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Research Article

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Clinical, Epidemiological Description and Implementation of Infection Prevention and Control Measures for Hospital Outbreak Intervention by Kluyvera Ascorbata Producer of Carbapenemase in Colombia

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Introduction

In 1936, AJ Kluyver and CB Niel Goes, postulate that could exist A group of organisms with polar flagellum in the family Pseudomonadae; that they had a type of acid-mixed fermentation similar to the delta Escherichia. Asai and Okumura described in 1956 five such organisms with polar flagellum and proposed the number of genus Kluyvera in honor of AC Kluyver In 1981, this group as integrates the Enterobacteriaceae family and will count back species [1].

Kluyveva, a genus included in the Enterobacteriaceae formerly known as Enteric Group 8, including a group of gram-negative mobile bacilli, positive methyl red and do not produce acetone, which is distinguished from other related genera by its ability to utilize citrate and malonate , decarboxylate of ornithine in medium Moeller there to produce large quantities of a-ketoglutaric aido during the fermentation of the glucose [2]. They have been identified very species of clinical importance: K. ascorbata; K.cryocrescens, K species [3]. First two can be differentiated by the ascorbate test and its sensitivity to carbenicillin and cephalothin. K species requires DNA hydridization for identification [3]. Kascorbata is the most frequently isolated species of clinical samples, whereas K. cryocrescens are the most common isolates in the environment [4]. The strain of K species is infrequently isolated from various sites [5].

Initially to commensal upper airways and gastrointestinal tract was considered. However, since about twenty-five years ago, it was implied as a true pathogen in a series of different cases, including bacteremia, severe sepsis and cases as serious as infection of the central nervous system (CNS); in a patient predisposed [6-9].

Isolates of the germ have been reported in immunocompetent patients and have been associated with moderate to severe infections, so it can not be considered an exclusively opportunistic pathogen; however, it is possible that the presence of diabetes, neutropenia, advanced age or cancer may be associated with an increased risk of infection by this microorganism [10-13].

It is difficult to correlate Kluyvera infections with specific clinical features. The origin of the infection is environmental in the case of soft tissue infections; probably enteric in the case of bile duct infection, urinary sepsis and bacteremia; and it is presumed to be of respiratory origin in the case of mediastinitis. In the medical literature there are deep reviews over the last twenty years, in which Kluyvera exhibits high-level resistance mechanisms that give it the character of a primary pathogen; however, it is an infrequent germ.

There is an increase in global reports of expanded spectrum beta-lactams of the CTX-M type in Enterobacteriaceae, and mostly in Escherichia coli; raising a question about its form of acquisition [14]. These enzymes are now widespread not only in the hospital setting, but also in pathogens acquired in the community [15].

Betalactams type 40 CTX-M can be divided into two main subgroups, one of which is the amino acid sequence (CTXM-1, -M-2, -M-8, -M-9 and -M-25) [16-19]. It is clear that different genetic elements are associated with the blaCTX-M genes. The insertion sequence ISEcp1 is the most frequently reported [20].

Betalactamases encoded by chromosomes of several *Kluyvera* species have been described, identified as progenitors of enzymes derived from CTX-M, have been described, which is related to the nature and complexity of the severe clinical conditions that it causes, as well as the cases of progression of the forms of resistance exhibited until reaching carbapenemases [21]. The subgroups CTX-M-1 and CTX-M-2 are derived from *Kluyvera ascorbata*, while the subgroups CTX-M-8 and CTX-M-9 are derived from *Kluyvera georgiana* [22-24].

Respect to the molecules available to fight the complex and growing associated infections to the emergence of resistance strains in gram-negative bacilli, colistin is the antimicrobial agent of last resort to treat them, however; the resistance to colistina has arises all over the world [25]. The mechanics responsible for the resistance to the colistin were mainly associated with mutations and insertions in chromosomal genes, such as the two-component system phoP-Q

and its regulatory gene mgrB [26].

