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Trans-complementation studies with the novel "Bungowannah" virus support the classification into the genus Pestivirus and provide new insights in the compatibility of pestivirus proteins

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In recent years several atypical pestiviruses have been described. Bungowannah virus, first recognised in a disease outbreak in 2003 from pigs in Australia, is the most divergent virus in this group. Therefore, heterologous complementation was used to clarify the phylogenetic relationship and to analyse the functional exchangeability of selected genome regions encoding structural proteins. Using a BVDV-1 backbone, several chimeric constructs, generated by the substitution of the envelope proteins E^{rns}, E1 and E2, were investigated. While all constructs replicated autonomously, infectious high-titre chimeric viruses could only be observed after exchanging the complete E1-E2 encoding region (vCP7_E1E2-Bungo). vCP7_E1E2-Bungo efficiently propagated in porcine as well as in bovine cells, indicating a broader host cell range compared to BVDV and similar to Bungowannah virus. In addition, complementation of BVDV-E^{rns} was only efficient if Bungowannah virus-E^{rns} was expressed from a bicistronic construct (vCP7_E^{rns}-Bungo_bi). The complementation of E1 or E2 alone resulted in replicons, not able to generate infectious virus progeny. In contrast, a BVDV chimera expressing the E2 protein of the atypical "HoBi" virus (vCP7_E2-HoBi) grew to high viral titres. In conclusion, our data encourage the classification of Bungowannah virus into the genus *Pestivirus*, since the envelope proteins E^{rns} and E1-E2 are in principle able to complement the classical pestivirus BVDV. However, in contrast to other atypical pestiviruses, the compatibility is severely reduced. In addition, it is shown here that heterologous complementation could be a useful tool for studying functional relationships and support the decision for the classification of new pestiviruses.