rabies remains enzootic and still threatens human and animal health.

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Harmonisation of research data for congenital Zika syndrome: need for core data sets for epidemic-prone infectious diseases

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Purpose: To reduce the delay in the clinical research response during outbreaks; we sought to define core variables for research on Congenital Zika Syndrome (CZS) based on the experiences of research responders in Recife, Brazil - a Zika affected region.

Methods & Materials: We employed a qualitative methodology with interviews and document review. Two sets of case record forms (CRFs) designed at the start of the Zika epidemic were reviewed; one developed by the Microcephaly Epidemic Research Group (MERG) in Recife and the other by ISARIC (International Consortium for Severe Acute Respiratory and Emerging Infections Consortium) and her collaborators. Semi-structured qualitative interviews were conducted to explore the views of the MERG team on core domains for research on CZS. Thematic discourse analysis was used to look for similarities and differences in the data.

Results: The document review indicated that the CRFs complemented each other and merging the domains from both sets of questionnaires produced a relatively comprehensive data set. The participants proposed a minimum set of domains for observational research on CZS and divided these into clinical and epidemiological domains based on the type of data generated. Cross-cutting themes which emerged were the importance of the research context and timing of research on the structure, construct and content of items in each domain. Participants underscored the need for dynamic CRFs at the start of an epidemic; because outbreaks are rapidly evolving, and questionnaires need to be adaptable to accommodate new information during the outbreak.

Conclusion: Developing a standardised case record form for clinical research involves various steps, each of which takes time. The domains recommended lend themselves to other arbovirus infections or infections with the potential for mother-to-child transmission. The study strengthens the need for an agreed core set of variables for various clinical syndromes and unique issues such as pregnant women and children. A methodology on how to decide on the data variables would be useful. A future study could be to identify what the generic research questions might be, to further refine the core data set in advance of an outbreak, given that CRFs should ideally be linked to predefined research questions and protocols.

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Rapid outbreak identification using point of need nanopore sequencing

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Purpose: Polymerase Chain Reaction (PCR) is considered as gold standard tests for molecular detection of pathogens. The PCR relies on the use of known sequences of specific target genes. A false negative PCR result might be obtained in case of new variant of a known pathogen or emerging diseases. Alternatively, Next Generation Sequencing (NGS) can be applied to identify the pathogen responsible for the outbreak through sequencing all nucleic acids existing in the collected sample. In addition, NGS gives insight about the origin and variant of the causative agent. In this study we have established a protocol for rapid identification of the cause of unknown fever as well as the origin of infection.

Methods & Materials: A RNA mock sample with fever of unknown origin was tested using a sequencing protocol relying on multiple displacement isothermal amplification and oxford nanopore sequencing. The yielded data were analysed using offline BLAST search data bases to facilitate its implementation at low resource settings.

Results: The procedure took around 400 minutes including sample preparation and data analysis. In total, 63,678 sequence files were yielded. After running a local BLAST against a viral genome database, approximately 4% of the reads were identified as ZIKV. The complete ZIKV genome sequence was recovered with 2454 reads with an average read length of 685 bases. The in-depth sequence analysis revealed that it was more related to ZIKV isolated from Senegal.

Conclusion: In conclusion, the protocol enables rapid and reliable virus identification and serotyping. The procedure has been conducted with a mobile suitcase laboratory, which is easy to use at the point of need in endemic countries. However, the protocol is still cooling chain dependent and the cost per sequencing run are very high.

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The development of the stochastic model for vivax malaria occurrence based on the climate factor in the Republic of Korea

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Purpose: We developed stochastic model for vivax malaria occurrence based on the climate factor in malaria risk areas.

Methods & Materials: We used the national suveillance database of registered malaria cases in period of 2001 to 2013 and malaria vector surveillance database in period of 2009 to 2013 from Centers for Disease Control and Prevention, Republic of Korea.