Brussels, 12 May 2023

COST 018/23

DECISION

Subject: Memorandum of Understanding for the implementation of the COST Action "Wildlife Malaria Network" (WIMANET) CA22108

The COST Member Countries will find attached the Memorandum of Understanding for the COST Action Wildlife Malaria Network approved by the Committee of Senior Officials through written procedure on 12 May 2023.

MEMORANDUM OF UNDERSTANDING

For the implementation of a COST Action designated as

COST Action CA22108
WILDLIFE MALARIA NETWORK (WIMANET)

The COST Members through the present Memorandum of Understanding (MoU) wish to undertake joint activities of mutual interest and declare their common intention to participate in the COST Action, referred to above and described in the Technical Annex of this MoU.

The Action will be carried out in accordance with the set of COST Implementation Rules approved by the Committee of Senior Officials (CSO), or any document amending or replacing them.

The main aim and objective of the Action is to The main aim and objective of the Action is to unite efforts of all major research groups dealing with wildlife malaria parasites across Europe and beyond. This will be achieved through the specific objectives detailed in the Technical Annex.

The present MoU enters into force on the date of the approval of the COST Action by the CSO.

OVERVIEW

Summary
Vector-borne diseases, and emerging infectious diseases of wildlife, are major contributors to the global disease burden and of increasing concern globally. Haemosporidian parasites are ubiquitous in nature, hugely diverse, and associated with morbidity and mortality across taxa, including humans, livestock and wildlife. Many research groups globally focus on these parasites as model systems for addressing a broad range of ecological and evolutionary questions with economic and health implications. This Action will bring together individuals and research groups to focus on coordinating research objectives to which multiple groups can contribute existing datasets, meaning that questions can be addressed at a global, rather than a local or regional, scale. Ornithologists, mammologists and herpetologists have a long history of investigating haemosporidian parasites in natural populations; these studies have provided insights into host-parasite associations, parasite geographic distributions, host-switching and the context-dependence of host-parasite relationships, alongside pathogenic impacts and conservation implications of haemosporidian infections. Increasingly, research groups are investigating the vectors of these parasites, and utilising novel genetic techniques to understand parasite gene expression, among many other examples. Coordinating and sharing research efforts between groups offers huge potential for large-scale collaborative research initiatives. This Action will promote the development of a common research agenda by providing opportunities for training, collaboration and knowledge exchange, targeting diverse researchers across disciplines to foster an interdisciplinary approach, whilst also recruiting and supporting a diversity of new researchers. The Action will target stakeholders, policymakers and the general public to endorse knowledge transfer and maximise the reach of the network.

Areas of Expertise Relevant for the Action	**Keywords**
● Biological sciences: Parasitology ● Biological sciences: Biodiversity, comparative biology ● Biological sciences: Ecology ● Biological sciences: Biogeography ● Biological sciences: Conservation biology, ecology, genetics	● disease ecology ● parasites ● vector borne parasitic diseases

Specific Objectives
To achieve the main objective described in this MoU, the following specific objectives shall be accomplished:

Research Coordination
● RCO1: Identify key molecular markers and develop coordinated protocols for genomics and transcriptomics
● RCO2: Incorporate molecular markers and morphology to assign wildlife malaria lineages to species and identify phylogenetic relationships
● RCO3: Determine what factors influence vector transmission success in wildlife malaria
● RCO4: Quantify the impact of anthropogenic activities and wildlife malaria on host haematology
● RCO5: Identify the drivers of spatiotemporal variation in multi-host-parasite communities

Capacity Building
● CBO1: Encourage the development of a common research agenda by providing opportunities for training, collaboration and knowledge exchange
● CBO2. Target researchers across disciplines to foster an interdisciplinary approach
● CBO3. Increase the proportion of underrepresented groups involved in haemosporidian research

● CBO4. Target stakeholders, policymakers and the general public to endorse knowledge transfer

TECHNICAL ANNEX

1. S&T EXCELLENCE

1.1. SOUNDNESS OF THE CHALLENGE

1.1.1. DESCRIPTION OF THE STATE OF THE ART

Vector-borne diseases, such as malaria, are major contributors to the global disease burden and responsible for almost 20% of infectious disease worldwide. The current unprecedented degradation of the global environment and other global change factors are altering rates and patterns of vector-borne disease with dramatic consequences for humans, wildlife and livestock. Haemosporidians (Sporozoa: Haemosporida) are one of the best-known groups of parasitic protozoans with remarkable diversity. They include the agents of human malaria, but the systematic and ecological diversity of these parasites is much larger, with more than 400 described species belonging to 15 genera within the order Haemosporida (Apicomplexa), infecting reptiles, amphibians, birds, and mammals, and depending on at least seven families of dipteran vectors for transmission. Wildlife malaria and related haemosporidian parasites (hereafter: wildlife malaria) have historically been an important model for the study of human malaria. Advances in medical parasitology, including characterization of the parasite life cycle, development of chemotherapy and anti-malarial compounds, and cultivation *in vitro*, were initially developed using bird parasite models. Moreover, ornithologists, mammologists, and herpetologists have a long history of sampling malaria in wildlife populations. Wildlife parasites can and do transmit into livestock systems, and wildlife malaria parasites can cause mortality in non-adapted hosts. Due to their global distribution and high prevalence in many host populations, wildlife malaria parasites are an attractive model system for investigating parasite-host relationships, including diversity, distribution, host switching, species formation, and community interactions. Such studies have contributed to our understanding of the dynamics of coevolution between hosts and parasites, emergence of new diseases in populations, variation in virulence of pathogens in natural populations, interactions between pathogens in host individuals and populations, and the evolutionary diversification of pathogenic organisms. Haemosporidian parasite studies are being conducted by a growing number of research groups with different interests, using different methods. Realizing the full potential of this global research depends upon coordination of these efforts within a research network. The targets of the present proposal are in accordance with the United Nations Sustainable Development Goals and Targets of the 2030 Agenda for Sustainable Development, and the “Global Challenges” of the European Commission within Horizon Europe plan for EU research. Specifically, our aims frame within the progress made in fighting malaria and other communicable diseases and epidemics, including by addressing growing treatment resistance and the problem of unattended diseases affecting developing countries.

Wildlife malaria parasites are highly diverse, with the global number of species potentially exceeding that of their hosts. Molecular techniques have dramatically improved the detection and description of parasite diversity, as well as identifying evolutionary relationships within and between parasite genera. Prior to the development of molecular tools, haemosporidian parasite detection and description were based primarily on morphological characteristics of blood stages and, for a few species, information about host specificity from experimental infections. However, gathering sufficient material from different life stages for morphological analysis is not trivial and requires substantial expertise. Incorrect species identification misleads or obscures inferences about the evolutionary and ecological processes responsible for parasite transmission and virulence. Furthermore, haemosporidian parasites switch hosts frequently and harbour extensive cryptic genetic diversity within morphospecies. As well as resolving parasite species limits, genomic data provide insights into lineage-specific evolution among host clades. Transcriptome studies enable insights into the genes involved in host cell invasion. These studies can be used to understand host-specific gene expression, also providing additional information for phylogenetic studies. Together, rapidly-growing genomic datasets can be used to identify sets of molecular markers for questions related to parasite evolution, ecology, and host-parasite compatibility.

Insect vectors play a central role in the transmission dynamics of wildlife malaria. Transmission success requires that a competent vector feeds on an infected vertebrate, and subsequently inoculates sporozoites into a susceptible host individual. Different insect groups are involved in the transmission of wildlife malaria parasites, of which most research has focussed on the mosquito vectors of *Plasmodium*. Even among mosquitoes, the competency of most species for transmitting malaria parasites is currently unknown. Recently, studies designed to identify potential vectors have used molecular identification of parasite DNA in insects collected in the wild. This method (molecular xenomonitoring) provides valuable information on potential vectors involved in the transmission of malaria parasites, but further studies are needed to identify the role of different vectors in their transmission. To do that, we must identify, amongst other things: the contact rates between vertebrate hosts of haemosporidians and vectors; the capacity of parasites to develop in, and be transmitted by, different insect species; and the cost of parasite infections for vectors. These goals are especially relevant under a global change perspective that affects the distributions of, and interactions among the three players: vectors, vertebrate hosts, and pathogens. Haemosporidians impact both their insect and vertebrate hosts, producing morbidity (anaemia, weight loss, reduced reproductive success) and increasing mortality due to organ failure and acute parasitaemia. However, malaria is generally neglected in wildlife health and management despite its identification as a causative agent of mortality. How different species cope with pathogenic malaria is mostly unknown. Recent eco-immunological studies have addressed this issue in birds by analysing haematological responses to infections, for example by using leucocyte profiles to measure stress. Haematology is the discipline that studies blood characteristics and their variation in vertebrates, both under normal conditions and in response to different factors, using such quantitative and qualitative parameters as haematocrit, haemoglobin concentration, and leucocyte profiles. The challenge of implementing these methods is the lack of reference values for wildlife that can be used to judge host health status: available data for wildlife species were obtained mostly from captive animals in zoos. Thus, to provide efficient health, conservation, and management responses for wildlife, we need to generate reference values, particularly for host species that are under an International Union for Conservation of Nature (IUCN) threat category.

