**Conclusion:** The antibiotic sensitivity of the common microbes differed significantly between CSOM and CRS with CSOM subjects in South Indian Population. The present study warrants the need for evaluation of antimicrobial susceptibility profile of the causative microbial pathogens before administration of antibiotics to treat CRS with CSOM in particular.

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**The emergence of cotrimoxazole and quinolone resistance in Shigella sonnei**

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**Background:** The emergence of cotrimoxazole resistance has been a dominant and consistent character in our isolates of Shigella sonnei. To study the behaviour of these emerging strains and characterise mechanisms of resistance to cotrimoxazole & ciprofloxacin the following study was performed.

**Methods & Materials:** Isolates of *Shigella sonnei* confirmed by standard methods from 2012 to 2015 were subjected to antimicrobial susceptibility testing using the Kirby Bauer method as per Clinical laboratory standards institute and PCR for the detection of virulence genes. The degree of relatedness between the isolates was assessed by ERIC PCR followed by gel image analysis. Dendrogram was generated using Pyleph. PCR was carried out to determine the mechanisms of resistance to cotrimoxazole and ciprofloxacin.

**Results:** Of 34 *Shigella sonnei* isolates, cotrimoxazole resistance was common (94.1%) followed by ciprofloxacin (47%). Majority carried the *ipaH* gene (97%) followed by *tul* (17.6%), *sen* (11.7%), *set 1 & set2* (5.8%). No six element was found. ERIC–PCR analysis of the isolates resulted in four major ERIC groups labelled ERIC group I, II, III and IV. Type III was the dominant (44.1%) type. Majority harboured *dfhr1* (94.1%), *sul2* (85.2%) followed by *sul3* (55.8%), *sul1* (11.7%). Two isolates that were resistant to cotrimoxazole were negative for the sul genes but harboured the *dfhr1* gene. All the phenotypically ciprofloxacin resistant isolates (47%) were positive for presence of *gyr A, gyr B, parC and parE*. Also, *qnrB* was the most prevalent PMQR gene (93.7%) while, *qnrC* was positive in 18.7% of isolates. None were positive for *qnrA* and *qnrS*. Two (0.1%) of the isolates were positive for *aac(6’)-Ib* gene. The *qepA* gene regulating the efflux pump was negative in all the isolates studied. One isolate that was susceptible to all antibiotics tested negative for all the genes.

**Conclusion:** The emergence of *Shigella sonnei* with a characteristic sulphamamide resistance needs to be addressed further in detail and the increasing trend of resistance to quinolones is a point of concern. This study also shows the emergence of a particular ERIC type in the background of this evolving resistance pattern.

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**Carriage of multiple gene cassettes mediated extended spectrum cephalosporinase within diverse incompatibility (Inc) plasmid groups among gram negative rods in a tertiary referral hospital of India**

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**Background:** Extended spectrum β-lactamases pose to be major health problem in hospital settings worldwide. Infection with ESBL producing organisms result in poor clinical outcome, overdue initiation of suitable antibiotic treatment, longer hospital stays and greater hospital operating cost. Management of treatment against these strains become complicated when the resistant determinants are associated with integron and horizontally transferable due to their location within plasmid. In this study, we report multiple gene cassettes mediated extended spectrum cephalosporinase within diverse Inc plasmid groups among gram negative rods for the first time in India.

**Methods & Materials:** A total number of 458 clinical isolates of gram negative rods were collected during November 2011 to October 2013 from Silchar Medical College and Hospital. ESBL status was detected by phenotypic screening as per CLSI criteria and multiplex PCR assay followed by sequencing. Genetic environment was determined by integrase gene PCR and location of *bla₆ESBL* within gene cassette was investigated by 59 base element PCR and sequencing. Plasmid transferability was done by transformation and conjugation while incompatibility profiling was done by PCR based replicon typing. DNA fingerprinting of isolates was done by ERIC and REP PCR.

**Results:** A total of 56 isolates were found harboring *bla₆ESBL* by PCR and sequencing. All of them were carrying class I integron and *bla₆ESBL* was found to be located within gene cassette and conjugative plasmid. Further, PCR based replicon typing established presence of diverse Inc plasmid types viz. FIA, FIB, P, FrepB, K, B/O, I1/Iy and Y. The isolates showed high MICs against cephalosporins (≥256 µg/ml) and monobactam (≥256 µg/ml) but was found in susceptible range against Ertapenem drug. The isolates were found clonally unrelated.

**Conclusion:** The study revealed presence of gene cassette mediated *bla₆ESBL* among gram negative rods within hospital environment. Presence of *bla₁₆ESBL* in diverse Inc plasmid groups suggests their diverse source of acquisition. Current study insists vital