surrounding the blαNDM-1 showed that at least a remnant of insertion sequence ISAba125 was methodically present upstream of the blαNDM-1. The entire ISAba125 element was identified upstream of the blαNDM-1 gene in most isolates. Downstream of the blαNDM-1, the bleMBR gene was quite systematically identified. The variable region of IntI1 presented different combinations of aac(6′)-Ie-aph(2′)-IIIa, dfrA1′ & aph(3′′)-Ila and dfrA14, but no NDM-1.

**Conclusion:** This work underlines how efficient the spread of the carbapenemase gene could be among Enterobacteriaceae. It also throws light on the association of multiple resistances and genetic diversity of the NDM-1 in a neonatal unit of a developing country.

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**Comparison of antimicrobial resistance determinants and Staphylococcal Cassette Chromosome mec elements of Staphylococci isolated from human and veterinary origin**

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**Background:** Staphylococcal species causing human infections have developed resistance to almost all the antimicrobial agents in clinical use today. In recent years, there has been an increase in reports of the isolation of multidrug-resistant (MDR) Staphylococcus spp. in veterinary medicine. The development of MDR is primarily due to the acquisition of multiple antibiotic resistance genes and its association with mobile genetic elements such as SCCmec. Asymptomatic colonization with MDR staphylococci in animal handlers represents a major risk factor for transfer of antibiotic-resistant determinants from animals to humans or vice versa. Hence, this study is aimed to compare the distribution of resistance determinants and SCCmec amongst isolates from human and veterinary origin and carrier isolates of animal handlers.

**Methods & Materials:** A total of 144 staphylococcal isolates were included for the study, viz., 48 clinical isolates of veterinary origin [Group-I], 47 human carrier isolates from animal handlers [Group-II] and 49 clinical isolates of human origin [Group-III]. Antibiotic sensitivity testing was carried out for routinely used antibiotics. Detection of determinants implicating resistance to β-lactams [blaZ, mecA], macrolides [ermA, ermC, msrA], tetracyclines [tetK, tetM], aminoglycosides [aac(6′)-Ie-aph(2′)-IIIa, ant(4′)-Ia, aph(3′)-IIla] and trimethoprim (dfrA) were amplified using PCR. Further, SCCmec typing was done to determine the genetic diversity of the isolates.

**Results:** Out of 144 isolates, 78 isolates (54%) were methicillin resistant. Resistance to penicillin was highest (72%) followed by quinupristin (43%), trimethoprim-sulfamethaxazole (41%), tetracycline (38%), erythromycin (33%), ciprofloxacin (30%), clindamycin (24%) and gentamicin (16%). Percentage of MDR strains was highest in Group-III (61%) followed by Group-II (53%) and Group-I (46%). blaZ, mecA, ermC, msrA & tetK showed highest prevalence in human carrier isolates, while dfr, aac(6′)-Ie-aph(2′)-IIla and aph(3′)-IIla were predominant in human clinical isolates and ermA in animal clinical isolates. Isolates of Group I & Group II predominantly exhibited SCCmec type I while, SCCmec type V in Group I. Combinations of SCCmec types were exhibited by isolates of Group II.

**Conclusion:** Amongst the study groups, carrier isolates from animal handlers are found to carry highest resistance determinants and combinations of SCCmec types indicating their acquiring these from both human and veterinary source and are potentially at risk of infections.

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**The impact of pre-hospital antibiotics on blood culture yields in a low resource setting**

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**Background:** Bacterial sepsis and severe focal infections are common admission diagnoses amongst Gambian children admitted to the Edward Francis Small Teaching Hospital (EFSTH) and the Medical Research Council (MRC) Unit, The Gambia. However, blood cultures are frequently negative. To understand the causes of the low blood culture yields we documented history of antibiotic use and measured antimicrobial activity in clean catch urine collected at the time of admission or before the start of antibiotic therapy.

**Methods & Materials:** Children aged between 1 month to 18 years presenting with sepsis or severe focal infections were recruited into the European Union Childhood Life-threatening Infectious Diseases Study (EUCLIDS) at the EFSTH and MRC wards. Participants were interviewed for history of antibiotic use in the last seven days. A sterile Whatman No.1 filter paper disc (6mm) was inoculated with 20 μl of patient urine collected pre-antibiotics and placed on a Mueller–Hinton agar plate pre-streaked with antibiotic sensitive Staphylococcus aureus (ATCC 25923 strain). After 18-24 hrs incubation at 35–37°C, growth inhibition around the disc was considered evidence of pre-hospital antibiotic exposure.

**Results:** Of 253 cases recruited, 128 (40%) were from MRC and the rest from EFSTH. Half of the cases were less than five yrs old. 182 (72%) were diagnosed with sepsis or focal infections with no organism identified. An organism was identified in 71 (28%) cases with the most common isolates Staphylococcus aureus 26 (35%), Streptococcus pneumoniae 13 (18%) and Neisseria meningitidis 10 (14%). Patients with osteomyelitis and meningitis were most likely to have a positive culture (80% and 46% respectively). The antimicrobial results did not tally with patient reports of antibiotic use: only 91 (36%) reported antibiotic use while antimicrobial activity was detected in 197 (78%).

**Conclusion:** A high rate of pre-hospital antibiotics in this setting makes conventional microbiology a poor diagnostic tool for sepsis and focal infections. The urine antibiogram assay is a sensitive