

Gene signatures associated with foot-and-mouth disease virus infection and persistence part I: persistent FMDV in a three-dimensional model of the bovine soft palate

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Gene signatures associated with foot-and-mouth disease virus infection and persistence. Part I:



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Persistent FMDV infection in a three-dimensional model of the bovine soft palate

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BACKGROUND

Foot-and-mouth disease virus (FMDV) causes devastating vesicular disease in livestock and persists in epithelial cells of the dorsal soft palate (DSP) in cattle.

OBJECTIVE





the study enable ΤΟ Of mechanisms, or the screening of molecules to detect or interfere in persistence, the objective was to persistent establish FMDV infection in vitro.

MATERIAL AND METHODS

SP cells were isolated after commercial slaughter and were cultured in multilayers at the airliquid interface. After 5 weeks of culture without passage, the cells were infected with a viral clone FMDV O derived from the FMDV/FRA/1/2001strain.

RESULTS AND DISCUSSION



At infection, ~20% of cells had a polygonal morphology and displayed tight junctions, such as in stratified squamous epithelia. Some cells expressed cytokeratin and most or all cells expressed vimentin, which characterises epithelial cells in culture.

A limited cytopathic effect was observed, restricted to the upper cell layers. FMDV antigen, FMDV **RNA and live FMDV were detected** • through day 1 to 28, with peaks at day 1 and 2. A maximum of infected cells (36%) was detected 24 hours after infection at an MOI of 1. At day 28, when animals are considered as carriers, FMDV antigen could still be detected in sparse cells (0.2%-2.1%) and live isolated from virus was supernatants of 6/8 cultures.

Isolation, characterisation and FMDV infection of bovine dorsal soft palate cells



http://www.afrivip.org/sites/default/files/ FMD/diagnosis.html



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Vesicular lesions caused by foot-and-mouth disease virus in cattle



CONCLUSION

Bovine dorsal soft palate cells were propagated in multilayers at the air-liquid interface. Persistent FMDV infection was established in sparse cells in all layers. The model will enable to get a better understanding of the mechanisms underlying persistence in order to develop ways to control this infection and to improve the diagnostics.

Transcriptomic data are presented in an oral communication and have been published (Pfaff et al., viruses, 2019).

Animal Health and Welfare ERA-Net

