



ISSN: 1697-090X

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### Letters to the Editor / Cartas al Editor

## "ONE HEALTH": STATE IN OUR ENVIRONMENT.

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**Rev Electron Biomed / Electron J Biomed 2023;1:60-63.**

Dear Editor:

The "*One Health*" concept is assimilated to the value represented by human and animal health and welfare as well as the optimization of environmental services. It is achieved through inter-, multi- and transdisciplinary collaboration between professionals and institutions related to Public Health, Animal Health, and other related disciplines, which goes beyond the results that could be obtained independently by each of the parties involved<sup>1</sup>. As glossed by Capua and Cattoli<sup>2</sup> the term was initially coined as "*One Medicine*" in 1890 by William Osler. In 1976 Calvin Schwabe, as pointed out by Zinsstag et al<sup>3</sup>, took up the concept in order to address infectious diseases from a holistic approach.

This field of knowledge evolved into "Global Health" with the emergence of avian influenza from 2003 to 2005, when wild birds spread the highly pathogenic influenza A H5N1 virus to poultry on three continents, its hemagglutinin (HA) diversified into several clades and the different isolates were grouped into different genetic lineages throughout the world<sup>4</sup>. It was undoubtedly more recent events that have contributed to consolidate the term. In 2009, there was the pandemic caused by a new influenza A H1N1 virus whose genome brought together segments of a quadruple origin: two porcine, one avian and one human lineage<sup>5</sup>. Then, in 2012, the world witnessed the emergence of the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) in Saudi Arabia from camelids<sup>6</sup>, which has caused several thousand cases to date with a case fatality rate of 36%. Subsequently during the Ebola outbreak between 2013 and 2016 in West Africa, almost thirty thousand cases were reported from this agent, with a lethality close to 50%<sup>7</sup>. In December 2019, the

SARS-CoV-2 pandemic appeared of which, according to the "Johns Hopkins" University, 676,609,955 cases and 6,881,955 deaths have been recorded, reported until March 10, 2023, date on which the prestigious North American Institution has stopped counting data in this regard<sup>8</sup>. In line with this trajectory, it seems imperative to monitor the evolution of viruses, especially in the natural environment and in animals, in order to minimize the potential emergence of new pathogens<sup>9</sup>.

An undeniable reflection of this human-animal-environment link is that 60% of all human pathogens known to date are zoonotic, the latter representing the majority of all emerging agents in our species<sup>10</sup>. Currently, rabies, zoonotic influenza viruses and antimicrobial resistance are included as priority lines of global action within the *One Health* strategy, to which SARS-CoV-2 have been added<sup>11</sup>.

In this sense, from the area of Microbiology of the University of Valladolid we contribute to the knowledge of these lines through the study of the microbial genome in three areas. Firstly, in the molecular characterization of influenza viruses in one of the 152 National Influenza Centers recognized by the WHO in the world<sup>12</sup>. Secondly, through the genetic study of SARS-CoV-2 and its variants<sup>13</sup> and other respiratory viruses<sup>14</sup> by coordinating the sequencing and monitoring of their evolution in Castilla y León, of which there was already experience in international platforms<sup>15</sup> and at present as part of the National Network of Laboratories dedicated to this field of knowledge. Thirdly, we have undertaken the definition of different mechanisms of bacterial resistance to antibiotics, collaborating with other groups and organizations to investigate the resistance genes circulating in humans, animals and food, making both methodological<sup>16,17</sup> and original contributions<sup>18-22</sup>.

To date, almost 50,000 viral genomes, 10,000 bacterial genomes and around 5,000 samples have been analyzed to determine microbiota. Of the total bacteria sequenced, we studied the resistome in 6,222 genomes of which 67.7% were found to be multidrug resistant, with *Enterobacteriaceae*, *Staphylococcus* and *Pseudomonas* being the most resistant. Among the antibiotics, resistance to aminoglycosides, beta-lactams and tetracyclines was documented, and in particular the most abundant resistance genes were against streptomycin, doxycycline, tetracycline and erythromycin. The *blaTEM*, *blaOXA*, *blaNDM* and *blaVIM* genes were identified in 17%, 14%, 7.5% and 7%, respectively, of the sequenced isolates. A higher number of plasmids carrying these genes have been identified in *Escherichia coli*, *Staphylococcus aureus*, *Klebsiella pneumoniae* and *Salmonella enterica species*<sup>23</sup>.

It seems appropriate to consolidate interdisciplinary collaborations and unify efforts to improve surveillance systems and characterization of relevant agents both in health care practice and in Public Health<sup>24</sup>. At the same time, it is obligatory to show recognition and gratitude to the microbiology and preventive medicine professionals of the network of public hospitals of the Castilla y León health system for their participation in the collection of samples and elaboration of epidemiological data on the patients to whom we provide care.

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