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Infection due to Roseomonas spp: a case report

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ABSTRACT

Male patient, 68 years old, immunocompromised, presented himself with fever and malaise for 15 days. At his hospitalization, peripheral blood and Schilley catheter blood cultures were collected, in addition to computed tomography that showed the presence of a peri-pancreatic collection. The material was drained and the samples were sent to the laboratory. Blood culture was positive for pink coconuts identified by mass spectrometry as *Roseomonas* spp. with the diagnosis of Bloodstream Infection being closed.

Key words: infection; blood flow; *roseomonas*; catheter.

INTRODUCTION

In 1984 Gilardi and Faur[1] described a new group of non-fermentative bacteria with unnamed pink pigmentation, which phenotypically resembled Methylobacterium extorquens. The term "pink coccoid" group was later coined by the Centers for Disease Control (CDC) to refer to this collection of phenotypically related organisms[2]. In 1993, Rihs and colleagues[3] proposed the genus name *Roseomonas* for this group of Gram-Negative bacteria with pink pigmentation, based on the results of DNA hybridization. Within the genus, six genome species were identified, and the following names were proposed for three of these groups (*Roseomonas gilardii*, *Roseomonas cervicalis* and *Roseomonas fauriae*). Currently, the genus Roseomonas comprises 15 valid species, including *R. aquatica, R. aerilata, R. cervicalis, R. gilardii, R. lacus, R. mucosa, R. terrae, R. stagni, R. vinacea, R. fauriae* and other unnamed genomespecies[4]. Although some *Roseomonas* isolates have been recovered from environmental sources (water and soil) or from non-sterile anatomical sites, including the respiratory and urogenital tracts[3], most strains have been isolated from potentially significant materials such as blood. It is known that *Roseomonas* has a low level of pathogenicity in humans, but can cause systemic infection in patients with underlying diseases or immunocompromised patients. The literature is very limited with regard to disease associations with this group of pink-pigmented bacteria[5,6].

CASE REPORT

A 68-year-old man, living in a rural area and a farmer, was admitted to Hospital São Paulo reporting that 02 weeks ago he had started with fever and generalized and unspecific malaise. With no other complaints or associated symptoms, the patient was admitted for investigation. Despite the patient's current condition having started 15 days ago, it should be noted that this is not the first episode of such clinical condition presented by him. In the period of 01 year, this was the fourth time that the patient had this condition and, previously, a Biliary Fistula with peri-pancreatic collection that had been drained by the General Surgery team had been found. Regarding the previous pathological history, the patient has Systemic Arterial Hypertension, Diabetes Mellitus 2, in addition to Hepatitis B, which progressed to Hepatocarcinoma and, finally, resulted in a liver transplant a few years earlier. The patient also has Chronic Kidney Disease undergoing renal replacement therapy with a Schilley catheter. Currently, he uses antihypertensive, Insulin NPH and immunosuppressant.

In his clinical examination, he was in a regular general condition, pale, afebrile and anicteric. Innocent abdomen with operative wound in good appearance and biliary drain with 18 ml of bilious content. Lower limbs unchanged. During the clinical investigation, an Abdominal and Pelvic Tomography was performed, which showed a new peri-pancreatic and peri-hepatic collection. He also performed an Upper Digestive Endoscopy that showed a Grade D Los Angeles Esophagitis and active duodenal

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ulcer. Laboratory tests showed an ongoing infectious process: blood count with anemia and neutrophilic leukocytosis (Hb 9.2g/dL; Ht 28.1%); leukocytes 14,000/uL (Bat 9% / Neutrophils 81%) and platelets 136,000/uL. Biochemical tests of renal function and altered liver injury markers (creatinine 6.55mg/dL; urea 184mg/dL; alkaline phosphatase 247U/L; gamma glutamyl transferase 279U/L). Electrolytes and bilirubin were normal (sodium 136mmol/L; potassium 4.8mmol/L; total bilirubin 0.42mg/dL and direct 0.32mg/dL). Peripheral blood and urine cultures were negative.

During the clinical investigation, a new drainage of the peripancreatic collection was performed and the material was sent to the laboratory in order to perform a new culture. Concomitantly, a new blood culture of peripheral blood and Schilley catheter was requested, and antibiotic therapy (carbapenem) was instituted, as the patient did not show improvement in the initial clinical picture. After 48 hours, the cultures remained negative, except for the Catheter culture, which was positive (Figures 1 and 2), and Gram stain was performed (Figure 3), which showed pink coccobacilli with a mucoid appearance and positive biochemical tests for catalase, oxidase and citrate (Figures 4, 5 and 6). The sample was used for identification, which was inconclusive and mass spectrometry identified the genus *Roseomonas* spp. Finally, the 16S gene sequencing was performed (Figure 7), the gold standard for identifying the genus and species of this bacterium, which showed a coverage of 100% and an identity of 99.16% for the strain of *Roseomonas* mucosa in comparison with the GenBank database provided by the National Center for Biotechnology Information (NCBI). On admission, the patient had the catheter changed, antibiotic therapy was maintained and received new guidelines on catheter handling.

