ONEPerú: Peruvian bioinformatics platform to contribute to the fight against antimicrobial resistance

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ABSTRACT

ONEPerú is a bioinformatics platform for genomic surveillance of antimicrobial resistance in priority bacterial pathogens. It integrates phenotypic, genomic, epidemiological, and clinical data from human, environmental, and animal sources under a One Health framework. The platform incorporates public and newly sequenced genomes, enabling resistome, virulome, and molecular epidemiology analyses to identify high-risk clones for national AMR surveillance.

INTRODUCTION

ONEPerú is a bioinformatics platform for genomic surveillance of antimicrobial-resistant bacterial isolates, including *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii*. The platform integrates phenotypic, genomic, epidemiological, and clinical data from clinical, environmental, and companion animal samples, supporting resistance pattern analysis and timely public health decision-making under the One Health approach.

MATERIALS & METHODS

Platform Development

Design and implementation of database structure and web application. Development of interactive maps and tables. integration of clinical, epidemiological, and genomic data.

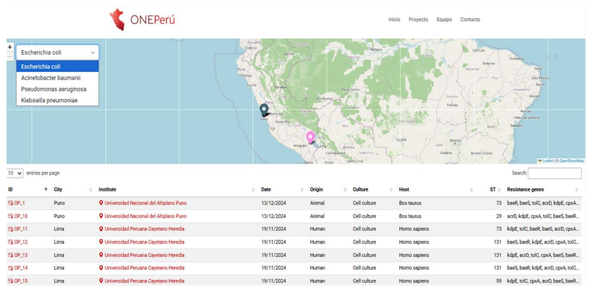

Figure 1. Website of the ONEPERU bioinformatics platform

Bioinformatics Analysis

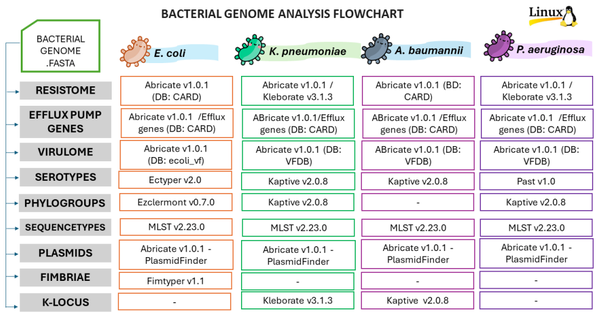

Figure 2. Flowchart of the bioinformatics analysis for the characterization of bacterial genomes

RESULTS

Genomic Data Sources

Species	Public Genomes (NCBI)	MinION Sequenced Isolates	Sample Origin
Escherichia coli	30	37	Human, Animal
Klebsiella pneumoniae	30	10	Human
Pseudomonas aeruginosa	30	34	Human, Env.
Acinetobacter baumannii	25	2	Human
Total	115	83	One Health

Figure 3. Overview of free and sequenced genomes

Using long-read sequencing Identification of resistance genes against: β-lactams Carbapenems Aminoglycosides, Efflux pump systems Detection of virulence factors linked to increased pathogenicity Molecular epidemiology

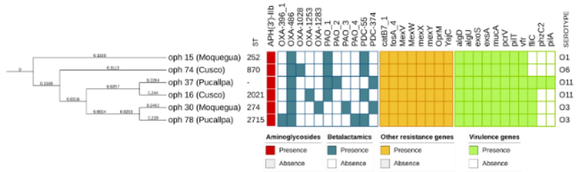

Figure 4. Phylogenetic analysis and resistance profile of *Pseudomonas aeruginosa* ST-486 isolates.

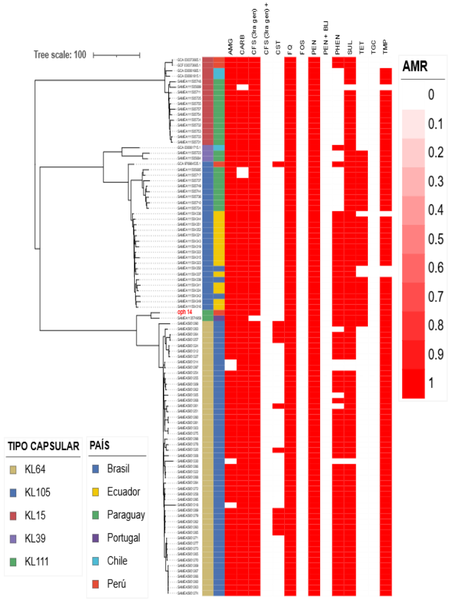

Figure 5. Phylogenetic analysis and resistance profile of Klebsiella pneumoniae ST11 isolates.

CONCLUSION

ONEPerú demonstrates the value of integrated genomic surveillance for AMR in Peru, enabling early detection of high-risk clones through long-read sequencing, automated bioinformatics, and One Health data integration to support national control strategies.

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