



Short Communication

Plasticity of *Corynebacterium diphtheriae* pathogenicity islands revealed by PCR

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ABSTRACT. Despite the existence of a vaccine against diphtheria, this disease remains endemic and is reemerging in several regions due to many factors, including variations in genes coding for virulence factors. One common feature of virulence factors is their high concentration in pathogenicity islands (PAIs), very unstable regions acquired via horizontal gene transfer, which has led to the emergence of various bacterial pathogens. The 13 putative PAIs in *Corynebacterium diphtheriae* NCTC 13129 and the reemergence of this disease point to the great variability in the PAIs of this species, which may reflect on bacterial life style and physiological versatility. We investigated the relationships between the large number of PAIs in *C. diphtheriae* and the possible implications of their plasticity in virulence. The GenoFrag software was used to design primers to analyze the genome plasticity of two pathogenicity islands of the reference strain (PiCds 3 and 8) in 11 different strains. We found that PiCd 3 was absent in only two

strains, showing genes playing putative important roles in virulence and that only one strain harbored PiCd 8, due to its location in a putative “hotspot” for horizontal gene transfer events.

Key words: *Corynebacterium diphtheriae*; Pathogenicity islands; Genome plasticity; PCR; GenoFrag; Horizontal gene transfer