Genomic characterization of *Klebsiella pneumoniae* isolates from deaths in children under 5 years of age identified through the CHAMPS network

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**BACKGROUND**

- *Klebsiella pneumoniae* (KP) is the predominant organism attributed to deaths at Child Health and Mortality Prevention Surveillance (CHAMPS) sites in sub-Saharan Africa and South Asia.
- Recent data indicate a rise in multidrug resistant and hypervirulent KP.
- We performed genomic characterization of KP isolates from CHAMPS cases to investigate diversity, virulence, and antimicrobial resistance (AMR) with the goal of informing development of vaccines and other therapeutics.

**METHODS**

- KP isolates cultured from post-mortem blood or cerebrospinal fluid (CSF) specimens from Mali (n=13), Kenya (n=38), Sierra Leone (n=39), Bangladesh (n=19) and Ethiopia (n=37) underwent whole genome sequencing (WGS) at International Centre for Diarrhoeal Diseases Research, Bangladesh (icddr,b) and Centers for Disease Control and Prevention, Atlanta (CDC).
- WGS data were analyzed by KP-specific genomic tools Kleborate (GitHub - kathol/Kleborate) and Pathogenwatch (Pathogenwatch | A Global Platform for Genomic Surveillance).

**RESULTS**

- Among 146 isolates identified as KP by various microbiological methods at CHAMPS site laboratories, 114 isolates were identified as KP by WGS (Figure 1). Among these, 54 STs were identified, including novel types in Sierra Leone (n=7), Mali (n=5) and Ethiopia (n=2).
- In total, 44 K-loci (capsular polysaccharide) and 7 O-loci (lipopolysaccharide) types were detected. Diverse K-loci (10-18 unique types) were observed within each country. O1/O2v1 comprised the majority of isolates in Kenya (50%), Sierra Leone (42%), Bangladesh (57%) and Ethiopia (44%) while O1/O2v2 was dominant in Mali (58%) (Figure 2).
- Over 50% of strains from Sierra Leone, Bangladesh and Ethiopia possessed yersiniabactin siderophores, a virulence factor common among hospital-associated KP strains (Table 1). Extended-spectrum beta-lactamase genes were detected in 58-92% of KP isolates from each country and a carbapenem resistance gene was identified in 57% of Bangladeshi isolates (Figure 3).

**FIGURES**

**Figure 1.** Number of *Klebsiella pneumoniae* (KP) and other *Klebsiella* spp. genomes from CHAMPS participate countries

**Figure 2.** Distribution of K (capsular polysaccharide; left pie) and O (lipopolysaccharide; right pie) locus in KP isolates by country.

**Figure 3.** AMR score in KP isolates by countries

**Table 1.** Virulence score in KP isolates by countries.

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<th>Virulence Score</th>
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Hypervirulence and AMR are common among *Klebsiella pneumoniae* isolates associated with child deaths in low-and-middle-income countries. Ongoing surveillance utilizing genomics tools is crucial for the development of vaccines and antimicrobial treatments.