DOI : 10.5958/2277-8934.2019.00005.5 Vol 26 No 1, p 29-40

SPECIES SPECIFICITY AND HOST AFFINITY RATHER THAN TISSUE TROPISM CONTROLS CODON USAGE PATTERN IN RESPIRATORY MYCOPLASMOSIS

Mahmoud Kandeel[1,2], Kamal Elshazly[2], El-Deeb WM[3], Mahmoud Fayez[4] and Ibrahim Ghonim[3]

[1]Department of Physiology, Biochemistry and Pharmacology, [3]Department of Clinical Studies,
Faculty of Veterinary Medicine, King Faisal University, Alahsa, 31982, Saudi Arabia
[2]Department of Pharmacology, Faculty of Veterinary Medicine, Kafrelshikh University, Kafrelshikh, 35255, Egypt
[4]Veterinary Serum and Vaccine Research Institute, Cairo, Egypt

ABSTRACT

Respiratory Mycoplasmosis (rMyc) is a devastating respiratory disease causing serious pneumonia in camels, cattle and human causing fatalities and high economic loss. Codon usage pattern is an important measure of host-parasite relationship, parasites adaptation and evolution. In this work, two important species of rMyc affecting human (*Mycoplasma pneumoniae*) and camels (*Mycoplasma mycoides*) were analysed for finding their codon usage bias, factors affecting their genomes composition and their relation to their host including adaptation and disease pathogenesis. In spite of their reduced genome size, rMyc showed comprehensive and host-independent codon usage machinery with wide variability and incompatibility with their host pattern. Although, rMyc are common infectious agents of respiratory tract, they showed completely diverse codon usage, adaptation and pathogenesis profiles. *M. mycoides* showed strict highly biased A/T selection in their genomic composition, preferred codons and at the 3rd position of codons as well as highly divergent codon usage pattern compared with its host. *M. pneumoniae* showed more attempts in adaptation to mammalian host environment by showing codon usage pattern almost similar to their host. High GC content in genome, low number of overbiased and underbiased codons, high ENc values and balanced use of GC and AT in preferred codons N3s were among the factors of adaptation to its habitat. There was immune selection among rMyc. *M. mycoides* is more immune resistant by showing lower CpG dinucleotide frequency compared with *M. pneumoniae*. The higher and faster gene expression in *M. mycoides*, and to a lesser extent *M. pneumoniae*, devoted from low ENc values accounts for high pathogenicity and acute disease. Common evolutionary origin and variable codon usage indices account for variable attempts among *Mycoplasma* species to adapt their habitat regardless their tissue tropism or host specificity.

Key words: Camel, codon, mycoplasmosis, pneumonia