Until recently, host-parasite interactions have been examined mostly in a context of single host species with single parasite species. In experimental research, studying single infections is an essential first step to reach clear answers to achieve better understanding of pathogens. However, such experiments only partly reflect the true epidemiological situation in wildlife populations. In nature, hosts occur in multi-species communities, parasite species or lineages infect multiple hosts, and multiple lineages may infect the same host individual or species. Among wildlife malaria parasites, coinfections predominate. Since the advent of PCR-based screening and identification of haemosporidian parasites nearly 20 years ago, attention has begun to shift focus toward these multi-host, multi-parasite communities. These systems are being used to test models of parasite diversification and host switching, and to examine changes in host-parasite associations across different environmental contexts. Determining parasite host breadth and interaction strengths will inform us about how parasite assemblages are organized, identify spatiotemporal responses of host-parasite assemblages to environmental change, and help identify when and where host-switching events (that can lead to disease outbreaks in novel hosts) may occur.

1.1.2. DESCRIPTION OF THE CHALLENGE (MAIN AIM)

Our overarching objective is to unite efforts of all major research groups dealing with wildlife malaria parasites across Europe and beyond. A strength of the Action is its originality, innovation, and inclusiveness. It brings together the proficiency of several disciplines (molecular genetics, parasitology, evolutionary biology, epidemiology, vector biology, pathology, and others) to address five research coordination objectives (RCOs) and four capacity-building objectives (CBOs). These range from the microscopic and molecular examination of parasites to resolve species limits, to quantifying impacts of infection across host species, to examining the drivers of host-parasite community composition across multiple biogeographic contexts on a global scale. The Action will decipher multiple facets of wildlife malaria, many of which are unexplored. This work will serve as a model for other invasive multi-host vector-borne diseases that are currently affected by anthropogenic changes, or may be extending their ranges into and within Europe in relation to climate change and other environmental impacts.

RCO1: Identify key molecular markers and develop coordinated protocols for genomics and transcriptomics. Sequencing the genomes of wildlife malaria parasites can provide information on the evolution of these important pathogens. Obtaining genomic data from non-mammalian haemosporidian parasites has encountered numerous challenges even with high-throughput sequencing, due to 1) the nucleated red blood cells of birds and reptiles; 2) the small proportions of parasitized cells in natural infections; and 3) the small size of the parasite genome compared to that of the host. Although >40 genomes are available for malaria parasites of primates and rodents (*Plasmodium* species; PlasmoDB), high quality data are generally lacking

for other major haemosporidian genera from vertebrate groups including bats (*Nycteria, Polychromophilus*, *Hepatocystis*), birds (*Plasmodium*, *Haemoproteus*, *Leucocytozoon*), amphibians (*Haemogregarina*, *Lankesterella*) and reptiles (*Plasmodium*, *Haemocystidium*). A stable synergy among interdisciplinary fields will provide immense opportunities for synthesis, innovation, and training, resulting in **specific** protocols and the identification of molecular markers, and **measurable** outputs in terms of protocols and an increase in collaborative proposals. The network of proposers contains individuals with experience in these techniques, making this RCO **achievable**. To create widely applicable and relevant solutions, the Action needs to combine expertise in diverse fields such as population ecology and genetics, classical parasitology, and bioinformatics, making this RCO highly **relevant**. The rapid evolution of sequencing methods and publication of genomic data has opened avenues for the **timely** resolution of this pressing challenge.

RCO2: Incorporate molecular markers and morphology to assign wildlife malaria lineages to species and identify phylogenetic relationships. There are over 300 morphologically described species of haemosporidians, and recent studies have shown that both morphology (with more than 130 characters) and molecular methods are essential for the correct interpretation of phylogenetic relationships and identification of life-histories for different parasite species. Thus, the challenge for us is to merge molecular and morphological methods to resolve systematic, evolutionary, and ecological relationships of wildlife haemosporidians, resulting in **specific** guidelines for defining haemosporidian species. This RCO is **measurable**, because it will deliver consistent and accurate criteria for haemosporidian species assignment. The RCO is **achievable**, because members of the network of proposers have access to high quality morphological specimens and unpublished data, and **relevant** because it will allow coordination of ongoing analyses of parasite isolates from multiple distinct localities, host species and vectors. Molecular analyses of the parasite cytochrome b gene, which has become the barcoding region for haemosporidians, have uncovered a remarkable diversity of >4000 unique haplotypes (lineages), and some lineages have now had additional genes sequenced, revealing unexpected complexities. To what extent each lineage represents good species, variation within species, or multiple species existing beyond the level of lineages, is an unresolved problem. It is thus **timely** to resolve these questions in order for comparative analyses of vector-host-parasite associations, measures of host specificity, and identifying the origin of emerging infectious diseases.

RCO3: Determine what factors influence vector transmission success in wildlife malaria. The identification of vectors of wildlife malaria and factors affecting transmission has encountered numerous challenges. This RCO is **specific** because it will identify the impact of the different approaches currently used for the study of the transmission capacity of insect vectors, providing **measurable** outputs in the form of guidelines for further studies in this respect. The RCO is **achievable** because multiple groups of researchers are currently working independently on similar questions across species and systems. The RCO is **relevant** because it represents the first attempt to consolidate global knowledge of impacts of key components on wildlife malaria transmission success by multiple insect vectors. The combination of approaches in this RCO is **timely** because it positions this Action to produce a major breakthrough in understanding the transmission dynamics of vector-borne pathogens across different wildlife systems, opening new horizons for research on pathogen surveillance and vector-borne disease control.

RCO4: Quantify the impact of anthropogenic activities and wildlife malaria on host haematology. Anthropogenic activities are rapidly destroying and fragmenting natural landscapes, increasing the number of species that are under an IUCN endangered category. The main engine behind such drastic and rapid changes is urbanization, which can alter relationships between host ecology, health and disease. While cities amount to a small fraction (~3%) of land surfaces, their environmental impacts (e.g., pollution, overexploitation, invasive species, land use change) extend for hundreds of km beyond city borders, leading us into the new epoch known as the Anthropocene. This objective seeks to compile **specific** haematological reference values for malaria-infected and uninfected individuals, resulting in a **measurable** output in terms of a database across different biogeographic regions, using blood smears, a cheap and accessible method. This RCO is **achievable** given the experience, existing datasets and contacts of the network of proposers, and enables the coordination of multiple existing databases and datasets, making the RCO **relevant**. The fast rate of environmental change will certainly impact the health of organisms on the planet, making this RCO **timely**.

RCO5: Identify the drivers of spatiotemporal variation in multi-host-parasite communities. It is increasingly apparent that host-parasite associations vary temporally and across relatively small spatial scales, but the drivers of these associations - whether stochastic, vector-driven, or related to host ecology - remain insufficiently investigated. Combining multiple existing datasets will allow us to investigate the **specific** drivers of host-switching: for example, climate variation, habitat destruction, and the introduction of alien species; on a global scale. The RCO will result in **measurable** outputs of publications and collaborative research proposals, and is **achievable** because the network of proposers encompasses multiple research groups with relevant data and field sites. This RCO cannot be achieved without the coordination of multiple datasets involving high resolution fieldwork on a broad spatial scale, making this RCO **relevant**. Environmental change and biodiversity loss favour generalist vectors and parasites, increasing the risk of host-switching and emerging

diseases in wildlife and humans. The Action is **timely** because it draws upon much new information available in taxonomy, parasite and vector ecology, and evolutionary biology, which have yet to be integrated from a multi-host-parasite community perspective.

Our four capacity-building objectives (CBOs) will work to:

CBO1: Encourage the development of a common research agenda by providing opportunities for training, collaboration and knowledge exchange. The Action will encourage the development of a **specific** common research agenda around haemosporidian research, improving data workflows among target groups and supporting the development of research careers through **measurable** outputs of joint publications and grant submissions. The CBO is **achievable** given the high number of haemosporidian research groups in Europe, and **relevant** given the current high level of interest in this topic and the lack of a current means to coordinate research efforts and training activities. The high proportion of Young Researchers and Innovators (YRIs) in the network of proposers mean this CBO is **timely**, allowing the coordination of multiple new research groups around collaborative RCOs.

