

**Spot Malaria Partner Study Proposal**

Spot Malaria aims to bring together malaria genetics with epidemiological information across both time and space. The project has two distinct but complementary goals;

* to simplify genetic data reporting so that more users are able to analyse and interpret the key features of their data, focusing on what is of most importance for field research and malaria control in a timely manner;
* and to create an open access global observatory across time and space for genetic variation and other relevant metadata such as malaria prevalence and deployment of control measures.

This form is to capture the key information for a potential partner study for genetic analysis of *P. falciparum* or *P. vivax* samples as a basis for discussion about potential collaboration under the Spot Malaria umbrella. For any questions, or to submit your completed forms, please contact support@malariagen.net

**People Information**

Please provide details of relevant stakeholders for this study. This information can be added to at a later stage.

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| Main contact(s) | Name | Affiliation | Email |
| Lead Investigator |  |  |  |
| Contact Person[[1]](#footnote-1) |  |  |  |

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| --- | --- | --- | --- |
| Key investigator(s) name | Role in Study | Affiliation | Email |
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**Study Information**

Please provide details about the study that was conducted to generate the samples.

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| Study Title |  |
| Study DescriptionBriefly describe the purpose of the study (<300 words) |  |

**Sample Information**

Please complete the relevant sections for your study.

***Dried Blood Spots (DBS) collected from malaria cases***

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| Malaria confirmed by RDT? | [ ]  Yes [ ]  No |
| Parasitaemia estimated by microscopy? | [ ]  Yes [ ]  No |
| Multiple samples from same patient? | [ ]  Yes [ ]  No |
| Samples collected using protocol we provide?***2*** | [ ]  Yes [ ]  No |
| If you did not use the protocol we provide, please complete below: |
| What type of filter paper was used? |  |
| Approx volume of blood per spot? |  |
| Number of blood spots collected per patient? |  |
| Country  | Site | Species | Sample number | ETA at Sanger |
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***Extracted Parasite DNA***

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| Malaria confirmed by RDT? | [ ]  Yes [ ]  No |
| Parasitaemia estimated by microscopy? | [ ]  Yes [ ]  No |
| Multiple samples from same patient? | [ ]  Yes [ ]  No |
| Samples filtered to deplete human DNA?3 | [ ]  Yes [ ]  No |
| Samples screened for human DNA contamination (ie by qPCR)? | [ ]  Yes [ ]  No |
| Time in culture will be provided | [ ]  Yes [ ]  No [ ]  Not applicable |
| DBS from same patient? | [ ]  Yes [ ]  No |
| Country  | Site | Species | Sample number | ETA at Sanger |
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***All samples***

Every sample submitted to the Sanger Malaria Programme for genetic analysis and to MalariaGEN Projects must:

* Have been collected in accordance with good research practice
* Have local ethics approval including appropriate informed consent
* Have approval from other local stakeholders (e.g. the local institutional review body) where appropriate

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| Please confirm that you will take responsibility for local ethics approval and for any other review processes that are required at the local level. | [ ]  Yes [ ]  No |
| Please provide details of the ethics Committees that approved the study and ethics approval number(s). |
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2, 3 A protocol for DBS collection is available on request and at <https://www.malariagen.net/network/capacity-building/methods>

Every sample submitted to the Sanger Malaria Programme for genetic analysis and to MalariaGEN Projects must:

* Be part of an approved partner study with a partner study reference code
* Be submitted with a complete Sample Manifest that provides collection date and location.

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| I understand that samples submitted without prior approval or without a complete sample manifest will not be processed and may be returned. | [ ]  Yes [ ]  No |

**How will samples be used**

State-of-the-art genetic and genomic technologies will be used to genotype Parasite DNA - either extracted from venous blood or isolated from the finger-prick blood samples of confirmed malaria patients. The processes may include DNA extraction, genotyping, targeted sequencing, selective whole genome amplification, genome sequencing, and the downstream statistical and computational analysis of these data. When a partner study is approved, it is our intent to use our best efforts to achieve high quality data on each sample within the limitation of the quality and quantity of parasite DNA and our capacity which will change over time.

**Data that will be returned to you**

Data products providing sample level information that that may be produced and returned include:

Genetic Report Card - A user-friendly summary of the main findings for each sample including information on drug resistance markers and other information such as multiplicity of infection and markers of geographical origin. As research progresses, assays are iteratively improving as new relevant markers can be reliably incorporated. From the time a sample and completed manifest is received we aim to return the Genetic Report Card within 6-8 weeks.

Whole Genome Data - When the parasite DNA is of high enough quality and quantity and capacity allows a sample may be submitted for whole genome sequencing. Sequence read data is deposited at ENA immediately after sequencing. The timeline for this is dependent on external factors therefore while we aim to return data within 9 months of receiving samples with a completed sample manifest although this cannot be guaranteed.

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| Which of the above products is most suitable for your needs? |
| [ ] Genetic Report Card  | [ ] Whole Genome Data  | [ ]  Other, please specify |  |
| If you said Other, please give details here |
|  |
| How do you anticipate using it? Please describe public health and research uses? |
|  |
| Who should receive products directly from the project? This can be updated at a later date. |
| Name of Product Recipient | Role in Study | Affiliation | Email |
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| Spot Malaria is planning on producing training materials to support the use of its products. Please let us know which, if any of the following you would be interested in using, if available?  |
| For the Genetic Report Card  | [ ]  How-to - document  | [ ] How-to – online course  |
|  | [ ] How-to – face-to-face course  | [ ] Other, please specify |
| For the Whole Genome Data  | [ ]  Advanced Course  | [ ] Other, please specify  |
| If you said Other, please give details here |
|  |

**Data that will be published and released**

Combined data from all partner studies will be used for two main purposes

1. To evaluate and develop the Spotmalaria methodology, e.g. (a) to determine the sensitivity and accuracy of this approach when applied to samples in the field; and (b) to develop a data report format and tools for data analysis that will be of practical utility for researchers working in the field and for control programmes.
2. To establish a prospective and systematic sampling framework for a global observatory that will provide open access information about how the parasite population is changing and evolving in different parts of the work, together with global analyses of drug resistance, malaria transmission and other factors relevant to malaria control and elimination.

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| Product | Mechanism for Release | Timeline and Restrictions on use |
| Partner Study DescriptionLead Investigator Contact Person with contact detailsStudy Site Information | MalariaGEN website | When a data product arising from the partner study has been shared publically |
| Sequence Read Data | Deposited in European Nucleotide Archive (ENA) | Immediate open access in line with Sanger Institute policy |
| Genetic Report CardWhole Genome Data | MalariaGEN website | As soon as possible and not later than 6 months after returning to partners |

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| Please confirm that you are happy for your samples to be used as above?  | [ ]  Yes [ ]  No |
| If you said No, please describe the ethical or institutional restrictions on the release of these data |
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**Key Information**

The Sanger Malaria Programme working through the MalariaGEN collaborative framework is committed to integrating genetic and epidemiological data to understand the evolutionary changes in malaria relevant genomes (human, parasite and vector) particularly in response to control measures. By partnering with research and public health programmes operating in endemic regions through the Spot Malaria Project we are committed to producing actionable knowledge for the purpose of controlling and eliminating malaria.

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1. Contact person is the publically named contact who will be the first point of contact for the Partner Study. Typically, this is the lead investigator but in some cases this could be the study coordinator of a larger study. [↑](#footnote-ref-1)