

Endogenous Parvovirus Sequences in Animal Genomes: A Critical Assessment

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In recent years, many RNA and DNA virus families have been recognized with capacity to colonize the germ line of multiple host genomes. Among them, presumed sequences of the ssDNA virus members of the *Parvoviridae* family, known as endogenous parvovirus elements (EPAV), have been identified inserted in the germ line of a wide range of animal genomes from insects to humans. In this study we have screened mammalian databases not only for previously described putative EPAV, but also for novel ones, aiming at: (i) clear identification of their presence and endogenous nature; (ii) characterization of their sequence and genetic structure; and (iii) assignment of their origin within *Parvoviridae* phylogeny. Our data suggest that some previously annotated small EPAV are of uncertain parvoviral origin, whereas in other cases the EPAV could be confirmed showing high sequence homology to known species of the currently circulating genera of the *Parvoviridae*. Genetic analyses of these EPAV indicate intricate and diverse genetic configurations, which may include partial or full non-structural (NS) and structural (VP) parvovirus genes. A wide survey of our findings will be presented and discussed.

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