CBO2. Target researchers across disciplines to foster an interdisciplinary approach. The Action will connect **specific** separate disciplines relevant to the study of haemosporidians (e.g., taxonomy, genetics, genomics and proteomics, ecology, biochemistry, veterinary science, bioinformatics, zoology, high-tech industry, parasitology, entomology, big-data management) to facilitate the implementation and standardization of newly developed techniques by training and education. The Action will promote knowledge sharing and collaboration among a wide range of sectors, by including scientists and specialists from different disciplines as part of the Action, making the CBO **measurable** by increasing the participation of multidisciplinary researchers in STSMs, conferences, and workshops. The CBO is **achievable**, since a number of the network of proposers have existing contacts with scientists across a range of disciplines. Additionally, Interdisciplinary Roundtables will be scheduled at Wildlife Malaria conferences over the lifetime of the Action to build connections among researchers across disciplines and industry services, making this CBO **relevant**. The CBO is **timely** due to the recent rapid expansion in interest in both avian haemosporidians specifically, and emerging infectious diseases in wildlife more generally. **CBO3**. Increase the proportion of underrepresented groups involved in haemosporidian research. The Action will encourage a wide diversity of participants traditionally underrepresented in the field in the Action, **specifically** ensuring gender equality, wider diversity, and the participation of newly established research groups, YRIs, and teams from participating countries with less capacity. This Action already involves a wide diversity of participants: for example, 49% of the network of proposers, including the main proposer, are female; 67% are from ITCs, and 49% are YRIs: either students, or creating their research groups. This objective aims to **measurably** increase the proportions of these participants in the network. All underrepresented groups will be prioritised for travel support and actively encouraged to participate in the activities. This objective is **achievable** as many of the network of proposers have experience in equality, diversity and inclusion work, in the context of inclusion in research. The CBO is **relevant**, since it can dramatically increase the capacity for undertaking haemosporidian research across the globe, and **timely** given the high proportion of underrepresented groups already involved in the network of proposers who would benefit from the Action.

CBO4. Target stakeholders, policymakers and the general public to endorse knowledge transfer. The Action will promote knowledge transfer and exchange to multiple **specific** audiences (citizens, industry, policy and decision makers, key stakeholders) at international, European, national and local scales, **measurable** because it will lead to an increase in stakeholders and policymakers involved in the Action. The Action will collate baseline information on the biodiversity and impacts of blood parasites present in their hosts globally. This information will be exchanged with government entities and stakeholders, who can support and design species conservation strategies, prevent the risk of spreading infections, and preserve environments: this is **achievable** by coordinating multiple existing contacts of the network of proposers. The CBO is **relevant** because it will develop and coordinate a wide range of outreach activities suitable for diverse audiences (e.g. website, press releases and articles, podcasts, social media channels and posts, videos, brochures, participation in public events dedicated to bringing researchers closer to the public, including European Researchers' Nights, local Science Fairs, and Pint of Science). Results from RCOs will be disseminated to a more specialist audience (scientific community, industry, policymakers, and professional organizations) by way of different dissemination activities (journal papers, publications, patents, dissemination materials for distribution to stakeholders, scheduled talks). Dissemination and communication activities will be carried out as a continuous process with a schedule from the beginning of the Action, involving all the partners of the consortium. This is **timely** given the increased importance of disseminating knowledge around vector-borne and wildlife diseases, and because this information can influence the improvement of the quality of life of local communities, taking into account that the conservation of habitats through sustainable use policies contributes to the implementation of economic activities such as ecological tourism.

This ambitious proposal puts forward objectives by which wildlife malaria can provide significant scientific

insights and capacity-building through coordination of existing research groups. The relevance for this proposal is based on (1) the absence of similar large-scale efforts to coordinate the research of investigators of haemosporidian parasites in wildlife, (2) a rapid increase in the number of laboratories using genetic markers to survey haemosporidian diversity, (3) absence of graduate courses and training programs specifically addressing issues and methodologies related to haemosporidian parasite research, (4) the potential for wildlife malaria as a productive model system for understanding host- parasite-vector relationships in natural populations, including the problem of emerging infectious diseases and related conservation issues, and (5) the particular expertise and prior interactions of the individuals who constitute the proposers of WIMANET. These investigators have a broad range of experience with the biology and taxonomy of Haemosporida and, increasingly, the vectors that transmit them. Many have a history of collaboration through NSF-funded Research Coordination Networks (RCN), forming a combination of individuals with experience of large, multi-investigator research and training enterprises, YRIs and students. The network of proposers is led by Young Researchers establishing their own laboratories who will benefit from the collaborations the Action will provide, and students for whom the Action will provide training and contacts to support career development.

1.2. PROGRESS BEYOND THE STATE-OF-THE-ART

1.2.1. APPROACH TO THE CHALLENGE AND PROGRESS BEYOND THE STATE OF THE ART

For the last 20 years, the primary state-of-the-art molecular technique for wildlife haemosporidian research has been the use of a molecular barcode, a short fragment of a mitochondrial gene (cytochrome b). However, it remains unclear how variation in this barcode relates to separate parasite species. By developing shared methods for barcoding and species identification, the Action will enable synchronized analyses across laboratories worldwide, allowing for direct comparisons across studies. On a larger scale, avian haemosporidian genomic data have been isolated from host DNA with varying degrees of success by applying innovative techniques that allow separation of parasite cells from host blood cells. Using this latter method, the first genome of an avian haemosporidian was published (*Haemoproteus tartakovskyi*). This genome provided the basis for developing probe kits for targeted sequence capture, a technique that successfully sequenced >100 loci from a variety of *Haemoproteus* species from birds with parasitemias as low as 0.02%. In addition to the *H. tartakovskyi* genome and two avian *Plasmodium* genomes, transcriptome assemblies from five additional avian haemosporidians have been published, adding to those mammalian genomes already available. These new resources, along with promising results from RNA-sequencing and genomic sequence capture, provide opportunities for comparative studies and continued advances in wildlife malaria genomics. First, the available transcriptome and genome datasets can be synthesized to identify probe sets of appropriate molecular markers for different types of questions related to evolution, biogeography, and host compatibility across all haemosporidian parasites. The Action will develop a coordinated plan to gather additional genomic data from other haemosporidian species, targeting groups of particular interest that form phylogenetically unique clades. As these new datasets are assembled, they will be included in additional comparative studies and be used to revise or design new probe sets.

Studying the role of insect vectors in the transmission of malaria parasites requires a multidisciplinary approach. This may be one of the main reasons why the study of parasite-vector assemblages has been one step behind the study of the interactions between vertebrate hosts and parasites. The lack of information includes basic aspects of the interaction between insect vectors and haemosporidians, including estimation of the vectorial capacity of the different insect species for the transmission of most haemosporidians. In addition, it is necessary to incorporate basic information on the transmission process, including vector biting behaviour, the ability of the parasite to develop in the vector (e.g., incubation period), and vector survival after infection. This information is essential to obtain a general overview of the transmission risk of vector-borne pathogens, and much of this will soon be available through the VectorBiTE RCN VecTrait database. Most studies conducted under natural conditions to identify potential insect vectors of these parasites are based on molecular xenomonitoring (the identification of pathogens in the insect vectors rather than in hosts), but confirming vector competence relies on more specialised techniques. Recently, different authors have conducted experimental infections to reveal the competence of insect species for the transmission of different parasite species or genetic lineages. However, the different approaches used (i.e., insect colonies, parasite strains maintained in lab passages, different parasite intensities of infection, feeding sources for vectors) strongly affect the conclusions obtained. The Action will review current data on the main factors affecting malaria transmission risk, identifying future research lines and developing standardized protocols for the study of vector competence for haemosporidians.

To determine the influence of parasites on their hosts, the development of haematological reference values represents a relatively easy and inexpensive process that can be implemented globally and under challenging environmental conditions, now even more with the availability of compact and inexpensive microscopes. Even physiological measurements such as haemoglobin concentration, which usually require expensive laboratory

equipment, can now be obtained under field conditions using portable point of care instruments such as hemoglobinometers. The use of such portable equipment allows data acquisition from remote areas, helping to build a solid reference-values database that can be used across the world to determine health status and guide management decisions, particularly for endangered species. Collaborations with veterinary pathology units are necessary in order to get access to organ samples of dead wildlife. For instance, outbreaks of viral infections in wild birds (e.g., Usutu virus in Europe, West Nile virus in the Americas, avian influenza globally) have fuelled dead bird monitoring programs, including investigation of tissue samples. These samples can also be useful for haemosporidian research due to the recent development of methods to identify haemosporidian parasite tissue stages.

