Studies on genetic diversity of bovine viral diarrhea viruses in Danish cattle herds - DTU Orbit (20/08/2019)

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Scandinavian countries have successfully pursued bovine viral diarrhea virus (BVDV) eradication without the use of vaccines. In Denmark, control and eradication of BVDV were achieved during the last two decades, but occasionally new BVDV infections are detected in some Danish cattle herds. The aim of this study was to determine recent BVDV subtypes isolated from 4 Danish herds (A, B, C, and D) isolated in 2009–2012 and to analyze the genetic variation of these isolates within the same herd and its relation with those of other herds. The results showed that three herds (B, C, D) were BVDV 1-b and only one herd (herd A) was BVDV 1-d, no other subtypes were detected. The deduced E2 amino acids result showed a high identity percent (99–100 %) between isolates originating from the same herd, but with higher variation compared to isolates of the other herds. Some of these new Danish strains have closer relationship to BVDVs from outside Denmark than to older Danish strains indicating that these are new introductions to Denmark. In conclusion, BVDV-1 subtypes recently detected in Denmark were only subtypes 1b and 1d, and BVDV infections established in a herd is genetically stable over a long time period.

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