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Investigation into the virome of Swiss water buffaloes

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Key words
Water buffaloes, virus, virome, next generation sequencing, interspecies transmission

Aim of the study
The Asian water buffalo (Bubalus bubalis) is gaining increasing importance in Swiss animal farming. Over the last two decades, the animal population has risen from 14 to over 1200. Where exotic animals like water buffaloes get in contact with native species such as cattle, sheep and goats, the species-associated difference in the clinical manifestation of viral infections may have severe impact on animal health. Since water buffaloes in Switzerland and their pathogens have not been investigated so far, the present study aims at gaining more information on the viral spectrum present in this species and about interspecies transmission from and to small ruminants. Due to financial restrictions, we concentrated on the virome that can be assessed from blood samples.

Material and methods
We analysed blood samples of 48 water buffaloes from three farms in the cantons Schwyz and Solothurn: 17 water buffaloes on farm 1, 26 water buffaloes and 19 sheep on farm 2, 5 water buffaloes and 7 goats on farm 3. The virome was investigated by two approaches: firstly, by Next Generation Sequencing (NGS), that allows unspecific detection of viruses and therefore also enables detection of unexpected and novel viruses, and secondly, by conventional specific diagnostic methods, including PCR, ELISA and SNT, that are not as broad as NGS but more sensitive. Our specific analyses covered herpesviruses of ruminants such as bovine Herpesvirus-1 as well as pestiviruses and emerging viruses such as Bluetongue virus (BTV) and Schmallenberg virus (SBV). Sequencing results of NGS suggestive of infection with a novel virus were confirmed by generation of conventional primers and overlapping Sanger sequencing.

Results and significance
In a nutshell, we detected evidence that the Water buffaloes had experienced infections with Gemycircularvirus (GyCV; NGS and PCR), bovine lymphotropic herpesvirus (BLHV; PCR), Bovine herpesvirus 2 (BoHV-2; serology), Bovine virus diarroea virus (BVDV; serology), and Bluetongue virus (BTV; serology). The significance of these observations is in the notion that water buffaloes have to be taken into account if any of those viruses should emerge in our cattle population and if their eradication would be addressed. At present, this may be the case particularly with regard to BVDV and BTV. The significance of the GyCV infection may need further evaluation.
Moreover, we detected evidence for the following viruses among the co-housed small ruminants: GyCV (PCR), Ovine herpesvirus 2 (OvHV-2; PCR), Ruminant rhadinovirus 2 (RuRHV-2; PCR), Caprine herpesvirus 2 (CpHV-2; PCR), BVDV and Border disease virus (BDV; serology), BTV (serology), Schmallenberg virus (SBV, serology). Thus, evidence for three viruses (BVDV, BTV, GyCV) was detected in both, the exotic water buffaloes and the domestic small ruminants, suggesting that inter-species transmission of these viruses may occur. Although we did not detect cases, it is known from the literature that water buffaloes may succumb to malignant catarrhal fever (MCF) due to either OvHV-2 or CpHV-2. The detection of these viruses among the co-housed small ruminants is, therefore, also of significance.

Importantly, we did not detect any evidence for the following infections, which are notifiable but considered eradicated from the Swiss cattle population: Bovine herpesviruses 1 and 5 (BoHV-1; BoHV-5) as well as Bovine leukaemia virus (BLV).
From the technical standpoint, it turned out that conventional methods (PCR, serology) were far more sensitive than the modern method of NGS. However, three caveats have to be taken into account: (1) Our census animals were all healthy, with no apparent signs of disease. The results might have been different if clinical problems would have been present at the time of sample collection. (2) Due to limited resources, we were restricted to analyse blood samples. As outlined in the original planning, it would have been most valuable to include also bodily secretions into our analysis. (3) Presence of CyGV among either water buffaloes or small ruminants would not have been detected without NGS.
Overall, we believe that the investment into this project turned out in a success: we made a very good technical advance in establishing NGS and, particularly, the methods of nucleic acid preparation for the purpose as well as in establishing the necessary bioinformatics tools. Moreover, we made some significant new observations about virus infections in water buffaloes. The knowledge of these may be valuable in the future.

Publications, posters and presentations

Oral presentation by Julia Lechmann, Münchenwiler meeting for Virology students, Münchenwiler (BE) 22.-23.10.2015

Poster presentation by Julia Lechmann, annual meeting of the Swiss society for microbiology, Bern, 13.-15.06.2016

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