Title
Draft genome sequence of Klebsiella pneumoniae UCD-JA29 isolated from a patient with sepsis

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Sepsis is caused by a systemic inflammatory response to bacteria and bacterial toxins in the bloodstream (1). Sepsis can result in multiple organ failure, which is associated with high rates of morbidity and mortality (2). Over the past 30 years, rates of sepsis have increased among hospitalized patients and sepsis-related costs have increased substantially. In 2009, sepsis was the most expensive reason for hospitalization, amounting to $15.4 billion in hospital costs (4.3% of all hospital costs), and was the sixth most common cause of hospitalization (1). *Klebsiella pneumoniae* is a Gram-negative, nonmotile, rod-shaped opportunistic pathogen that is common in nature and is frequently found in the human nasopharynx and intestines (3). In addition, it is one of the most common causes of Gram-negative multidrug-resistant nosocomial infections (4). Little is known about how host susceptibility and virulence-associated factors relate to the severity of human sepsis. This project aimed to use a genomics-based approach to identify pathogen genomic features associated with high severity of illness in patients with sepsis. *Klebsiella pneumoniae* UCD-JA29 was isolated from a blood culture from a patient with sepsis at the University of California, Davis Medical Center in Sacramento, California, USA. The genome sequencing project was performed at the UC Davis Genome Center with the support of the UC Davis Clinical and Translational Science Center (CTSC). The project was supported by the National Center for Advancing Translational Sciences, National Institutes of Health, through grant number UL1 TR000002. The content is solely the responsibility of the authors and does not necessarily represent the official views of the NIH.

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**REFERENCES**