Raoultella spp. was dismembered from the genus Klebsiella in 2001, and now it is composed by R. electrica, R. ornithinolytica, R. planticola, and R. terrigena. Although Raoultella spp. is routinely recovered from environmental sources, recent reports have evidenced the emergence of infections caused by such group of microorganisms. Herein, we aimed to analyze a collection of Raoultella, which were misidentified as Klebsiella spp. strains, and to characterize their pathogenic potential. We analyzed 67 Klebsiella spp. strains recovered from intestinal and extraintestinal infections during the 80s-90s in the city of São Paulo, Brazil. The identification at genus and species levels was confirmed by MALDI-TOF MS and, for those isolates identified as Raoultella spp., a total of 24 distinct virulence-encoding genes frequently found in Klebsiella spp. strains were screened by PCR. The ability to form biofilm on abiotic surface, the hypermucoviscosity phenotype, hemolytic activity in blood agar, and adherence on HeLa and polarized Caco-2 cells (6 h) were also evaluated. The antimicrobial susceptibility profile was determined against 14 antimicrobials by disk diffusion method according to EUCAST guidelines. A total of 6/67 (8.9%) strains obtained from fecal samples of patients with intestinal infections in 1987, where no other enteropathogen was found, were identified as belonging to the genus Raoultella. Among them, three isolates were identified as R. ornithinolytica followed by R. planticola (n=2), and Raoultella spp. (n=1). The virulence-encoding genes entB, ybtS, iutA, aerol, and mrkD were present in 100% of the strains. In addition, the kpn (83.3%), aer2 (83.3%), irp2 (50%), fyuA (50%), pagO (50%), fimH (50%), shIF (33.3%), traT (33.3%), and kfu (33.3%) genes were also detected. The number of positive virulence determinants varied from seven to nine. Only one strain (16.7%) formed a strong biofilm. All strains were negative for hypermucoviscosity phenotype and hemolytic activity but were able to adhere on HeLa and Caco-2 cells at different intensities. Finally, the Raoultella spp. strains were susceptible to most of the antimicrobials tested, except for five strains (83.3%) that showed resistance to fosfomycin. Our results identified Raoultella spp. strains in feces of diarrheagenic patients, which carried many virulence genes, suggesting the potential of Raoultella species to cause diarrhea in humans.

Keywords: virulence, Raoultella spp., Gram-negative bacilli, Enterobacteriales, diarrhea.

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