cultures from sterile isolates, indicating infection. Positive MRSA and CRKP colonization or infection were identified, and patient notes were collected. Our exclusion criteria included patients with a of stay of <48 hours and patients with MRSA or CRKP before admission. **Results:** Of 3,641 of persons admitted 2,801 cases fit the study criteria. Overall, 161 (5.3%) were colonized or infected with MRSA alone, 215 (7.67%) were colonized or infected with CRKP alone, and 15 (0.53%) were colonized or infected with both MRSA and CRKP. In addition, 10 (66.6%) of patients colonized or infected with MRSA and CRKP died. Average length of stay of patients who died was 50 days. **Conclusions:** The results of this study demonstrate that MRSA and CRKP cocolonization and coinfection is associated with high mortality in patients within the ICU and HDU units. Patients admitted to the ICU and HDU with an average length of stay of 50 days are at a higher risk for cocolonization and coinfection with MRSA and CRKP. Stronger IPC measures must be implemented to reduce the spread and occurrence of MRSA and CRKP.

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Colonization and Genetic Diversity of MRSA Among ICU Patients and Healthcare Workers From a Hospital of Northeastern India

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Background: The prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) is diverse in different geographic regions, and transmission of MRSA in hospital settings occurs either through the patients or asymptomatic healthcare workers who MRSA colonized in the nares and thus act as a potential reservoir of infection for susceptible patients. **Methods:** *S. aureus* isolates were collected from ICU patients and healthcare workers at Gauhati Medical College and Hospital, Assam, India, from May 2010 to April 2015. Premoistened swab samples were obtained from the ICU patients from 4 different sites (ie, nares, axilla, groin, and perianal region) within 48 hours of admission. For healthcare workers (HCWs) a nasal swab was obtained. The isolates were identified by phenotypic and genotypic methods using CLSI guidelines and PCR (fem B, MecA, and PVL). The antibiograms were obtained using a Vitek 2 system. **Results:** For 84 patients admitted to the ICU, swab samples were obtained from various sites, and *S. aureus* was observed in 34 samples (40.5%). Among the isolates, 13 (38%) were MRSA and 21 (62%) were methicillin-susceptible *Staphylococcus aureus* (MSSA). Among the HCWs from the ICU, growth of *S. aureus* was obtained in 10 of 30 samples (33.34%), of which 3 (30%) were MRSA and 7 (70%) were MSSA. *S. aureus* isolates were genotypically identified as fem B among colonized patients (40.5%) and HCWs (33.34%). MRSA (mecA positive) was detected in 3% of colonized patients and 30% of HCWs. Among the ICU patients, 78.56% were PVL-positive *S. aureus*: 21.42% were PVL-positive MRSA and 57.14% were PVL-positive MSSA. Multilocus sequence typing of the 7 housekeeping genes against 2 *S. aureus* isolates showed the presence of ST1428, which had not been reported in India, whereas the other sequence was entirely novel. The MDR rates were 68% and 75% among ICU patients and HCWs, respectively, and all the strains were mupirocin sensitive. The *S. aureus* isolates were significantly proportional among HCWs compared to the colonized group ($P = .031$). **Conclusions:** The study results show a high prevalence of PVL-positive MSSA and MRSA among ICU patients. This finding indicates its transmission among hospitalized patients through the HCWs, for which constant monitoring of the pathogen, particularly its phenotypic and genotypic variations and antimicrobial resistance pattern, is needed to develop effective strategies for infection prevention.

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Colonization of Resistant Microorganisms in Renal Transplants

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Background: Kidney transplant recipients are a group of patients at risk for healthcare-related infections. The results of this study make an important clinical contribution and contribute to findings options to decrease the infection-related morbidity and mortality that affects this patient population. **Objectives:** We evaluated the prevalence of colonization by multidrug-resistant bacteria, *Klebsiella pneumoniae* carbapenemase (KPC)–producing bacteria, vancomycin-resistant enterococci (VRE), and methicillin-resistant *Staphylococcus aureus* (MRSA) in renal transplant patients; we identified the infection rate, morbidity, and mortality in this population. **Methods:** Prospective cohort study was conducted at the Kidney and Hypertension Hospital from 2012 to 2015. This project was approved by the Unifesp Research Ethics Committee (no. 1630/11) and an informed consent form was obtained from patients included in the study. **Study protocol:** Data collection was performed in 2 phases: within the first 24 hours after transplantation and 7 days after transplantation. For all included patients, the following data were collected: identification data, clinical data, and laboratory tests of the first day in the study. All included patients (colonized or not) were followed prospectively for 6 months or until treatment change or death. **Results:** The study included 200 renal transplant patients in accordance with the inclusion and exclusion criteria. We observed that 76 (38%) patients included in our sample were colonized; 8% *S. aureus*, 11% *Enterococcus*, and 19% *K. pneumoniae*. We verified the presence of concomitant colonization of 1 or more of these pathogens. The most prevalent concomitance identified in our population was *E. coli* and *K. pneumoniae*. We identified the presence of diabetes and diabetes associated with hypertension as risk factor for colonization. Thus, patients with more systemic complications may be at risk for colonization by multidrug-resistant bacteria. Another risk factor for colonization was antibiotic use in the 6 months prior to transplantation. Transplant-related outcomes

