TITLE: ONE HEALTH BRAZILIAN RESISTANCE (ONEBR): FIRST INTEGRATED DATABASE FOR GENOMIC SURVEILLANCE OF ANTIMICROBIAL RESISTANT PATHOGENS AT THE HUMAN-ANIMAL-ENVIRONMENTAL INTERFACE

AUTHORS: FONTANA, H. CARDOSO, B. ESPOSITO, F. FUGA, B. SANO, E. NEVES, I. RODRIGUES, L. CARDENAS-ARIAS, A. FUENTES-CASTILLO, D. LINCOPAN, N.

INSTITUTION: UNIVERSIDADE DE SÃO PAULO, SP. (AV. PROF. LINEU PRESTES, 1372, 2˚ ANDAR, CEP 05508-000, SÃO PAULO – SP, BRAZIL)

ABSTRACT:

A One Health approach for antimicrobial resistance must integrate whole-genome sequencing WGS) surveillance data of critical priority pathogens from human, animal and environmental sources to track hotspots and routes of transmission, and developing effective prevention and control strategies. As part of the Grand Challenges Explorations: New Approaches to Characterize the Global Burden of Antimicrobial Resistance Program, we developed the OneBR (One Health Brazilian Resistance) Platform, an integrated genomic database for surveillance, diagnosis, management and treatment of antimicrobial resistance in the human-animal-environment interface, in Brazil. In this regard, we performed WGS of *Escherichia coli* (n = 104), *Klebsiella pneumoniae* (n = 101), and *Salmonella enterica* (n = 85) obtained from different cities, covering all Brazilian geographical regions, and from different sources, including humans (n = 153), animals (n = 72), environment (n = 29) and food products (n = 45). Genomes were analyzed extracting clinically relevant information [i.e., resistome, virulome, mobilome, sequence types (STs), and phylogenomic], which was included in the platform (http://www.onehealthbr.com/), along to clinical, epidemiological and geolocation data distributed in a Brazilian map. Overall, antimicrobial resistance genes to carbapenems (bla_{KPC-2}, bla_{NDM-1}, bla_{IMP}), broad-spectrum cephalosporins (bla_{CTX-M}, bla_{TEM}, bla_{CMY-2}), colistin (*mcr*-type), and fluoroquinolones (*oqxAB*, *qnrB19*, *qnrE1*, *qnrS1*) were identified among international clones of *E. coli* (ST10, ST131, ST648, ST224, ST90, ST58, ST410), *K. pneumoniae* Clonal Complex (CC) [(CC258: ST11, ST258, ST340, ST437)], ST307, ST15, ST29 and *S. enterica* (ST15, ST112, ST548). Additionally, data from *Pseudomonas aeruginosa* (ST235, ST277), *Staphylococcus aureus* (ST5, ST8, ST105), and emergent bacterial pathogens co-infecting COVID-19-positive inpatients have been included. In summary, a wide resistome (antibiotics, biocides, and heavy-metals) has contributed to adaptation and dissemination of WHO critical priority clones in human and non-human hosts, in Brazil, which is a serious problem that needs urgent actions that includes both more strict surveillance and more judicious use of antimicrobials, under a One Health perspective.

Keywords: Critical Priority Pathogens, Enterobacterales, *P. aeruginosa*, COVID-19, Genomic surveillance.

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