

Antimicrobial resistance as a worldwide problem. Ecology of antibiotic resistance genes

Resistencia a los antimicrobianos como un problema mundial. Ecología de los genes para la resistencia a los antibióticos

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Abstract

Bacterial resistance is a worldwide problem, affecting both industrialized and developing countries. At present, among other aspects, acute respiratory infections continue to be a major cause of morbidity and mortality among children in low-income countries; *Shigella dysenteriae* is responsible for the most severe morbidity in many parts of the world; *Vibrio cholerae* 01 and 0139 strains resistant to tetracycline and chloramphenicol from different parts of Africa have been reported, and multiple antimicrobial resistance (ampicillin, tetracycline, and chloramphenicol) in typhoid and other *Salmonella* infections was described in an increasing number of the countries from 1990s. In Cuba, studies conducted at the Institute of Food Nutrition and Hygiene, found high values of resistance in *Salmonella* and *E. coli* strains isolated from search and sanitary surveillance of foods and outbreaks. In theory, DNA is constantly flowing into and out of bacterial cells to be found in the environment. Thus, according to the old idea of “reservoir hypothesis” commensal bacteria in the colon exchange DNA with one another, resistance genes that can be acquired from ingested bacteria. In fact, several animal species could be reservoir to the existence and evolution of drug resistant and multidrug resistant strains for transmission to humans.

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