At a community level, the Action provides an ideal opportunity to combine data from multiple, spatially independent study systems, using both single- and multiple-species models to address fundamental questions about how these multi-host multi-parasite communities are shaped. These datasets (on a global scale) can be combined and analysed in a geographically- and phylogenetically- controlled way to address broad questions, such as determining what factors influence host-parasite associations, or whether some characteristics consistently predict host switching. For the first time, the Action will provide opportunities to share comparable datasets that are currently dispersed across different research groups, but include the same hosts, vectors, and parasites sampled during the same seasons. Analysis of such datasets is essential to determine patterns of complex host-parasite interactions and pathogen transmission, but remains unexplored broadly because of insufficiently developed collaboration between groups. It is timely to unite efforts of researchers in wildlife malaria because they use similar methods of sampling and parasite analysis, and we now have the opportunity to merge and analyse datasets available within different groups. The Action will bring a new approach in the field of wildlife parasitology, providing opportunities for better understanding mechanisms of transmission of zoonotic infections in multi-host parasite communities, with implications for animal and human health.

Coordinating existing datasets and research groups around common objectives will allow significant advances in our understanding of wildlife malaria, including patterns of transmission, and the environmental drivers of community assembly in Europe. Following the collation and coordination of existing outputs during this proposal, the Action will enable the research community to develop grant proposals targeting national and EU funding streams during and beyond WIMANET. These results will provide information and recommendations for policy about most vulnerable groups of wild species and how to minimize the transmission risk of wildlife malaria in Europe under global climate change.

1.2.2. OBJECTIVES

1.2.2.1. Research Coordination Objectives

RCO1 will 1) identify existing sets of appropriate molecular markers for different types of questions related to evolution, biogeography, and host compatibility across wildlife *haemosporidia*; 2) develop protocols to coordinate ongoing sequencing efforts to expand genomic resources across geographic regions and wildlife host diversity; 3) identify funding sources and develop collaborative proposals to collect novel genomic and transcriptomic data from target host species, parasite lineages, and regions. RCO2 will 1) compile all published morphological species of wildlife malaria parasite that have attached to them a mtDNA cytb barcode, to determine phylogenetically informative characters for taxonomic identification of vertebrate haemosporidians; 2) identify priority molecular lineages for morphological analysis; 3) coordinate existing data into open-source databases for easy access in comparative and meta-analyses; 4) facilitate collaborations across laboratories to develop a global standard for species identification of wildlife malarias.

RCO3 will 1) synthesize existing information on the vector species of wildlife malaria and summarize the conditions used to identify their vector competence; 2) develop plans to coordinate standard strategies to conduct studies on the vector capacity of haemosporidians across geographic regions and wildlife species; 3) identify funding sources and develop collaborative proposals to perform experimental studies testing vector competence across insect species, parasite lineages, and hosts.

RCO4 will1) coordinate existing datasets to compile a database of reference haematological values for different wildlife that can be used to determine host health in reference to parasitism; 2) determine spatiotemporal host physiological responses to environmental challenges; 3) identify funding to develop collaborative proposals that address wildlife health in relation to parasitism and climate change.

RCO5 will 1) synthesis existing datasets to determine the spatiotemporal similarities and differences of multi-host multi-parasite communities across geographical scales to identify ecological drivers promoting or repressing parasite host switches; 2) examine coevolutionary dynamics, particularly of generalist and/or invasive parasite species; 3) develop collaborative proposals to allow detailed analysis of datasets.

1.2.2.2. Capacity-building Objectives

CBO1 will 1) organise and deliver four week-long Training schools for 25 participants, spanning RCOs, for students, YRIs, and those new to the field; 2) organise two dedicated Wildlife Malaria conferences during the Action; 3) coordinate a symposium during at least one international conference to publicise the Action and research findings of its members; 4) organise annual workshops, at which RCO WGs meet to work on collaborative papers and proposals; 5) arrange and support STSMs of 1-4 weeks. CBO2 will 1) advertise the Action across a wide range of disciplines to diversify our existing network of proposers and maximise our interdisciplinary reach; 2) organise an interdisciplinary round table event at each Wildlife Malaria conference; 3) arrange virtual meetings on remote meeting platforms and publicise these events to the general public, to maximise our reach across regions and audiences of different careers, ages, and backgrounds.

CBO3 will 1) target students (including undergraduates) and scientists from groups traditionally under-represented in the research field for funded travel support; 2) ensure gender balance in all activities; 3) prioritise YRI WIMANET members for conference attendance and STSMs.

CBO4 will 1) design, publicise and maintain a dedicated WIMANET website to advertise events and contain compiled datasets, protocols and open access resources; 2) develop and carry out a wide range of outreach activities; 3) disseminate results from RCOs.

2. NETWORKING EXCELLENCE

2.1. ADDED VALUE OF NETWORKING IN S&T EXCELLENCE

2.1.1. ADDED VALUE IN RELATION TO EXISTING EFFORTS AT EUROPEAN AND/OR INTERNATIONAL LEVEL

WIMANET has important European added value because the Action will: (1) link and make optimal use of highly specialized expertise in various disciplines that complement each other, possible to achieve geographically only at the international level of this consortium; (2) create new networks, thus building multidisciplinary teams with strength in biodiversity sciences; (3) take advantage of existing datasets, databases, and infrastructures already available in different countries; (4) deliver scientific results to fill knowledge gaps at the European level, which are needed for biodiversity policy decisions; (5) integrate national infrastructure, knowledge and experience about malaria species; (6) promise improved understanding of Emerging Infectious vector-borne diseases in Europe beyond wildlife malaria parasites. WIMANET builds on two previous RCNs relevant to this topic: Malaria RCN, and VectorBiTE.

WIMANET will coordinate the study of malaria parasites in laboratories throughout the world, particularly among YRIs in Inclusiveness Target Countries (ITCs), paying special attention to gender balance and diversity. Key to the Action is the coordination of sharing, integration, and use of existing datasets from a range of research institutions, to coordinate existing resources around the five RCOs and understand the evolution, distribution, ecology, and disease consequences of the haemosporidian parasites of terrestrial vertebrates. WIMANET CBOs will provide mechanisms for knowledge sharing among research groups by facilitating mobility and networking, and developing collaborative research programs based on the integration of data produced by independent groups.

WIMANET will engage in collaborative activities with other operational networks and existing EU- projects focused on vector-borne diseases, public health and wildlife conservation. We have contacts with several management and Action chairs of networks (e.g. *Malaria Network*, *MalariaGEN*, and *European Network for Neglected Vectors and Vector-Borne Infections*) and running Actions (CA17108- Aedes Invasive Mosquitoes, CA16224-European Raptor Biomonitoring Facility, CA18107-Climate change and bats: from science to conservation, CA16227-Investigation and Mathematical Analysis of Avant-garde Disease Control via Mosquito Nano-Tech-Repellents), who have expressed their willingness to participate in workshops, meetings and interdisciplinary round tables at WIMANET conferences during the Action. WIMANET will bring together experts from disciplines such as Genetics, Epidemiology, Entomology, Biostatistics, Chemistry and Nanotechnology, thus providing an excellent scenario for interdisciplinary research collaborations and knowledge exchanges (RCO1–RCO5).

2.2. ADDED VALUE OF NETWORKING IN IMPACT

2.2.1. SECURING THE CRITICAL MASS, EXPERTISE AND GEOGRAPHICAL BALANCE WITHIN THE COST MEMBERS AND BEYOND

WIMANET contains both advanced and early-career investigators from European countries and partner countries in the Americas, spanning both temperate and tropical regions. Haemosporidians are globally

distributed and in some cases, both parasites and their vectors have been transported between continents via human-mediated transfer, leading to drastic consequences for wildlife. It is therefore imperative to consider variation on a global scale to better understand the biology, evolution, and potential impacts of parasites and vectors on wildlife hosts. Including IPCs and NNCs in WIMANET enables the *global* coordination of research efforts across our research objectives. New genomic techniques are being developed in parallel around the world (RCO1), and the taxonomic identification of parasites (RCO2) and species assignment require geographically disparate data to encompass global variation in morphologically and molecularly similar lineages to confirm species identity (RCO2). The inclusion of community-level datasets from study systems across the globe, across different biogeographic regions, and host clades, is vital to identify general patterns driving parasite transmission via vectors in both native and introduced ranges (RCO3), identify impacts on host health (RCO4), and identify drivers of host-vector-parasite associations across biogeographic regions (RCO5).

