

## Differential replication of two porcine parvovirus strains in bovine cell lines ensues from initial DNA processing and NS1 expression

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Porcine parvovirus (PPV) is a small DNA virus with restricted coding capacity. The 5 kb genome expresses three major non-structural proteins (NS1, NS2 and SAT), and two structural proteins (VP1 and VP2). These few viral proteins are pleiotropic and interact with cellular components throughout viral replication. In this regard, very few cell lines have been shown to replicate the virus efficiently. Cell lines were established from a primary culture of bovine cells that allowed allotropic variants of PPV to be distinguished. Three cell lines were differentially sensitive to infection by two prototype PPV strains, NADL-2 and Kresse. In the first cell line (D10), infection was restricted early in the infectious cycle and was not productive. Infection of the second cell line (G11) was 1000 times less efficient with the NADL-2 strain compared with porcine cells, while production of infectious virus of the Kresse strain was barely detectable. Restriction points in these cells were the initial generation of DNA replication intermediates and NS1 production. Infection with chimeras between NADL-2 and Kresse showed that residues outside the previously described allotropic determinant were also partially responsible for the restriction to Kresse replication in G11 cells. F4 cells were permissive to both strains, although genome replication and infectious virus production were lower than in the porcine cells used for comparison. These results highlight the dependent nature of parvovirus tropism on host factors and suggest that cells from a non-host origin can fully support a productive infection by both strains.

Received 20 September 2013

Accepted 13 December 2013