Table 1: Characteristics of Patients with MRSA and CRKP

Demographics	MRSA alone n-161	CRKP alone n-215	MRSA & CRKP n-15
Age			
18-35	53	36	5
36-50	25	85	7
Above 50	83	94	3
Sex			
Female	72	80	7
Male	89	135	8
Length of Stay(Average)	92	110	9
>50 days	69	105	6
<49 days			

Fig 2: MRSA, CRKP in ICU and HDU 2013-2017

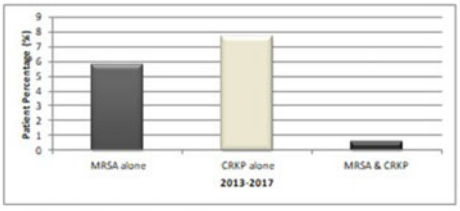

Fig 1: Total Patients on ICU and HDU during the period of Study

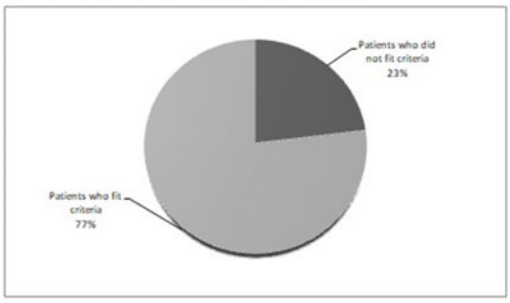

Fig3: MRSA & CRKP co-colonization and co-infection Death 2013-2017

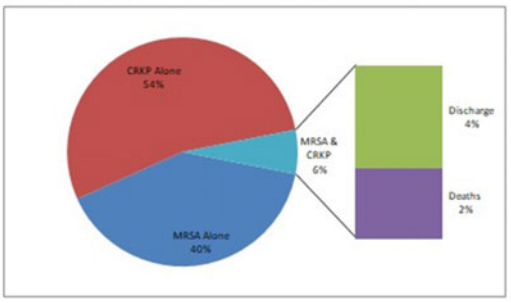

Fig. 1.

were length of stay after transplantation, delayed graft function (ie, dialysis after the transplantation) and postoperative care in an intensive care unit. At the 6-month follow-up, we identified urinary infection and surgical site infection as risk factors. One death occurred due to stroke in the group of colonized patients, unrelated to infectious causes. **Conclusions:** These results show fundamental aspects for health professionals for bacterial characterization, transmission, and resistance mechanisms and, mainly, tools for prevention and control of multidrug-resistant bacteria from patients colonized under conservative treatment before the complexity of high-risk procedures begins, such as dialysis and transplantation to reduce morbidity and mortality.

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Colonization With Antibiotic-Resistant Gram-Negative Bacteria in Population-Based Hospital and Community Settings in Chile

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Background: Estimating the burden of intestinal colonization with antibiotic-resistant gram-negative bacteria (AR-GNB) is critical to understanding their global epidemiology and spread. We aimed to determine the prevalence of, and risk factors for, intestinal colonization due to AR-GNB in population-based hospital and community settings in Chile. **Methods:** Between December 2018 and May 2019, we enrolled randomly selected hospitalized adults in 4 tertiary-care public hospitals (Antofagasta, Santiago, Curico and Puerto Montt), and adults residing in a community-based cohort in the rural town of Molina. Following informed consent, we collected rectal swabs and epidemiological information through a standardized questionnaire. Swabs were plated onto MacConkey agar with 2 μg/mL ciprofloxacin or ceftazidime. All recovered morphotypes were identified, and antibiotic susceptibility testing was performed via disk diffusion. The primary outcome was the prevalence of colonization with fluoroquinolone (FQ)- or third-generation cephalosporin (3GC)–resistant GNB. The secondary outcome was the prevalence of colonization with multidrug-resistant (MDR) GNB, defined as GNB resistant to ≥3 antibiotic classes.