DISCUSSION

Roseomonas spp is a genus of pink coccobacillus bacteria, which forms fastidious, elevated mucoid colonies, with slow growth, on average, 72 hours and has a single malformed flagellum[4]. It is worth mentioning that the identification of the infection of the genus is not performed by the usual bacteriological laboratory techniques, but by genetic sequencing in which there is an alteration in the 16S rRNA gene[4]. The clinical significance of *Roseomonas* species is not well understood, mainly because of the uncommon infections caused by this pathogen. In a retrospective

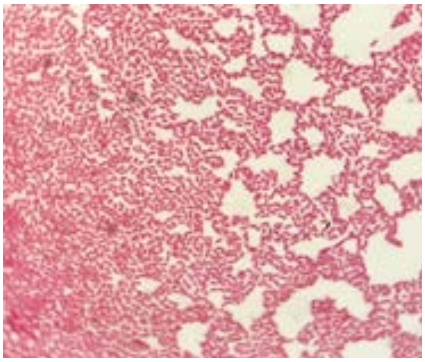
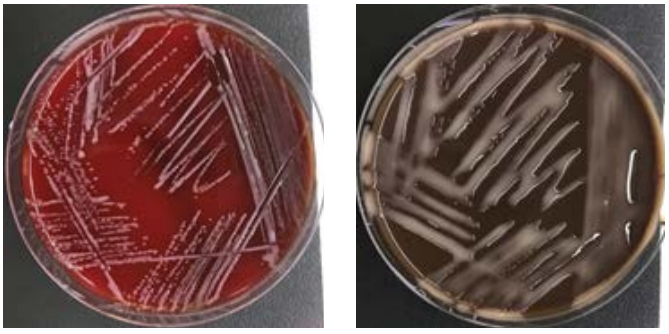


FIGURE 3 – *Microscopy (Gram): pink coccobacilli*



FIGURES 1&2 – *Bacterial Culture: Roseomonas spp*

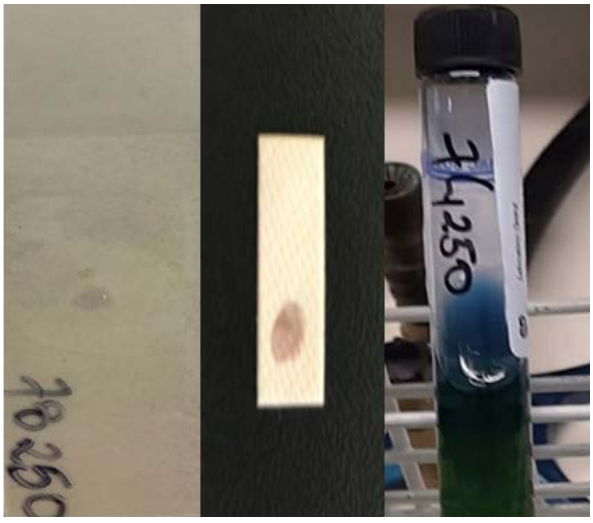


FIGURE 4,5,6 – *Biochemical Tests of Catalase, Oxidase and Citrate*

select all 100 sequences selected GenBank Graphics Distance tree of results MSA Viewer

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per Ident	Acc. Len	Accession
Roseomonas mucosa strain 191NCU262 16S ribosomal RNA gene, partial sequence	Roseomonas mucosa	1504	1504	100%	0.0	99.16%	1390	MT225639.1
Roseomonas mucosa strain B_MAR_18_176 16S ribosomal RNA gene, partial sequence	Roseomonas mucosa	1504	1504	100%	0.0	99.16%	1141	MN396252.1
Roseomonas mucosa strain AA31 16S ribosomal RNA gene, partial sequence	Roseomonas mucosa	1504	1504	100%	0.0	99.16%	1092	MN618721.1

FIGURE 7 – *Genetic Sequencing: Gene 16S*

laboratory analysis of 35 patients with *Roseomonas* isolates, only 60% were considered to be clinically significant pathogens[5] bacteria[3,5].

Catheter-related infections were the most common type of infection and nearly all patients with these infections had associated cancer. A common finding in this infection is that it appears to be a feature of patients with comorbidities or those who are immunosuppressed: 80% of reported patients had underlying disease, most commonly malignancy, followed by kidney disease, inflammatory bowel disease, diabetes mellitus, and others[5,6] . Further analysis reveals that in 88% of cases, the microorganism was isolated from the blood. Often, it was isolated from only one of several samples collected or from a central venous catheter and not from a peripheral blood sample. Other sites are rarer to find the bacteria, for example wounds, respiratory tract or peritoneum[5-8]. The genus *Roseomonas* spp cannot be identified in the routine laboratory by usual microbiological methods and requires sequencing of the 16S rRNA gene as a gold standard method[8].

Although different antibiotic regimens were administered, reports indicate that all patients had favorable outcomes after removing their catheters. These findings are consistent with those reported and suggest the low pathogenicity of *Roseomonas* species[6,9,10]. Another common feature of this Gram-Negative organism is its pattern of susceptibility to antibiotics, especially with regard to its behavior with cephalosporins, which appear to be ineffective against any of the *Roseomonas* species. It was noted that all six species exhibited 96% resistance to first, second and third generation cephalosporins[3]. There are no data on susceptibility to fourth-generation cephalosporins such as cefepime[3,7]. The bacterium has universal susceptibility to imipenem, amikacin, gentamicin, tobramycin and tetracycline[3,7,8]. There are no data on susceptibility to the newer quinolones, but 65% of the isolates studied were susceptible to ciprofloxacin and all other isolates that were tested were also susceptible to this antibiotic[3].

CONCLUSION

Although the microorganism can cause disease, it has a low pathogenicity and, even in individuals with comorbidities or immunosuppressed individuals, its mortality rate is also low. Further studies detailing the association between the *Roseomonas* genus with specific disease processes are needed to delineate their role as human pathogens.

Authors' Contribution: Mirela Carla da Costa Baretta - performance of laboratory tests; Thomás Cardoso Chagas-Neto - realization and structuring of the case; Leandro da Silva Fernandes and Adagmar Andriolo - case structuring, discussion and final writing of the manuscript. All authors read and agreed to the final wording.

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