

**Densovirus Experimental Evolution in Insecta: The Appearance Can be Deceptive**

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To understand the mechanisms underlying the evolution of insect parvoviruses and their adaptation to a new host, we set up an experimental evolution protocol with JcDV, a “generalist” ambidensovirus pathogenic for several caterpillar species. Starting with a single genotype of JcDV (infectious clone), we realised serial oral infections in parallel lines of two caterpillar species for ten passages, either passaging the virus in the same species (constant environment) or by alternating host species (variable environment). The resulting phenotypes (virulence) and genotypes (sequencing) were compared to the ancestral ones. Results showed that virulence dropped in constant environment but remained at similar high levels when alternating host species, suggesting that mutations were differentially selected with passages depending on environment. However, deep sequencing analysis of viral populations showed that no adaptive mutations were selected and thus that the phenotypic outcomes were not explained by genetic changes in the viral genomes. Although distinct polymorphisms were generated depending on species and conditions. Instead, we found that JcDV infection induced an original mechanism that specifically restricts gut recognition during horizontal transmission to conspecifics.