

Título: ANALYSIS OF RESISTANCE TO ANTIMICROBIAL AND DETERMINATION OF PHYLOGENETIC GROUPS IN *Escherichia coli* ISOLATED FROM LAGUNA TRAMANDAÍ, RS

Autores: ¹Amorim, L. M.; ¹Rodrigues, B. L.; ¹Meneghetti, K. L.; ¹Chaves, M. A e ¹Corção, G.

Instituição: ¹Departamento de Microbiologia do Instituto de Ciências Básicas da Saúde da Universidade Federal do Rio Grande do Sul

Resumo:

In nature, microbial cells live associated with other cells into populations. Estuarine systems are strongly influenced by anthropogenic activity, accumulating high levels of pollutants and often becoming eutrophic. *Escherichia coli* is a natural member of the gastrointestinal tract of poultry and warm-blooded animals and involved in many metabolic pathways. The species of *E. coli* are divided into at least four major phylogenetic groups (A, B1, B2 and D). The objectives of this study were to isolate and identify *E. coli* from water samples from Laguna Tramandaí, Rio Grande do Sul, Brazil; to analyze the resistance of these isolates to different classes of antimicrobial of isolates and to determine the phylogenetic groups of isolates. Two collections were held in Laguna Tramandaí, North Coast of Rio Grande do Sul, one in winter (august 2014) and another in the summer (january 2015). Approximately 2L of water each point were sampled and analyzed. Four sampling points with different degrees of environmental impact were selected: near the mouth of the lagoon at sea (1), at the exit of a residential condominium in Imbé (2), a point located in the central part of the lagoon (3) and another point in the surge margins with no residences (4). Samples were inoculated in specific media for enterobacteria and typical colonies were identified by Gram staining and biochemical testing. The resistance was determined by disk diffusion method (Amikacin, Ampicillin, Amoxicillin + Clavulanic acid, Aztreonam, Cefepime, Cefotaxime, Cefoxitin, Ceftazidime, Choramphenicol, Cotrimoxazole, Gentamicin, Imipenem, Norfloxacin, Piperacillin + Tazobactam and Tetracycline) . Determination of phylogenetic groups will follow the protocol proposed by Clermont et al. (2000) which uses three sets of oligonucleotides (*Chua*, *yjaA* and Tsp E4. C2). Sixty one *Escherichia coli* were isolated and identified in the first collection (8 in point 1, 29 in point 2, 14 in point 3 and 10 in point 4) and 96 in the second collection (36 in point 1, 23 in point 2, 4 in point 3 and 33 in point 4). To date, it performed the antibiogram from 20 isolated from the first collection (5 isolates for each point). These isolates exhibit sensitivity to all antibiotics tested.

Palavras-chaves: *Escherichia coli*, water, phylogenetic groups and disk diffusion method

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