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Experiences from the current voluntary bovine viral diarrhea control efforts in Hungary

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Introduction. Bovine viral diarrhea (BVD) is caused by Pestivirus A viruses (BVDV), occurs worldwide, and compromises cattle husbandry via direct and/or indirect damages. Some distinct characteristics, such as the existence and differing pathogenesis of infection by the two biotypes of the virus, the emergence, and the epidemiological and ecological role of persistently infected and immunosuppressed calves, complicate the epidemiology of BVD.
It is not mandatory to control/eradicate BVD in Hungary, however, several farm owners decided to undertake a voluntary program, supported by laboratory investigations.
Herein we provide a summary of the relevant methodology and preliminary results.

Methods. The programs are organized according to the established principles of BVDV control, i.e. screening for and eliminating persistently infected (PI) immunotolerant animals, vaccination to provide the necessary immune status of the dams to prevent intrauterine infections, and monitoring the BVDV status of the herd by direct (virus detection) and indirect (serology) ways. Biosecurity, as another key pillar of BVD control, is beyond the lab service competencies.
The samples comprise of bulk milk, sera, and organ specimens. The laboratory methodology includes a screening RT-qPCR (commercial), a vaccine strain-specific RT-qPCR (in-house), a BVDV total antibody ELISA (commercial), a virus neutralization assay, cell-mediated immunity (CMI) evaluation through IFN-? mRNA and/or protein detection, and nucleotide sequencing protocols (Sanger and Next Generation Sequencing).

Results. A preliminary survey indicated the presence of Pestivirus A 1b, 1d, and 1f subtype viruses in Hungary, and supposed a cross-protection by the applied subtype 1a MLV type vaccine associated with a high IFN-? production. Over a hundred farms were interested in their BVDV status, approximately 30 considered control measures, and in the end, five have embarked on the voluntary eradication program since 2020. Out of these four have not identified PI animals for the last 1-1.5 years, and the vaccinated population seroconverted against the virus, a pre-requisite for preventing the emergence of PI animals. These findings demonstrate the efficient control of BVD on these farms. Scrutinizing selected isolates, a few identified cytopathogenic strains in particular is an ongoing project.

Conclusions. The willingness of the farm owners and the appropriate combination of the relevant toolkits enabled a rather fast progression of BVD control, which should be broadened geographically because the next challenge will be to maintain the favorable status and prevent re-introduction.