The network of proposers consists of 65 researchers from 19 countries, within which **66.7% of COST Country Institutions are ITCs, with 49% females, and 49% YRIs**. This team of researchers brings together expertise in parasitology, entomology, ornithology, ecology, evolutionary biology, genomics and veterinary medicine, including identification of haemosporidians using morphological and molecular methods, fieldwork resulting in material for molecular analysis, and laboratory techniques, including the use of emerging technologies for genomic and transcriptomic data collection and bioinformatic processing (RCO1, RCO2, RCO4). The network also contains multiple proposers with expertise in big data storage and management; from both a database perspective and a genomics perspective. The network of proposers contains groups with either established field systems (usually one or a handful of host species) across the globe, as well as those with relatively recently established host-vector-parasite community systems (with a European focus; RCO3, RCO5). The Action provides a unique opportunity, first, to examine how host-parasite relationships differ between different populations of the same species, and between different communities, and, second, to test hypotheses that may explain these differences both in a geographic and in a community context by combining existing datasets (RCO5). Altogether members of WIMANET provide a general overview of the different methods required to develop studies on the importance of insect vectors for parasite transmission (RCO3). These include basic approaches to insect collection, identification and maintenance, experimental infections of potential vectors, and morphological and molecular identifications of parasites in the vectors (RCO3). Members also have ample experience working in remote areas and using molecular and microscopic methods (RCO2, RCO4). Many of the research groups have addressed how human impacts are altering wildlife malaria dynamics across the world from temperate to tropical areas (RCO4), and the Action anticipate recruiting additional researchers with complementary skillsets to the Action.

Research into malaria parasites and related haemosporidians in wildlife is experiencing an explosion of interest. This is indicated by a several-fold increase in both citations and publications in this area over the past 15 years. This research is particularly active in Europe and the USA, but has yet to be coordinated in a single network. WIMANET will attract attention from a range of wildlife malariologists, including YRIs and students from laboratories around the world who may not have been initially targeted as proposers for the Action. Additional expertise will be recruited to the network through open calls and wide advertisement (through routes such as the “evoldir” and “ecolog” distribution lists, existing social media channels, and through different parasitological and other international associations to which the Action members belong) as well as targeted e-mails to departments with existing expertise in areas such as (but not limited to) disease ecology, database and big data management, and genomic analysis). Members of the Action will also advertise the network at national and international (in person and virtual) conferences. Wildlife malaria conferences have occurred on an approximately biennial basis since 2011, and were previously coordinated through the NSF sponsored Malaria RCN or by a handful of research groups. WIMANET offers the opportunity to continue these popular conferences, alongside Training Schools and STSMs, to provide opportunities for established and younger researchers to share findings, knowledge and expertise, and for YRIs, establishing their own research groups in the field, and students to undertake training in specific methods relevant to wildlife malaria studies.

2.2.2. INVOLVEMENT OF STAKEHOLDERS

The Action will result in new knowledge and recommendations essential to end users and stakeholders to improve responses to socio-economic needs of the community, under a scenario of global change which has a direct impact on biodiversity loss. Beneficiaries of our scientific products include non- governmental organizations (NGOs) involved in nature conservation across Europe and beyond, municipal authorities, business, government departments and agencies, and industry. With many of them, members of the network of proposers have already established fruitful interactions. Government, environmental and health authorities, zoo veterinarians, and administrations of European ornithological observatories will use the outcomes of the Action to take scientifically based decisions on prevention, mitigation, and control of wildlife vector-borne diseases. Some examples are in the areas of population management, changes of landscapes, man-made changes in ecosystems, species conservation, monitoring of vectors, control of invasive species, climate

change impacts on parasite community composition and virulence, threats to biodiversity and smuggling of birds. Our data will be available for immediate use on the public website, free to download and regularly updated. The dissemination efforts are in line with Council Directive 90/313/EEC of 7 June 1990 on the freedom of access to information on the environment. The Action plans activities to engage public and students at all levels, interest groups, scientists and the industry. Outputs generated by the Action will be disseminated to stakeholders through targeted national and international workshops; for example, findings relevant to birds will be publicised through workshops targeting national BirdLife partners, who work with on-the- ground conservation organisations and policy-makers. Technical reports related to conservation and health of wildlife can be prepared as needed, depending on the actual challenges faced across different geographic locations (e.g., a technical report on land use change effects on bird health focused on species of conservation concern [endemic, migratory] and how to reduce development impacts). Dedicated meetings are planned to directly involve stakeholders. To engage with industry, policy makers, government agencies, national authorities, and any other stakeholders relevant to the topic, objectives and deliverables of WIMANET (such as those identified above), they will be invited to WIMANET workshops and conferences. At each conference, one full day will be dedicated to interdisciplinary roundtables and dissemination activity for stakeholders. During annual workshops (CBO1 and CBO2), there will be one dedicated session for the participation of relevant stakeholders. The Action will also create and upload on the WIMANET webpage brochures, flyers, videos and interesting case studies that will be freely accessible, in both the native languages of each WIMANET country participant and English. This multimedia material will achieve a broader dissemination, available also to students and the general public (CBO2 and CBO4). WIMANET will also participate in COST Connect events scheduled during the Action execution. These events will provide an interactive format for WIMANET researchers, policy makers and R&I stakeholders to implement networks targeting vector- borne diseases, public health, climate change impacts on disease, and wildlife conservation.

This research addresses the Directive 2009/147/EC of the European Parliament and of the Council of 30 November 2009 on the Conservation of all species of naturally occurring wild birds in the European territory, providing scientific basis for their protection, management and use of the populations. The Directive states that measurements taken in conservation of the species of wild birds must apply to the various factors that may affect bird numbers. A large number of species of wild birds naturally occurring in Europe are declining, creating a serious threat to the natural environment and the ecological balance. Emerging infectious diseases represent a major threat to the conservation of global biodiversity, but there are insufficient studies in wildlife. Wildlife malaria is caused by numerous parasite species with high potential to expand their geographical and host range as a result of environmental change. Consequences for the health of wildlife populations and potential threats to biodiversity are poorly understood, with the exception of the Hawaiian avifauna where it is well documented that invasive malaria parasites resulted in extinction and range contraction of many endemic bird species. It remains unclear whether similar processes are occurring in European wildlife populations.

The scientific knowledge generated through the coordination of research activities as outlined in the proposal will answer urgent questions about Emerging Infectious Diseases and wildlife populations that may have high impact on conservation and the impacts of global change. Such questions are addressed under the Council Directive 92/43/EEC of 21 May 1992 on the conservation of natural habitats and of wild fauna and flora, the Council of Europe; Convention on the Conservation of European Wildlife and Natural Habitats (Bern Convention, 1979, including recommendations in 2008), the UNESCO: Programme MAB (Programme on Man and the Biosphere), 1970, actualized in 2008, the UNESCO: World Heritage Convention, 1972, last Committee decisions, July 2008, the UN: Convention on Biological Diversity and the associated 2010 Biodiversity Target , the IUCN: International Convention for Wetlands Especially as Habitat for Waterfowl (Ramsar Convention, 1971) and especially its current Ramsar Strategic Plan (2009-2015), DIVERSITAS: and international programme for biodiversity science (1996), and its core projects BioDISCOVERY and BioGENESIS (2006). The Action is relevant to the 2019 UN Intergovernmental Panel on Biodiversity and Ecosystem Services (IPBES) report which, as well as highlighting that a million wildlife species may be threatened with extinction, also identifies the entire lack of parasite assemblage data available and thus the potential for unrecorded parasite species to add to the global extinction debt.

3. IMPACT

3.1. IMPACT TO SCIENCE, SOCIETY AND COMPETITIVENESS, AND POTENTIAL FOR INNOVATION/BREAK-THROUGHS

3.1.1. SCIENTIFIC, TECHNOLOGICAL, AND/OR SOCIOECONOMIC IMPACTS (INCLUDING POTENTIAL INNOVATIONS AND/OR BREAKTHROUGHS)

WIMANET was initiated because there was a clear need identified by the community following the conclusion of previous relevant RCNs, and because the field is rapidly expanding, particularly in Europe. The ability to

coordinate research groups and stimulate collaborations on a global scale will lead to scientific advances that add up to more than just a sum of their individual parts.

