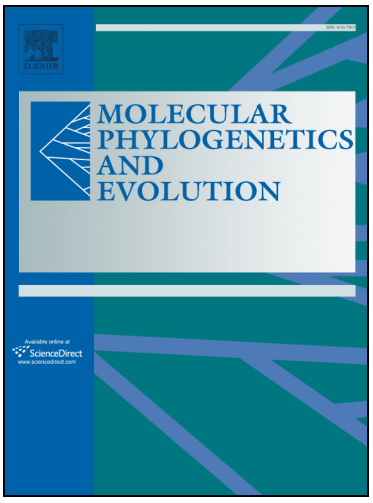

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Canine parvovirus type 2 (CPV-2) and *Feline panleukopenia virus* (FPV) codon bias analysis reveals a progressive adaptation to the new niche after the host jump.

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Abstract

Based on virus dependence from host cell machinery, their codon usage is expected to show a strong relation with the host one. Even if this association has been stated, especially for bacteria viruses, the linkage is considered to be less consistent for more complex organisms and a codon bias adaptation after host jump has never been proven. *Canine parvovirus type 2* (CPV-2) was selected as a model because it represents a well characterized case of host jump, originating from *Feline panleukopenia virus* (FPV). The current study demonstrates that the adaptation to specific tissue and host codon bias affected CPV-2 evolution. Remarkably, FPV and CPV-2 showed a higher closeness toward the codon bias of the tissues they display the higher tropism for. Moreover, after the host jump, a clear and significant trend was evidenced toward a reduction in the distance between CPV-2 and the dog codon bias over time. This evidence was not confirmed for FPV, suggesting that an equilibrium has been reached during the prolonged virus-host co-evolution. Additionally, the presence of an intermediate pattern displayed by some strains infecting wild species suggests that these could have facilitated the host switch also by acting on codon bias.

Keywords

Codon bias; Canine parvovirus type 2; Feline parvovirus; Evolution over time; Tissue adaptation.