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# Patients colonization and infection in wards after discharge from a polyvalent intensive care unit with selective digestive decontamination: preliminary results

C Sánchez Ramirez<sup>1\*</sup>, R Prada Osorio<sup>1</sup>, CF Lübbe Vazquez<sup>1</sup>, R Argandoña Primicia<sup>1</sup>, J Cabrera Arrocha<sup>1</sup>, F Artiles Campelo<sup>2</sup>, S Ruiz Santana<sup>1</sup>

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**POSTER PRESENTATION** 

# **Objectives**

To analyze the colonization and infection rate of patients after discharge from an the Intensive Care Unit (ICU) with Selective Digestive Decontamination (SDD).

## Methods

In a polyvalent ICU of 30 beds, from October 7<sup>th</sup> to December 30<sup>th</sup> 2014, SDD was applied to all patients requiring endotracheal intubation for more than 48 hours. We administered during the first four days intravenous cefotaxime plus enteral solution and a paste with colistin, tobramycin, and nystatin every 8 hours. Oropharyngeal, rectal and nasal swabs were obtained on admission, whether or not they received SDD and once weekly. To assess in the wards, after ICU discharge, colonization and development of hospital infections with germs originated in the ICU, pharyngeal and rectal swabs on the 3<sup>th</sup> and 10<sup>th</sup> day after ICU discharge were obtained and analyzed. Categorical variables were summarized as frequencies and percentages and number in means and standard deviations (SD) or median with interquartile ranges (IQR).

### Results

Forty one patients were analyzed, 26 of them received SDD (63,4%) and 24 of them (92.3%) received standard SDD. Demographic data, and admission types are shown in Figure 1.

Isolates with germs at ICU discharge and at hospital ward are shown in Figure 2.

The most frequent findings were negative isolates. Those who were positive at ICU discharge remained positive, and the negative ones remained negative except in 2 patients (one patient with a yeast at discharge changed to *Klebsiella pneumoniae*, and the other one changed from normal flora to *Pseudomonas aeruginosa*). There was only 1 patient who developed an infection in the ward originated in the UCI independently of receiving or not SDD. The patient was colonized by *Klebsiella pneumoniae* in the ICU and later developed a *Klebsiella pneumoniae* urinary infection in the hospital ward. The most frequent isolated germs at discharge and in the ward were *Pseudomona aeruginosa* and *Klebisella pneumoniae* (9%).

#### Conclusions

All but two of patients the investigated patients receiving SDD in ICU did not have any change in the etiology of colonization after ICU discharge. Only another patient developed an attributable multi-resistant ICU infection.

#### Authors' details

<sup>1</sup>University Hospital of Gran Canaria Dr Negrín, Intensive Care Unit, Las Palmas de Gran Canaria, Spain. <sup>2</sup>University Hospital of Gran Canaria Dr Negrín, Microbiology Department, Las Palmas de Gran Canaria, Spain.

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<sup>1</sup>University Hospital of Gran Canaria Dr Negrín, Intensive Care Unit, Las Palmas de Gran Canaria, Spain

Full list of author information is available at the end of the article



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N Age, years Male/Female, n SDD, n

	41	
	61.6 ± 12.1	
1	32/9	
	26 24 (92 3)	
	2 (7.7)	
	18.3 ± 6.3	
	115 + 42	

Mixed, n, %	2 (7.7)
Apache II	18.3 ± 6.3
Glasgow Coma Score	11.5 ± 4,3
Trauma patient, n (%)	1 (2.4)
Coronary patient, n (%)	11 (26.8)
Patients, n (%)	0.000
Medical	23 (56.1)
Emergency surgery	5 (12.2)
Scheduled surgery	12 (29.3)
ICU stay, days	15.6 ( 9.5; 17.2
Hospital stay, days	35.5 (17;54)
Ward stay in ICU discharged patients, days	16.4 (7;23)
ICU Mortality	0
Hospital mortality, n (%)	1 (2.4)
Previous surgery. n (%)	16 (39)
Urgent surgery n (%)	6 (14.6)
Diabetes mellitus n (%)	14 (34.1)
Cirrhosis n (%)	2 (4.9)
COPD n (%)	3 (7.3)
Renal failure n (%)	8 (3.8)
Neoplasia n (%)	1 (2.4)
Renal replacement therapy n (%)	7 (17.1)
Parenteral nutrition n (%)	4 (9.8)
Immunosuppression n (%)	2 (4.9)
Neutropenia n (%)	0
Malnutrition n (%)	3 (7.3)

### Figure 1 Patients data.

Type of germs	R 8 01 019	Rectal Swab at ICU discharge		Pharyngeel swab at ICU discharge		Roctal swab day 3 hospital ward		Pharyngeel swab day 3 hospital ward		Rectal swab day 10 hospital ward		Phatyngoal swab day 10 hospital ward	
	p	8		*	F	5		*		5	=		
At hospital discharge	0	0	0	0	3	7.3	7	17	14	34.1	14	34.1	
Normal Flora	26	63.5	32	78.1	26	63.4	29	70.7	19	45	27	65.8	
Enterococcus Faecals	0	0	0	0	0	0	1	2.4	0	0	0	0	
Acinetobacter Baurmanii	0	0	1	2.4	0	0	0	0	0	0	0	0	
Klebsielle preumoniee ESBL	4	9.8	0	0	5	12	0	0	3	7.3	0	0	
Oxacilin Resistant Streptococcus ES8L	2	4.9	0	0	1	2.4	0	0	0	٥	0	0	
Escherichia coli ESBL	2	4.9	1	2.4	2	4.9	0	0	4	9.8	0	0	
Pseudomonas aeruginosa	2	4.9	0	0	3	7.3	0	0	0	0	0	0	
Multidrug resistant Pseudomonas aeruginosa	0	0	1	2.4	0	0	1	2.4	0	0	0	0	
Achromobacter sylosoxidans	1	2.4	0	0	1	2.4	0	0	0	0	٥	0	
MRSA	0	0	1	2.4	0	0	2	4.9	0	0	0	0	
Yeasts	4	9.8	3	7.3	0	0	1	24	1	2.4	0	0	
Oxacilin Resistant Streptococcus	0	0	0	0	0	0	0	0	0	0	0	0	
Total patients with isofates	41	100	41	100	41	0	41	100	41	100	41	100	

Figure 2 Germs.

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