TITLE: GENOMIC SURVEILLANCE OF CLINICAL KLEBSIELLA PNEUMONIAE FROM DIFFENT BRAZILIAN STATES

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ABSTRACT:

Klebsiella pneumoniae is a critical worldwide pathogen in healthcare settings, causing serious and hard to treat infections. The detection of antimicrobial resistance and virulence genes are crucial in the characterization of this scenario. The Whole Genome Sequencing (WGS) combined with efficient analyses are powerful tools, making possible to get wide and fast results. In this study 68 *K. pneumoniae* clinical strains isolates between 2019 and 2020 were analyzed through the tool Kleborate, using data produced by WGS. The analyzed strains cover 4 Brazilian regions: 53% from Southeast [Espírito Santo (22), Rio de Janeiro (9) and Minas Gerais (5)], 31% from Northeast [Bahia (11) and Ceará (10)], 10% from the North [Pará (1) and Tocantis (6)] and 6% from the Midwest (represented only by the Goiás state, with 4 strains). Altogether, 24 STs were identified. In the Southeast and Northeast regions, 12 different STs were observed, while in the North and the Midwest 6 and 3 STs were detected, respectively. Among the strains analyzed, 57% were characterized with virulence score 0 (absence of *ybt, clb* and *iuc*), 26.5% received a virulence score of 1 (only *ybt*) and 16.5% assigned to 2 (*clb* without *iuc*, which may have *ybt*). In the former case all of them are from ST11. All strains positive for *ybt10* and *ybt0* belonged to this same ST, as well as strains positive for *clb*. Most strains (60%) had a resistance score of 2 (presence of carbapenemases), 34% with a score of 3 (carbapenemase plus colistin resistance), and only 6% with a resistance score of 1 (presence of ESBLs). A total of 63% of the strains were positive only for KPC-2, 25% only for NDM-1 and 3 stains from different STs were positive for KPC-2 and NDM-1, simultaneously. In addition, one sample was positive for IMP-1. Among strains characterized as colistin resistance, 10 were confirmed by microdilution test. Considering OmpK35 and OmpK36 most frequent mutations, 9% of the strains had truncated OmpK35 (25% present) and GD insertion in OmpK36, all belonging to ST258. Following, 16% of the strains showed truncated OmpK35 (35-40% present) and the GD insertion in OmpK36, allocated mainly in ST11, and only 2 in ST874. The most prevalent capsule antigens (K locus) were KL64 (9%), the vast majority from ST11 and one from ST147, followed by KL107 (7%), all from ST258. Regarding the O antigen, 42.5% of the samples were positive for type O2 and 22% for type O1. Kleborate has already been widely adopted in larger-scale genome surveillance studies in Europe, Asia, Caribbean and United States. Here we presented Brazilian data, which have its own characteristics. These results make possible comparing our profile with other regions in the world. The surveillance can help deal with multidrug resistant infection causing by *K. pneumoniae*, directing corrective and preventive actions.

Keywords: *Klebsiella pneumoniae*, whole genome sequencing, multidrug resistant, genomic

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