The *scientific* impacts envisaged to result from WIMANET are broad, ranging from the small but fundamental scale of how parasite species are detected, identified, and defined (RCO1, RCO2), and what can be learned about parasite biology from combining morphological data with molecular markers (RCO2), to what drives parasite transmission (RCO3), impacts on host health (RCO4), and community composition and disease emergence on a global scale (RCO5). WIMANET will actively promote Haemosporida as a model system for integrated studies of host-parasite coevolution, immune function, and life-history evolution, and the development of a global database for haemosporidian parasites to include non-avian haemosporidians, promoting wider research and collaboration. The Action will facilitate the investigation of questions that require large-scale data, where enabling data-sharing and collaborations will lead to far greater advances than those possible from individual studies. These datasets include host and geographic distribution, mechanisms of speciation, host-switching and potential for emerging disease, and conservation implications of malaria parasites (RCO3, RCO5). WIMANET represents the first attempt to coordinate studies of key components of the transmission success of vector-borne pathogens by different groups of insect vectors; the combination of approaches used here makes the Action a major breakthrough for understanding pathogen transmission dynamics, opening new horizons for research on pathogen surveillance and vector-borne disease control (RCO3). Coordination of existing data will provide the first worldwide database of haematology and cytology reference values for wild non-captive wildlife (RCO4). This database will include different environmental conditions and will be regularly updated to monitor temporal patterns, allowing the spatiotemporal analysis of responses to different environmental changes/challenges across the world (e.g., habitat alterations, species introductions, global warming), which can lead to the identification of general patterns that can be later used to take health and management decisions, particularly in species of conservation concern (RCO4 and RCO5). The haemosporidian parasite species and lineages leading to severe disease and mortality in resident wildlife populations will be identified on a global scale (RCO2). In the longer term, this knowledge can be used in wildlife management, and in the development of disease prevention measures, and has the potential to be extrapolated to other multi-host vector- borne disease systems. Training activities (CBO1) developed and implemented during the Action will provide the tools and build capacity for further research on this topic in the long-term. This will undoubtedly contribute to the wider field of disease ecology and evolution. By consolidating current knowledge and encouraging an interdisciplinary approach (CBO2), WIMANET will identify future research requirements and submit collaborative grant applications to national and EU funding bodies.

Technological advances will include improved and consistent methods of disease diagnostics and species/lineage identification (RCO1, RCO2), coordinating and comparing new PCR and other molecular diagnostic protocols (e.g., new molecular markers, in situ hybridisation, immunodiagnostics, etc.; RCO1), contributing to technology transfer of molecular techniques (CBO1), and improving current portable technologies that are currently calibrated for humans and a limited range of wildlife (RCO4). The development of more precise instruments is likely in the long term once the Action develops enough information in such a way that it is possible to interact with engineers. Interoperability scientific standards, such as standard operation procedures for laboratory protocols developed during the Action will be made openly available (e.g., taxonomy and morphological parasite identification; CBO4) and incorporated into Training Schools (CBO1). For dissemination in the scientific community, results will be published in open access peer-reviewed journals (both specialist and multidisciplinary; CBO4).

Socioeconomic Our proposal addresses issues of concern to different sectors of society and will benefit society as a whole by informing the general public, interest groups, scientists, politicians and decision-makers about the consequences of climate change on the dynamics of vector-borne diseases and impacts on biodiversity (CBO4). Knowledge acquired during training schools and STSMs (CBO1) will help YRIs gain professional experience of both specific techniques and transferrable skills that can be broadly applied, to improve employability and transition into regular employment, paying special attention to researchers from underrepresented groups and ensuring gender balance (CBO3). Traineeships will also benefit employers by giving them access to an interdisciplinary group of talented young researchers (CBO2). The Action is embedded in the important One Health - One Medicine concept, linking human, animal, and environmental health. Wildlife parasites can be transmitted into domestic animals and livestock systems, and wildlife malaria parasites can cause mortality in non- adapted hosts. WIMANET will provide a better understanding of wildlife health under normal and modified conditions, so all information generated is for the well-being of wild animals, and informed decisions can be made on how best to proceed for their welfare and management. Local societies know their wildlife and the benefits of having and understanding such animals, as well knowing how they can help to protect them. Having a diverse wildlife community can help to dilute infection risks by harmful pathogens for both humans and animals. All of the above translates into economic benefits because baseline information allows a more rapid response in case of a health emergency. The lack of reference information can delay actions and elevate medical and veterinary costs. This problem will be addressed and society will be informed

about endemic infections, which formerly were neglected in wildlife health and management. Data obtained on the impact of these parasites will enable the research community to continue with insightful analyses to address several urgent questions, particularly: assessing impacts of invasive malaria on the health and fitness of susceptible wildlife populations across Europe; defining the epidemiological role of various species (reservoirs, spill-over, target species) on the risk of successful establishment and spread of invasive malaria; determining ecosystems in which invasive malaria parasites and related parasites may thrive; predicting the impact of human activity on infection; and predicting the effects of environmental changes, particularly climate change on distribution of malaria and other haemosporidians in Europe. The RCO results will provide information and recommendations relevant to policy regarding the most vulnerable wildlife groups and how to minimize transmission risk of invasive wildlife malaria in Europe.

3.2. MEASURES TO MAXIMISE IMPACT

3.2.1. KNOWLEDGE CREATION, TRANSFER OF KNOWLEDGE AND CAREER DEVELOPMENT

Knowledge creation: The compilation of existing resources and datasets across RCOs will, in itself, create valuable tools for wildlife malaria researchers. For most of our RCOs, we have only just reached a point at which data from sufficient study systems are available to allow us to address these kinds of broad questions on a global scale. Coordination of molecular and morphological datasets will provide novel insights into the fundamental question of species definition (RCO2). New knowledge will be generated on how these organisms have coevolved with hosts and the Action will gain a greater understanding of their host specificity (RCO1), creating an opportunity to study the morphological evolution of the entire Haemosporida order for the first time (RCO2). Study of vector competence for the transmission of pathogens affecting wildlife is an emerging research area, where basic information is currently lacking. The development and dissemination of the different tools essential for the study of the transmission risk of vector-borne parasites (CBO1; CBO3; CBO4) will allow the study of new vector- parasite assemblages currently unknown (RCO3), along with the coordination of existing data and the identification and targeting of knowledge gaps for future research proposals. The study of multi-host multi-parasite systems is a relatively young field, and we are just reaching the stage where data from sufficient study systems are available to allow us to address questions examining drivers of the similarities and differences across biogeographical contexts (RCO5). To our knowledge, WIMANET will allow the first attempt to gather health reference information for wildlife across the world, in such a way that will create an invaluable tool to determine host health under different non-captive scenarios (RCO4).

Transfer of knowledge: For all RCOs, the Action will utilise CBOs to disseminate newly attained knowledge through publication of results, and discussions at workshops, and conferences. Databases compiled by WIMANET will be made publicly available alongside publication of the analyses proposed in RCOs. The Action will allow its members to work across different biogeographic regions in meetings, workshops, training sessions, and the writing of both high impact research papers and future grant applications via data sharing. Moreover, results from technical publications can be used to prepare information for the general public in the form of talks, workshops, popular science papers, and press coverage. Working together to achieve the RCOs, both in person at workshops and meetings, and remotely over e-mail, Skype, and through document sharing tools such as Google Drive and OneDrive, will allow the transfer of skills and knowledge within Working Groups (WGs). Knowledge generated through the compilation of databases will be publicised to relevant professionals and may have practical uses: e.g., the generated knowledge can easily be used to determine wild animal health status by different professionals (e.g., veterinarians, biologists) and by anyone after basic training on interpretating the available data. Local people can easily acquire this information after proper training during a workshop initially aimed at zoo veterinarians. Thus, local capacity can be easily developed, which will aid in the acquisition of long-term data. Furthermore, the generation of non-specialist audience materials such as articles, talks, leaflets, and open sessions with games and workshops, will help encourage local people to embrace and protect their biodiversity, benefiting both conservation and health.

