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Editorial: Recent advances in "omics" of tropical diseases

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Editorial on the Research Topic
Recent advances in "omics" of tropical diseases

Over the past two decades, technological and computational advances in big biological data have enabled a revolution in our understanding of diverse diseases. Starting with genomics, where whole genome sequences are determined for infectious agents and their hosts, now all types of biological sources can generate global data. Transcriptomes, methylomes, immunomes, metabolomes, lipidomes, and microbiomes are commonly generated and assessed for establishing correlates of disease states, both for noncommunicable and communicable conditions. Infectious diseases have been intensively studied in this regard, and systems biology has allowed us to understand the molecular mechanisms driving diseases in greater detail (1). Direct application of this knowledge has also led to the real-time identification of new pathogens and the rapid design of new vaccines.

Infectious diseases of great impact such as HIV/AIDS, influenza, and more recently COVID-19, have drawn great attention from the research community due mainly to their established or potential pandemic impact (2). Research groups have assessed those diseases by "omics" techniques, and substantial advances to their mitigation have been achieved. On the other hand, infectious diseases that disproportionately affect low-income countries and parts of the world have been somewhat neglected in those kinds of studies, until recently (3), because "omic"-wide studies were expensive and were not being conducted in developed countries with the most research infrastructure and resources; this is true in the case of tropical diseases. Recently, with decreasing costs of the "omics" experimental approaches, and the dissemination of tropical diseases to temperate regions due to the global warming phenomenon, both middle and high-income countries have invested into the research of those diseases.

In this Research Topic of Frontiers in Tropical Diseases, we have assembled four different studies (and a *corrigendum* for one of them) that applied distinct "omics" techniques to diverse diseases, advancing the knowledge on understanding and fighting them. The studies also came from different parts of the world, and included bacteria, viruses, and parasites as topics, thus corroborating the disseminated interest on the subject.

In the study *Microbial RNA: The new PAMP of many faces*, Milillo et al. addressed and reviewed the many different aspects of bacterial RNA, not only limited to triggering pro-inflammatory immune responses, but also capable of inducing down-modulatory

responses, which are used by pathogens as an immune evasion mechanism. Bacterial RNAs are part of what the authors call *vita*-PAMPs, i.e., pathogen-associated molecular patterns linked to the viability of the pathogen. Bacteria like *Escherichia coli*, *Streptococcus pyogenes*, and *Klebsiella pneumonia*, and viruses such as HIV and HCV, can all produce RNAs in the cytosol of infected cells, which induce down-modulation of MHC-I and II, as well as TLR-7/8 from the cell surface to protect them from recognition and killing.

In the second study, *From helping to regulating—A transcriptomic profile of Ifng^{+} Il10^{+} Il21^{+}Cd4^{+} Th1 cells indicates their role in regulating inflammation during experimental trypanosomosis*", Nguyen et al. discussed the role of CD4+ Th1 cells during experimental *Trypanosoma evansi* infection in a mouse model. Using the modern transcriptomic technique of single-cell RNA sequencing (scRNA-seq), the author discovered that this cell subset, which is prevalent during infection, provides an anti-inflammatory response by producing high levels of IL-10, an anti-inflammatory cytokine, rather than "helping" the immune inflammatory response. This regulatory response is likely to dampen inflammation during *T.evansi* infection. The corrigendum to this study (Nguyen et al.) has not changed any of the results or conclusions found, but it was rather related to data availability.

The third study, *Challenges and opportunities of molecular epidemiology: using –omics to address complex One Health issues in tropical settings* (Tigistu-Sahle et al.), provides a comprehensive review on the different "omics" techniques and how they can be used for molecular epidemiology studies in One Health approaches. Through a collaboration among authors from three distinct countries (USA, Brazil. and Ethiopia), the review used the two developing countries as models to identify gaps and opportunities for such approaches. The authors highlighted capacity building in tropical areas as in need of utmost attention to establish global health.

Finally, in the fourth study (*Beyond surveillance: leveraging the potential of next generation sequencing in clinical virology*), Aulicino and Kimata shared their perspective on the use of the infrastructure and capacity building in NGS and bioinformatics that took place during the COVID-19 pandemic for future applications in molecular virology. The authors highlighted a scale back of those efforts after the end of the pandemic, and despite the use of the structure for other health problems worldwide, they called for the importance of keeping viral surveillance conducted in this setting for managing diagnosis of viral infections and devising treatment options.

The field of tropical diseases is provided expanding opportunities to develop in view of current lower-cost experimental procedures and equipment platforms, a growth in bioinformatics hardware, software and human resources, and the expanding geographic dissemination of tropical infectious agents worldwide. Such opportunities should not be neglected so that the field is brought back to the spotlight of quality hardcore science.

Author contributions

MS: Conceptualization, Writing – original draft, Writing – review & editing. GK: Conceptualization, Writing – original draft, Writing – review & editing.

Conflict of interest

Author GK was employed by the company AstraZeneca.

The remaining author declares that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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