[1]Institute of Diagnostic Virology, Friedrich-Loeffler-Institut, Greifswald-Riems, Germany
[2]Veterinary Laboratories Agency, Woodham Lane, New Haw, Addlestone, Surrey, KT15 3NB, UK

VALIDATION AND ESTABLISHMENT OF AN OPTIMIZED DNA-MICROARRAY SYSTEM FOR THE NON TARGETED DETECTION OF VIRUSES

B. Abendroth[1], B. Hoffmann[1], D. Höper[1], A. Dastjerdi[2], M. Beer[1]

DNA microarrays are highly parallel biosensors which allow a fast, standardized, simultaneous detection and identification of many different viruses in one or more samples. In this study we used an 8x15k Pan Viral Chip developed within the European Network of Excellence project "EPIZONE" and printed by Agilent. These arrays contain catcher oligonucleotides specifically detecting 1960 different virus families/species. The array was validated and its sensitivity was determined using two different viruses. On the one hand, we used the classical swine fever virus (CSFV) strain "Kozlov", a positive stranded RNA virus. On the other hand, a double stranded DNA virus (modified Vaccinia Ankara; MVA) was used. The nucleic acid samples (DNA or RNA) were processed prior to hybridization onto the array using three different workflows in comparison. In order to distinguish between positive and negative signals in the raw data, data were analysed with three different methods in comparison. First, data were processed using the "DetectiV" R-package, initially developed for analysis of the EPIZONE chip data. Second, the well-established "Limma" R-package was used for data analysis. Third, Z-score transformation in combination with calculation of the accompanying P-values was done. The results of the different data analysis methods were compared. With the established optimal combination of sample processing and subsequent data evaluation, a series of different RNA and DNA viruses, including the novel Schmallenberg virus, and numerous sample materials were analysed. It could be shown that the established workflow can successfully be used for the very broad virus detection in cell culture and diagnostic samples.

Corresponding author
Björn Abendroth
Friedrich-Loeffler-Institut
Institute of Diagnostic Virology
Südufer 10
17493 Greifswald-Insel Riems, Germany
E-Mail: bjoern.abendroth@fli.bund.de

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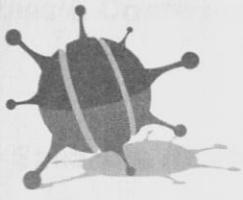

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