

**TITLE:** OCCURRENCE OF GENOMIC RESISTANCE ISLANDS WITHIN CLINICAL ISOLATES MULTIDRUG-RESISTANT *CORYNEBACTERIUM STRIATUM*

**AUTHORS:** RAMOS, J.N.<sup>1</sup>; BAIO, P.V.P.<sup>2</sup>; VERAS, J.F.C.<sup>3</sup>; VIEIRA, E.M.D.<sup>3</sup>; MATTOS-GUARALDI, A.L.<sup>1</sup>; VIEIRA, V.V.<sup>3</sup>

**INSTITUTION:** <sup>1</sup>LABORATÓRIO DE DIFTERIA E CORINEBACTÉRIAS DE IMPORTÂNCIA CLÍNICA, FACULDADE DE CIÊNCIAS MÉDICAS, UNIVERSIDADE DO ESTADO DO RIO DE JANEIRO, BRAZIL (Boulevard 28 de Setembro, 87 Fundos, 3º andar, Vila Isabel, Rio de Janeiro, RJ – CEP: 20551-030); <sup>2</sup>LABORATÓRIO QUÍMICO-FARMACÊUTICO DO EXÉRCITO BRASILEIRO, BRAZIL (Rua Licínio Cardoso, 96 – São Francisco Xavier, Rio de Janeiro, RJ, CEP: 20960-015); <sup>3</sup>LABORATÓRIO INTERDISCIPLINAR DE PESQUISAS MÉDICAS, INSTITUTO OSWALDO CRUZ, FUNDAÇÃO OSWALDO CRUZ, RIO DE JANEIRO, RJ; BRAZIL (Av. Brasil, 4365, Manguinhos, Rio de Janeiro, RJ – CEP: 21040-360).

**ABSTRACT:**

Genomic islands are mobile genetic elements that can harbor virulence, antibiotic resistance, pathogenicity, symbiosis or metabolism genes, making bacteria highly diversified organisms, capable of adapting to various environments and hosts due to their high genomic plasticity. Genomic islands are acquired by horizontal gene transfer and play an important role in genomic plasticity and consequently in bacterial evolution. Genomic resistance islands (GRI) carry genes encoding proteins associated with antibiotic resistance and are unknown in the emerging multidrug-resistant (MDR) pathogen *Corynebacterium striatum*, a Gram-positive rod that has been isolated in nosocomial outbreaks in several countries, including Brazil, in a variety of invasive diseases. This study aimed to identify genomic resistance islands in MDR *C. striatum* isolated from bloodstream infections during an outbreak nosocomial that occurred in a public hospital in the city of Rio de Janeiro, RJ, Brazil. The occurrence and diversity of GRI were investigated by bioinformatics tools in 8 genomes of *C. striatum* that presented 5 antimicrobial susceptibility profiles. The PFGE profile I and II isolates were susceptible only to tetracycline, vancomycin, linezolid and daptomycin. No GRI shared was found between all genomes, nor between the genomes of the PFGE I profile (2023 and 2308) and VI (2230 and 2237). In each isolate, several GRI were predicted carrying resistance genes to tetracycline, macrolide, aminoglycoside and chloramphenicol. In all GRI it was possible to observe genes related to mobility such as transposases and insertion sequences. Several hypothetical proteins were found, in addition to genes belonging to the efflux protein superfamily called Major Facilitator Superfamily (MFS) and related to the transport of metals such as zinc and arsenic. Except in 2296 isolate, tetracycline resistance genes *tetAB* were not found in GRI, but another tetracycline resistance gene, *tetW*, was located on an island that also contained aminoglycoside resistance genes (*strA-strB* and *aph(3')-Ia*). Class 1 integrons from 2296 and 2425 isolates were not located in GRI. The presence of these GRI demonstrates the plasticity of MDR *C. striatum* genomes isolated from invasive nosocomial infections. This impacts in the spread of resistance and the control of these infections.

**Keywords:** *Corynebacterium striatum*, genomic resistance island, multidrug-resistance, nosocomial outbreak.

**Development Agency:** FAPERJ, INOVA-FIOCRUZ, SR-2/UERJ, CNPq.