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Bacterial infections and emerging resistance in renal transplant recipients

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Background: Renal transplantation is frequently complicated by bacterial infections in the scenario of immunosuppression, altered metabolism and interventions resulting in prolonged morbidity. Subdued clinical presentation, antimicrobial resistance and toxicity tend to jeopardize the outcome of transplantation. This study conducted at tertiary care apex transplant centre highlights colonization, clinical infection and antimicrobial resistance patterns in Renal Transplant Recipients (RTR) in comparison with nephrology ward in-patients (NIP).

Methods: Infection and antimicrobial resistance patterns in 65 RTR in comparison with 80 NIP were studied. Clinico demographic and transplant parameters were noted. Infection screening in the post-transplant period along with antimicrobial susceptibility were used to analyze data in a post-transplant time frame.

Results: Culture positivity timeline was dominated by post-surgical infections in the first week post- transplant. Urinary infections followed by blood stream infections were noted. Infection profile included simultaneous poly microbial, prolonged and widespread infections. Multiresistant organisms producing beta lactamases and extended spectrum beta lactamases were isolated.

Conclusion: Transplant recipients remain prone to bacterial infections with multiresistant organisms which may persist due to immunosuppression, altered metabolism and toxicity and further contribute to nosocomial hazard. Infection control may be strengthened at avoidance of donor derived infections, surgical complications, epidemiologic exposures, antimicrobial prophylaxis and anti-infection engineering. Antimicrobial stewardship, outbreak and epidemic preparedness should be ensured.

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Analysis of type IV pilus biogenesis genes between *Neisseria meningitidis*, *Neisseria Gonorrhoea, Pseudomonas aeruginosa* and *Vibrio cholerae*

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Type IV pili are long, thin and flexible filaments which play an important role in bacterial pathogenesis. In current study, structural and sequences similarities of type IV pili proteins and their associated proteins were analysed in *Pseudomonas aeruginosa, Vibrio cholerae, Neisseria meningitidis* and *Neisseria gonorrhoeae. P. aeruginosa* and the pathogenic *Neisseria* species possess pil-genes for structural and assembly proteins of type IV pili. In opposite to *P. aeruginosa* and *Neisseria*, *V. cholerae* expresses toxin-co-regulated pili (tcp). In *V. cholera* typical type IV pil genes are often pseudogenes. The major pilin subunit of *P. aeruginosa* and *Neisseria* contains a short signal peptide region whereas pilin of *V. cholera* lacks this type of signal peptide. Pre-pilins are cleaved by signal sequence peptidases which are similar in all the three bacterial species. The secretin PilQ of *P. aeruginosa* and pathogenic *Neisseria* are more similar as compared to the secretin TcpC in *V. cholerae*. A set of assembly proteins denoted PilM, PilN, PilO and PilP show homology between *Neisseria* and *P. aeruginosa*. In *V. cholerae*, these proteins have functional counterparts denoted TcpD, TcpR and TcpS. The pilus retraction and assembly ATPases, PilT, PilU and PilB/PilF are homologous in *P. aeruginosa* and *Neisseria* whereas *V. cholerae* possesses only one ATPase called TcpT. In this work the type IV pilus machinery of *P. aeruginosa* shows high resemblance with the type IV pilus machinery of pathogenic *Neisseria* whereas the pilus assembly machinery in *V. cholera* is different. Finally, the role of type IV pili in biofilm formation of *P. aeruginosa V. cholerae,* and *Neisseria* is summarized.

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