PERITONEAL DIALYSIS: INFECTIOUS AGENTS OR NORMAL MICROBIOTA

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INTRODUCTION and AIMS

Peritoneal dialysis (PD) is a home-based renal replacement therapy, currently treating 11% of the global dialysis population across 130 countries worldwide.

Infection-related morbidity remains one of the major complications in peritoneal dialysis (PD) patients. In our center there is a low but persistent number of PD related peritonitis every year, mainly attributed to *Staphylococcus* and *Pseudomonas* species (spp.). This work aimed to characterize possible sources of peritonitis agents focusing on normal microbiota.

Keywords: Peritoneal Dialysis: Peritonitis, Catheter exit-site (CES) infection.

RESULTS

Table 1: Characterization of PD patients.

	PD patients
Average age	47±12 years
Mean duration of PD	12.8±15.6 months
Intra-oral exame	poor oral hygiene ; high index of decayed, missing or filled teeth
With previous Peritonitis Episodes	26.0%
Staphylococcus spp.	37.5%
With previous CES infection Episodes	55.5%
Staphylococcus spp.	34.4%
Pseudomonas spp.	37.5%

Table 2: Prevalence of PD patients colonization by *Staphylococcus* and *Pseudomonas* in saliva, nasal cavity and catheter exit-site.

	Saliva	Nasal Cavity	Catheter exit-site
Staphylococcus	91.7%	100%	51.8%
Pseudomonas	2%*	-	-

Table 3: Microorganism frequency in the saliva, nasal cavity and catheter exit-site of PD patients.

Staphylococcus species	Saliva	Nasal cavity	Catheter exit-site
S. epidermidis	75.0%	85.2%	33.3%
S. aureus	20.8%	18.5%	0%
S. warneri	12.5%	3.7%	0%
S. hominis	4.2%	3.7%	3.7%
Other *S.* species	41.7%	33.3%	22.2%
Micrococcus luteus	4.2%	3.7%	0%

Thirteen different *Staphylococcus* species were found, as well as one species from other genus.

Interestingly, 60% of the saliva samples presented simultaneously 2 or more *Staphylococcus* spp. and in 7.4% of these patients the same microorganism was identified in the 3 body locations examined.

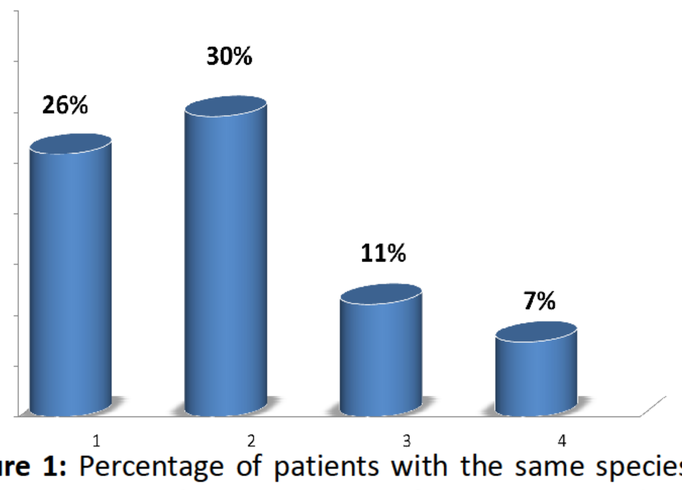

Figure 1: Percentage of patients with the same species as the peritonitis or catheter exit site infectious agents detected in different body locations.

The *Staphylococcus* spp. responsible for a previous infectious episode was identified in the normal microbiota of 25.9% of saliva samples, in 29.6% of nasal cavity samples and in 11.1% of CES samples.

Pseudomonas colonization was detected in the saliva of only one PD patient and was not related to a previous *Pseudomonas* infection.

MATERIALS & METHODS

A group of 27 PD patients of S. João Hospital was studied. Microbiological analysis of saliva, nose and catheter exit-site comprised the isolation and identification of *Staphylococcus* and *Pseudomonas*. The following strategies were employed for microbial identification:

- ***Staphylococcus* spp.**- growth in Mannitol-Salt medium, gram-staining, catalase-test followed by sequencing analysis of *DnaJ* or Multi-test system API 32 STAPH (Biomerieux®);
- ***Pseudomonas* sp.-** Cetrimide selective agar 10 mL/L glycerol, gram-staining and oxidase-test.

Staphylococcus and *Pseudomonas* normal colonization of PD patients were correlated to previous peritonitis episodes and CES infections.

CONCLUSIONS

Our results suggest that Staphylococci PD-related infections may be strongly related to normal human microbiota, since the *Staphylococcus* spp. most commonly found in the saliva, nasal cavity or CES of our population corresponded to the most prevalent spp. associated with infections. No correlation was found between PD-related infection and normal *Pseudomonas* colonization, suggesting that *Pseudomonas* infections may occur through other routes of infection.

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