However, a colistin-resistance gene transmitted by plasmid, mcr-1; It was recently found in isolates of *Escherichia coli* and *Klebsiella pneumoniae* from humans and animals in eastern and southern China. As the mcr-1 gene can be transferred by a plasmid, its dissemination is not infrequent to other enterobacteria species other than E-coli and *Klebsiella pneumoniae*, and in November 2015; the WCH1410 strain of K. ascorbata was recovered from the wastewater of a hospital, which were collected from the main tributary of a wastewater treatment plant at a Western China Hospital in Chengdu, western China [28].

Objective

This work describes the clinical and epidemiological characteristics of *Kluyvera ascorbata*, and the success of the intervention strategies of the prevention and control committee of infections before a hospital outbreak Of carbapenemase-producing bacterial strains in a tertiary care hospital in Magangué - Bolívar, Colombia.

Methods

Descriptive and retrospective study. The clinical and epidemiological aspects of patients with *Kluyvera ascorbata* infection were recorded taking into account the different specimens analyzed and the increasing nature of the resistance mechanisms exhibited during the period from June 2016 to August 15, 2017 [29].

Antimicrobial susceptibility was determined by disc-diffusion antibiogram and by automated method (MicroScan WalkAway Plus System). The detection of extended-spectrum beta-lactamases (ESBLs) was carried out using double disc synergy. The search for carbapenemase type KPC was carried out with the inhibition test with 3-aminophenyl boronic acid (APB), modified Hodge test, EDTA. Molecular typing of the isolated strains was not performed.

Results

A total of 1065 microbiological isolates were recorded in all samples derived from the institution's laboratory between July 5, 2016 and August 2, 2017, with a total of 45 cases of infection by *Kluyvera ascorbata*. (Figure 1). Distribuyed: (external consultation: n = 22; internal medicine : n = 4, surgical hospitalization: n = 4, surgery room: n = 1, adult ICU: n = 4, adult emergencies: n = 4, gynecological emergencies, n 2, pediatric emergencies: n = 4). The sites of infection or anatomical site were: urinary tract (35 isolates), secretion (4 isolates), skin (3 isolates), blood (1 isolate), respiratory tract / tracheal aspirate (1 isolate), others (1 isolate).

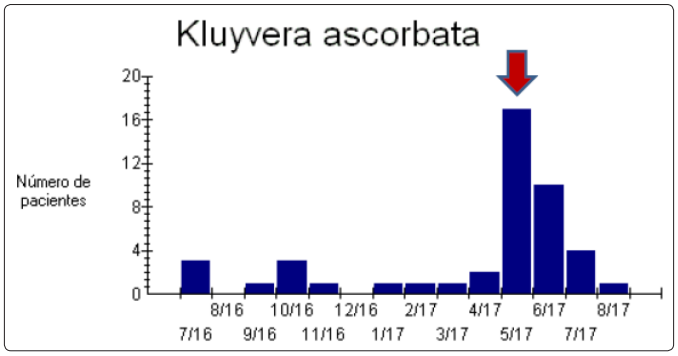

Figura 1: Frequencies of isolates by date in the period June 2016 to August 2017

Conclusion

The emergence of a hospital outbreak of *Kluyvera ascorbata* in Magangué, Colombia is described; with high dissemination capacity and associated mortality.

Betalactamases encoded by chromosomes of several Kluyvera species, identified as progenitors of enzymes derived from CTX-M, have been described, which is related to the nature and complexity of the severe clinical conditions that it causes, as well as the cases of progression of the forms of resistance exhibited until reaching carbapenemases.

The subgroups CTX-M-1 and CTX-M-2 are derived from *Kluyvera ascorbata*, while the subgroups CTX-M-8 and CTX-M-9 are derived from *Kluyvera georgiana* [30-33].

The month with the highest isolation report was May 2017 with 17 cases, followed by 10 in the month of June; coinciding with the implementation of the Cohort of patients with confirmed cases as a strategy to contain the outbreak, conjugate antibiotic schemes, hand hygiene campaign and cohort of health care personnel trained in hospital isolations.

The implementation of infection control measures is essential to reduce the hospital transmission of entereobacteria with capacity to produce resistance mechanisms with ESBL and KPC phenotypes and contribute to the reduction of the spread of the emergence of strains and clones of gram-negative bacilli. multi resistant.

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