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Letter to the Editor

How to detect new viral outbreaks or epidemics? We need to survey the circulation of viruses in humans and other animals using fast, sensible, cheap, and broad-spectrum methodologies

Dear Editor,

"One Health" is the concept that unifies (I) human, (II) animal, and (III) environmental health.[1,2] According to this concept, any condition that affects one of these three actors will affect the health of all of them. Emerging and reemerging diseases can be recognized as disorders in the One Health. Such diseases can arise in response to environmental disturbances caused by human action. For example, interferences on wildlife habitats can predispose wild animals to approach or even to live in urban areas, creating ideal conditions for pathogens to jump from these animals to humans. In other words, the emergence of a disease can be the result of lack of synergism between various socioecological factors.

When a new zoonotic disease arises in a human population, it is mandatory to quickly detect and identify such a new pathological agent. This early detection is an important way to prevent outbreaks and avoid epidemics. For example, if the circulation of HIV had been identified in Africa right after the virus transition from wild primates to humans, perhaps the HIV pandemic could have been avoided. Similarly, to prevent the reemergence of a viral disease in a human population, early identification, monitoring, and survey of the viruses circulating among humans is essential. This monitoring should be primarily done in sentinel populations (I) living in places near to the habitats of animals considered to be important viral reservoirs (for example rodents, bats, pigs, and monkeys); (II) living or working near animal breeding regions or regions of slaughtering of livestock animals, since these sites provide ideal conditions for the emergence of human viral diseases due to cohabitation of humans and non-human animals; and (III) living in areas infested by viral vectors (especially mosquitoes). Still, this monitoring should be carried out among patients that seek health services showing signs of viral infections. However, a practical problem is the lack of tools and methodologies to perform this control.

Recently, a Brazilian research group developed a DNA microarray methodology (SMAvirusChip) that allows the screening of more than 400 viruses transmitted by arthropods and small mammals, using only one biological sample.[3] It is important to highlight that the SMAvirusChip can identify viruses that pose a constant concern for public health authorities (Chikungunya, Dengue, Zika, among others) or intrigue the scientific community, as is the case of Sabiá and Rocio viruses (both viruses identified in human patients but for which still lacks genetic/evolutionary or even ecological information). Based on oligonucleotide probes, this tool allows the precise identification of viruses that are often difficult to diagnose by conventional immunoassays due to cross-reactivity. For example, the results of immunoassays aiming at detecting the Zika virus can be inconclusive due to cross-reactivity of antibodies induced by other flaviviruses, such as Dengue or Yellow Fever. For us, the detection of a broad spectrum of viruses is a unique feature of the SMAvirusChip. On the other hand, the feasibility of large-scale use of methodologies such as SMAvirusChip still needs to be evaluated. Of course, the cost for the application of this microarray methodology may be an important obstacle, especially in developing countries. However, this is an example of a tool that could be used for monitoring the circulation of viruses among humans and other animal species.

The development of tools to identify a broad spectrum of viral pathogens in a fast, sensible, and cheap way is a global need. Such tools would primarily be applied to healthcare services of developing countries located in tropical regions. Knowing the pathogens that circulate in a given population will allow the detection of even small variations in circulation patterns. Several fronts could be envisaged in such survey: first, methodologies such as these would facilitate the diagnosis of viral diseases of which the causative agents often remains unidentified. In these cases, even if the identification of the pathogens does not have clinical implications or therapeutic consequences, the data is of epidemiological importance. Second, it would allow the survey of different viruses hosted in human populations. Third, these tools could be used in health services for the screening of blood bags, for

example. Fourth, in viral ecology studies, these tools would facilitate the work of researchers that target viral diversity amongst non-human animals. In these different contexts, the spectrum of pathogens detected in research activities would also be expanded.

Permanent monitoring of the circulation of viruses in risk areas can be considered a strategy within the scope of "constant interventions". Matua et al.[4] defined this term as strategies "undertaken at individual, community, and institutional levels following an epidemic and to be continued in the aftermath, that is in-between the outbreaks". The "constant interventions" were recommended by the authors in the context of the last outbreak of Ebola in Africa; we consider it useful to be applied in other situations, previous to the establishment of a significant number of infectious cases, in the monitoring of endemic, emerging, and reemerging diseases. The same authors state that "In essence, 'constant interventions' are intended to keep populations and institutions in 'high-risk' areas ready, fully prepared, and constantly aware of the risk of Ebola outbreak recurrence". In our opinion, this definition fits properly not only for Ebola but for many other viral diseases.

In conclusion, viruses with a great potential to trigger new epidemics are already "out there". Monitoring of the circulation of viruses in biological samples (human and non-human) is essential for early identification of the next outbreaks or epidemics. The need for such a surveillance and monitoring behavior is even greater in developing tropical countries where so often humans live disharmoniously with many domestic and wild animals. The proposed surveillance would be even more effective if performed with samples from (I) vectors, (II) resident viral reservoirs, and (III) migratory animals such as birds, and (IV) humans. Together, data gathered from humans and other animals (wild, livestock, and domesticated) would show where the viral hotspots are, enabling measures to control the spread of viral pathogens. Such strategy could not only reduce health problems but also the economic losses caused by the infection and even death of animals of economic interest (for the food industry, for example). Importantly, only with the development of methodologies that allow the identification of a broad spectrum of viruses this monitoring can be achieved effectively. In developing and tropical countries like Brazil, this type of initiative should be encouraged not only as a form of support for technological development, but mainly as a public health strategy and a way to preserve the One Health.

Conflicts of interest

The authors declare no conflicts of interest.

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