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**The Extent of Diversity in Parvovirus Expression is Paramount with Densoviruses**

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Densoviruses have evolved with many of the million-odd invertebrate species that have adapted to different niches of the ecosystem resulting in a greater variation in genome sequence and expression than for the vertebrate parvoviruses. Although many densoviruses are highly pathogenic, some are essential for the life cycle of the host. These viruses have small icosahedral capsids with a diameter of 18-27 nm with a limited packaging capacity. The variation in genome sizes led to a co-evolution of the expression strategy with the packaging capacity of the capsids and in some cases even necessitated a split genome. The definition of a parvovirus, such as in metagenomic studies, is not always clear for densoviruses and may have to be revised in some cases. In addition, not all reported transcription strategies are correct, especially those for densoviruses with a high AT content. Although leaky scanning was common in the initial studies on expression strategies, lately very complex splicing strategies have been observed. Moreover, we isolated new densoviruses with conserved genome structures but very low sequence identities.