**TITLE: DNA FINGERPRINT USING (GTG-5)-PCR IN COMMUNITY-ASSOCIATED AND HOSPITAL-ASSOCIATED *PSEUDOMONAS AERUGINOSA* STRAINS.**

**Authors:** Tanabe, I. S. B.[1]; Pedrosa, B. C. M. [1]; Kamiya, R. U. [2]

**Institution:** Universidade Federal de Alagoas, Campus A.C. Simões, Av. Lourival Melo Mota, s/n, Tabuleiro dos Martins, CEP:57072-900, Maceió - AL.

**Resume:**

*Pseudomonas aeruginosa* is a opportunist pathogen commonly associated with community and nosocomial infections, in immunocompromised individuals. **Objectives:** The objective of this study was to analysis the genotypic diversity of 19 *P. aeruginosa* isolated from 19 patients admitted in public hospital of Maceió, AL (hospital-associated-HA) and 16 *P. aeruginosa* isolated from oral cavity of 10 individuals diagnosed with oral or cervical-thoracic cancer (community-associated-CA) using the (GTG)5 – PCR. **Methodology:** Biochemical tests were used to identify *P. aeruginosa* isolates. The bacteria were isolated in Cetrimide Agar and the species was confirmed by biochemical tests, as well as Gram, catalase, oxidase, pyoverdin production, motility test, triple sugar iron test and sodium citrate assimilation. The DNA extraction followed the SDS 10% method and the PCR products were submitted to electrophoresis in agarose gel at 2% and photographed in UV transilluminator. The amplicon most prevalent were marked in polarized array in *Winclada* software and *TNT* software to generate the tree and reorganized with *"Most Foals"* option. The Simpson's index of diversity was used to test the discriminatory index of technique. **Results:** The discriminatory index of (GTG)5-PCR was about 97%. The dendogram showed larger consensus and distributed CA-*P.aeruginosa* and HA-*P. aeruginosa* in 10 distinct clusters. The tree analysis showed that four individuals carry more than one genotype of CA-*P. aeruginosa* in the oral cavity. HA-strains had varied distribution in the tree and genetic diversity higher than CA-*P. aeruginosa*, although epidemiological unrelated individuals share similar genotypes in hospital environment, suggesting cross-infection or higher genetic proximity with the same ancestor. **Conclusion:** Although the technique (GTG) 5-PCR has provided high capacity discriminatory, it is necessary to associate it with other typing methods to obtain more accurate results in epidemiological studies.

**Key words:** *Pseudomonas aeruginosa*, DNA fingerprint, (GTG)5-PCR, Infections, Genotyping.

**Acknowledgment:** CNPq, FAPEAL, MS and SESAU (PPSUS process number: 60030.000710/2013 and PPP process number 20110830-011-0025-002)