Career development: 32 (49%) of the proposed WG members and leaders are YRIs, from a range of disciplines. YRIs will be actively encouraged to take up positions on the Management Committee of the Action, and will benefit from collaborations and information transfer with more established members of the WGs, and from their experience in writing high-impact scientific publications and grant proposals. The landscape of biological research is changing quickly and training researchers in specific techniques such as vector capture and analysis, genomic techniques, meta-analyses, and working with “big data” (CBO1, CBO2) has particular importance in the context of environmental change, biodiversity conservation and infectious disease dynamics. Many practical techniques used in the study of wildlife malarias are inexpensive and easy to implement under different conditions, opening the door for aspiring researchers of different socioeconomic backgrounds (CBO3). Membership of WIMANET will be open and publicised via social media channels (CBO4), training schools and

STSMs (CBO1), which will help guide common research objectives, and will be targeted toward underrepresented minorities and COST ITCs (CBO3). One 5-day training course per year will provide for up to 25 participants per course with training relevant to each RO (one day per RO), alongside the opportunity to share their work and discuss potential collaborations with each other and the course leads. 10 STSMs per year will provide opportunities for visits or exchanges with laboratories willing and able to provide training in specific skills, and to progress projects with identified research outputs where an in-person visit is necessary. WIMANET will bring together researchers at the forefront of a rapidly advancing field; WG activities will contribute to the development of the scientific workforce with skills applicable to e.g., ecology, evolution, parasitology, biomedicine, and big data (CBO2). Access to website resources will require (free) website registration, allowing the circulation of relevant information (e.g., workshops, external training courses, etc.) to all interested parties (CBO4).

3.2.2. PLAN FOR DISSEMINATION AND/OR EXPLOITATION AND DIALOGUE WITH THE GENERAL PUBLIC OR POLICY

Dissemination activities will be developed throughout the 4-years of the Action, aimed at raising the impact of the Action as well as reinforcing the widespread nature of the Action results. Protocols (both wet lab, e.g., library preparation, genomic/transcriptome sequencing; and dry lab, e.g. bioinformatic pipelines) and marker sets will be shared on open-access sites, coordinated via the WIMANET website. Unpublished genetic sequences identified within RCOs will be submitted to public databases including GenBank, the NIH genetic sequence database, and MalAvi. Each RCO will result in multiple collaborative high impact papers, published in highly ranked peer-reviewed journals (both specialist and interdisciplinary) with associated datasets and results uploaded to open-access repositories (e.g., FigShare, Dryad). Researchers involved in this Action are highly productive and enthusiastic, which together with the innovative nature of this proposal support the fact that, multiple resulting papers will be published in high-profile peer-reviewed journals such as Nature, PNAS and Molecular Ecology. Links to all publications will be shared on the WIMANET website and publicised through social media.

To enhance dissemination to a wider audience and open up the potential for new networking activities, outcomes presented during WIMANET workshops and conferences will be published as special issues, conference proceedings or book of abstracts, made available open access through publishers' websites (through e.g. Malaria Journal, International Journal for Parasitology, Philosophical Transactions of the Royal Society B) in order to achieve a closer approach to the target audiences of the Action. All publications and activities will be disseminated or advertised through social media platforms for which a dedicated WIMANET account will be created (e.g., Twitter, Facebook, Instagram), and an effective communication will involve the design of tailored messages in different languages, appropriated for each target audience (e.g., information about current research, raising awareness), as well as attractive content for mass-media, as multipliers of the impact. Publications will be advertised through departmental websites of authors, press releases, and science news outlets (radio, newspapers, etc.); lay summaries of papers will be published as blogs on the WIMANET website. The Action will use the public interest in health-related stories to gain media coverage across countries and in multiple languages. WIMANET members based in universities will incorporate findings into research-led lectures on wildlife malaria, enthusing the next generation of wildlife malaria researchers. Results will be presented at scientific society meetings (including WIMANET-organised conferences and symposia) to which stakeholders will be invited, as well as to international collaborators and networks, to guarantee dissemination at national and international levels, and in presentations to the general public (e.g., museum open houses, local wildlife society meetings, zoo lectures). The Action will specifically offer talks to NGOs and other stakeholders. Wildlife disease is a topic of great relevance to the general public, particularly this group of parasites that includes organisms of biomedical importance (*Plasmodium* species causing malaria in humans). Presentations and materials for stakeholders, for the public, and for distribution at scientific conferences, will emphasize the benefits of understanding genomic variation of related parasites for wildlife conservation and human health, as well as the training opportunities that are provided to the next generation of scientists and professionals using new technologies. Some of the institutions of the proposer network have press offices that will aid in the work of disseminating the generated information to the general public. The Action will use different outreach activities, such as European Researchers' Night, or Pint of Science, to publicise the findings of the Action, as well as to educate the public on wildlife malaria more generally. The Action will target relevant stakeholders in the latter two workshops and the second conference, and will arrange interactive meetings with interested stakeholders and policymakers to gauge their interest and requirements for inclusion and outputs of subsequent research.

Measurable outputs obtained during WIMANET will support both European and national public health and wildlife conservation policymakers with independent scientific evidence of vector-host- parasite associations, identifying the origin of emerging infectious diseases (RCO2), determining spatiotemporal dynamics in the transmission of vector-borne pathogens across wildlife systems (RCO3, RCO5), and quantifying the impact of

anthropogenic activities on vector-borne diseases (RCO4). These outcomes can be exploited by the European Environmental Bureau (EEB), the European Environment Agency (EEA) and NGOs (e.g., European Wildlife, SEO/Birdlife international, Royal Society for the Protection of Birds) to conserve biological diversity and reduce anthropogenic impacts on wildlife (CBO4). After completion of the Action, WIMANET will continue through consortium projects in other programmes such as ERANET calls, LIFE 2021-2027 and Horizon Europe 2021-2027 (Cluster 1: Health; Cluster 6: Food, Bioeconomy, Natural Resources Agriculture & Environment.).

4. IMPLEMENTATION

4.1. COHERENCE AND EFFECTIVENESS OF THE WORK PLAN

4.1.1. DESCRIPTION OF WORKING GROUPS, TASKS AND ACTIVITIES

WIMANET will be implemented through the formation of six Working Groups (WGs), tightly linked to RCOs and CBOs. All RCOs will undertake dissemination activities and contribute to CBOs. Each RCO WG will have at least one member responsible for CBO liaison for that RCO, who will sit on both RCO and CBO WGs. Each WG will have a nominated leader and deputy leader, responsible for overseeing the smooth running of the tasks, reviewing progress against milestones, and communicating progress with the Management Committee (MC). The MC will comprise the leader and deputy leader of each WG, with >50% YRIs. The expectation is that WG members will be able to contribute to multiple WGs. Specific tasks and activities for each RCO are below:

RCO1 (WG1): 1) synthesize existing data to identify sets of markers to consolidate protocols and sequence capture methods, and prioritise target species and geographic regions for further genomic and transcriptome sequencing; 2) submit review manuscript from 1; 3) identify potential funding sources;

4) make first set of protocols available; 5) submit collaborative grant proposals to sequence additional genomes/transcriptomes.

RCO2 (WG2): 1) collate available information and identify a candidate set of morphological traits alongside additional molecular markers to be used for species identification of haemosporidians; 2) overlay molecular phylogeny with available morphological data to identify phylogenetically informative traits; 3) identify priority clades for morphological species descriptions and submit collaborative grant proposals for funding; 4) pinpoint key identification criteria and define a global standard for species identification; 5) describe the detailed workflow for species identification, from easy cases to complicated situations that will require a large combination of informative characters (genes and morphology).

RCO3 (WG3): 1) update existing data in the public MalAvi database on the identification of the potential insect vectors of wildlife haemosporidians; 2) identify the different approaches used to determine the parasite vectors and develop standardized protocols to feed into subsequent Training Schools; 3) analyse and publish compiled datasets and information from 1 and 2; 4) make protocols available to the scientific community; 5) identify funding sources and develop collaborative grant proposals to perform further studies on the transmission capacity of haemosporidians by native and invasive vector species.

RCO4 (WG4): 1) identify blood smear collections across the globe available to determine haematological values from wildlife. 2) determine relevant haematological variables to be regularly determined from wildlife, and consolidate field and laboratory protocols for microscopic analysis of haematological samples as required for haemosporidian parasites. 3) identify target species and regions for further collection of blood smears and blood for molecular analyses. 4) identify funding sources and write collaborative grants in order to sample target species and regions. 5) write and submit manuscripts.

RCO5 (WG5): 1) extract existing datasets of host-parasite relationships from both i) focal species (to be identified dependent upon availability) sampled intensively across multiple geographically independent sites, and ii) multi-species communities sampled over multiple years; 2) analyse datasets and outline manuscripts; 3) Allocate specific analyses and tasks among the WG; 4) submit manuscripts; 5) identify knowledge gaps and funders and write collaborative grant applications.

CBO1 (WG6): 1) Identify locations and timings for training schools, workshops, symposia and conferences; 2) plan and deliver one 5-day training school for 25 participants each in each of four years, designing the curriculum so as to cover skills relevant to 1 RO per day; 3) plan and deliver conferences in Years 2 and 4, and a symposium at an international conference in Yr. 3; 4) arrange annual workshops for progression of RCOs with regular remote progress meetings; 5) form gender-balanced and diverse panel to assess and award applications for STSMs; ensure unconscious bias training is undertaken by all with a role in selection and award of funding recipients; monitor diversity of STSM participants and rebalance as necessary.

