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## Emerging bacteria in a tertiary healthcare set up

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**Background:** Emerging organisms are organisms that have newly appeared in a cohort/population or have existed but are rapidly increasing in incidence, geographic or host range. While, one-tenth of all infectious diseases are attributable to emerging organisms, operationally defining an organism as emerging is a subjective endeavor. As emerging organisms sporadically affect a relatively small percentage of population, they are not studied at large. This study was aimed at studying the characteristics of emerging bacteria at an Indian tertiary care hospital.

**Methods:** 16918 positive isolates obtained from 66323 processed samples during 2013-14 were included. Identification percentage >85% along with inbuilt standards for identification comparison were considered for final validation through automated systems. Non repeat positive cultures were interpreted in conjunction with colony characteristics, cellular morphology, disc-diffusion antifungal susceptibility patterns, clinical correlates and environmental surveillance. The frequency of isolation, sources, referring centers, susceptibility profiles and phenotypic characteristics. A literature search was done to identify reports on human pathogenicity and yeasts and algae reported less than 100 times on PubMed were defined as emerging.

**Results:** 13498 (79.78%) Gram negative and 3254 (19.23%) Gram positive bacteria were isolated from 16918 isolates, of which 445 (2.63%) were emerging bacterial isolates. Emerging *Enterobacteriaceae* comprised of 40 species in 15 genera, non-fermenters 33 species in 21 genera and Gram-positive bacteria 45 species in 14 genera. The emerging bacteria were isolated from multiple sources and centers. Most of the isolates were multi-resistant while only a few were susceptible to commonly used drugs. Environmental surveillance was not corroborative.

**Conclusion:** Emerging bacteria have the potential to infect compromised hosts, posing difficulty in management due to multidrug resistance. They are likely to evade routine identification or be disregarded as non-contributory. Astute efforts directed at identification of emerging isolates, decisions by clinical microbiologists and treating physicians and containment of infection are required.

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