CBO2 (WG6): 1) advertise the Action across disciplines and encourage scientists and specialists from different

disciplines to participate, prioritising YRIs and participants from ITCs; 2) organise interdisciplinary round table at conferences in Years 2 and 4; 3) Identify regions to target to encourage public engagement with the network; deliver virtual meetings.

CBO3 (WG6): 1) advertise travel support for meetings highlighting the promotion of diversity within the Action; 2) review and ensure equal gender balance in all activities; 3) prioritise funding allocation to members from ITCs and underrepresented groups; review this prior to confirmation of award to ensure support for those in underrepresented groups.

CBO4 (WG6): 1) construct and publicise a WIMANET website; 2) develop a range of outreach activities; 3) disseminate RCO results to both specialist and generalist audiences.

4.1.2. DESCRIPTION OF DELIVERABLES AND TIMEFRAME

The Action will start with an initial meeting within the first month, with WGs being established and determining specific plans for recruitment of new WG members, compilation of existing data (as above), and remote progress meetings to monitor progress until the next in-person meeting. When organising WGs, care will be taken to ensure gender balance. Full meetings of each WG will occur in person (COVID-dependent) on an annual basis and remote progress update meetings once every 3-4 months, with the intention that individuals can contribute to multiple WGs. Deliverables and milestones are detailed below, with specific timeframes for both provided in the GANTT chart (Section 4.1.4).

WG1: Coordinating genomics, transcriptomics, and molecular markers. Year 1: Summary of target species and geographic regions to expand genomic/transcriptomic resources (M1.1); Year 2: First set of protocols available (D1.1); submit first collaborative grant proposals to collect additional genomic/transcriptomic data (M1.2); Year 3: Submit for peer-review a manuscript analysing existing genomic, transcriptomics, and molecular marker data (D1.2); Year 4: Complete dissemination plan (M1.2) making all training materials and protocols available (D1.3).

WG2: Incorporate molecular markers and morphology to assign wildlife malaria lineages to species and identify phylogenetic relationships. Year 1: Identify species with morphological descriptions and attached molecular sequence information (M2.1). Year 2: Compile morphological and molecular data, constructing phylogenetic hypotheses and identifying phylogenetically informative characters (D2.1); identify priority clades for detailed morphological characterisation (M2.2) and submit funding proposals (M2.3). Year 3: Develop a global consensus for classifying haemosporidian species (M2.4). Year 4: Produce a detailed workflow for species identification using a combination of morphological characteristics and molecular markers (D2.2).

WG3: Determining what influences vector transmission success in wildlife malaria. Year 1: Summarise current knowledge on the vector competence of haemosporidians and the experimental designs and conditions used in previous studies (e.g., feeding sources, temperature, humidity) (M3.1). Year 2: Organize and make first available the first set of standardised protocols to work with vectors of haemosporidian parasites (D3.1). Year 3: Reach a consensus on key knowledge gaps for drafting and submitting collaborative grant proposals (M3.2). Year 4: Submit manuscripts (D3.2); complete dissemination plan (M3.3); Make training materials and finalised protocols for working with the vectors of haemosporidians available (D3.3).

WG4: Quantifying the impact of anthropogenic activities and wildlife malaria on host haematology. Year 1: Compile existing datasets from researchers and museums for analysis and reference (M4.1). Year 2: Organize and make first set of protocols for quantifying host haematology available for implementation through existing research programmes (D4.1). Year 3: Submit first manuscript summarising existing knowledge and compiling existing datasets to quantify the impact of anthropogenic activities and wildlife malaria on host haematology (D4.2), progress evaluation to identify relevant findings and knowledge gaps for developing collaborative grant proposals and priorities for future work (M4.2). Year 4: Disseminate protocols and training materials to assess baseline host haematology parameters (D4.3).

WG5: Identifying the drivers of spatiotemporal variation in multi-host-parasite communities. Year 1: Identify and summarise key variables and clarify statistical methods, structure of models, task allocation (M5.1). Year 2: Determine tweaks to sampling design for existing field programmes in subsequent years and produce protocols that can be implemented through existing research programmes to identify the drivers of spatiotemporal variation in multi-host-parasite communities (D5.1). Year 3: Identify key findings from analyses and knowledge gaps for collaborative grant proposals (M5.2). Submit for peer review a manuscript examining environmental drivers of host-switching (D5.2). Year 4: Identify priorities for future work (M5.3); submit a second manuscript (D5.3).

WG6: Coordinating and implementing the CBOs. Year 1: Identify locations and timings for training schools, workshops, symposia, conferences and annual workshops for progression of RCOs (M6.1); Construct and publicise a WIMANET website, including space for network member profiles, information about networking

activities, and space for protocols (D6.1); implement unconscious bias training for all network members who will be involved in the selection of participants in summer schools and short-term scientific missions (D6.2); advertise the Action and travel support across disciplines and encourage scientists and specialists from different disciplines to participate (D6.3); identify regions to target to encourage public engagement with the network, and deliver virtual meetings (M6.2) alongside outreach activities disseminating RCO results to both specialist and generalist audiences (D6.4). Years 1-4: deliver one training school per year alongside annual workshops in each of four years (M6.3); deliver conferences incorporating interdisciplinary round tables in Years 2 and 4 (M6.4), and a symposium at an international conference in Year 3 (M6.5).

4.1.3. RISK ANALYSIS AND CONTINGENCY PLANS

This is an ambitious proposal, and with that comes a risk that parts of the proposal may fail to be completed within the four-year program. Specific risks are considered below:

- *The risk of **not attracting a critical mass of excellent researchers** is considered low: the network of proposers is already substantial, containing multiple pre-existing and productive collaborations, alongside enthusiastic YRIs and students, most of whom have contributed to the writing of the proposal and whose labs' research aligns with the RCOs in the proposal.*
- *The risk of **not involving relevant stakeholders** is considered low. The network of proposers has existing engagement with relevant stakeholders at national and international levels.*
- *The risk of **management failure** is considered medium. A Management Committee of one key member from each RCO, along with a deputy for each RCO who will liaise with the MC member and step in if necessary, will be assigned, having the responsibility to monitor overall progress on the deliveries with checkpoints at 6 month intervals.*
- *The risk of **not achieving consensus on difficult decisions** is considered medium. At each meeting, efforts will be taken to reach consensus on any problems encountered. For important issues not resolved at meetings, subgroups will be allocated consisting of members of alternative views, with a commitment to either solve the issue democratically or deliver a plan for how this will be achieved, and reported to all meeting participants within 3 months.*
- *The risk of **restricted freedom of movement for some participants due to** political and health situations in some countries is considered high; however, the Action will ensure that conferences and workshops are held in countries that are accessible, and if freedom of movement of some participants is impacted then the Action will ensure remote participation (through e.g. Zoom) wherever possible.*
- *The risk of **not delivering on targets** is considered low. Each RCO is aligned with the research objectives of the labs of multiple proposers, providing the necessary expertise. This proposal will facilitate these objectives by attracting and enabling additional collaboration from outside the network of proposers, alongside focussed time through WG meetings to achieve these objectives. Regular WG update meetings will allow the identification of any lack of progress alongside the formulation of plans to implement any corrective actions that may be required.*

4.1.4. GANTT DIAGRAM

	Year 1				Year 2				Year 3				Year 4			
	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4
WG1			M1.1			D1.1				D1.2				M1.2	D1.3	
WG2			M2.1			D2.1	M2.2					M2.3		D2.2		
WG3			M3.1			D3.1				M3.2			D3.2	M3.3	D3.3	
WG4	M4.1				D4.1					D4.2	M4.2		D4.3			
WG5			M5.1			D5.1			M5.2	D5.2				M5.3		
WG6	*	D6.3			D6.3				D6.3							D6.4
MC																
Reporting				PR1				PR2								FR

	Workshop/meeting	**PR**	Progress report	**M**	Milestone
	Management committee (MC) meeting	**FR**	Final report	**D**	Deliverable

* M6.1, D6.1, D6.2, D6.3

Figure 1. GANTT chart of the time schedule for activities, deliverables and reporting for WIMANET. Wherever possible, meetings, conferences, Training Schools and workshops will be organised in succession to optimise the use of available funds. It should be noted that D6.4 and D6.5 are not included in the timeline as these will occur on a continuous basis.

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