

# Widespread Skin Lesions in Tanzanian Horses Caused by Molluscum Contagiosum Virus-like Poxvirus

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## Introduction:

In a herd of horses used for horseback safaris in Tanzania several animals showed wart-like masses in variable number distributed across the body. Lesions exacerbate in sick or stressed horses and disappeared over time when horses recovered. This case report describes the skin lesions and the investigation of the causative agent in one of these horses.

## Acknowledgement

Many thanks to Prof. Dr. Frank Dombrowski and Dr. Artur Gontarewicz, Institute of Pathology, Greifswald University Hospital and Prof. Dr. Christiane Herden, Institute of Veterinary Pathology, Justus-Liebig-University Gießen for making available case material of human molluscum contagiosum and bovine stomatitis. Additionally, we thank G. Zöller, C. Kahlhofer and A. Lorber for the excellent technical assistance.

## Material and methods:

A 10-year-old, female horse presented clinically numerous papular and verrucous lesions. Before disease came up the mare showed signs of colic and neurologic deficits. One of these masses was surgically removed, fixed in 4% formalin and processed for histopathology, electron microscopy, PCR, *in-situ*-hybridisation and next generation sequencing.



Fig. 1: Hair-coated trunk of the horse. Numerous verrucous masses distributed over the surface.

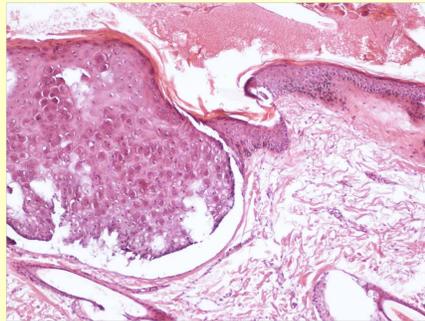


Fig. 2: Overview. Note abrupt transition between epidermal hyperplasia and normal epidermis. HE, 10x.

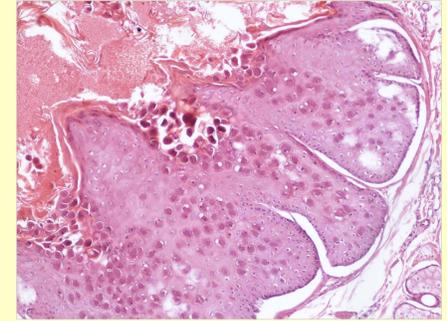


Fig. 3: Skin lesion. Focal epidermal hyperplasia with numerous large, eosinophilic, intracytoplasmic inclusion bodies within keratinocytes. Superficially infected epithelial cells scale off. HE, 10x.

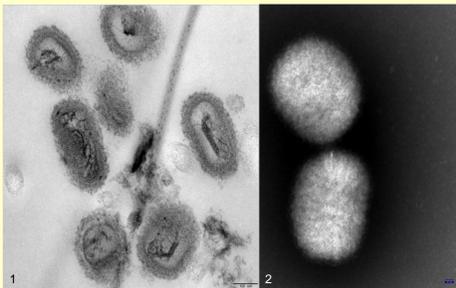


Fig. 4: Electron microscopy. 1. Ultra-thin section showing brick-shaped virions with core structures characteristic for Molluscum contagiosum virus (bar=100 nm). 2. Negative staining of isolated virions (bar=200 nm).

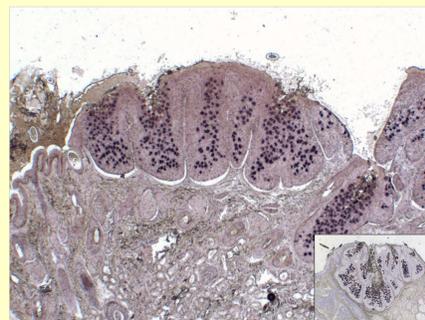


Fig. 5: *In-situ*-hybridisation. Positive signals within the intracytoplasmic inclusions in equine keratinocytes. Insert: identical staining pattern in a human case of molluscum contagiosum.

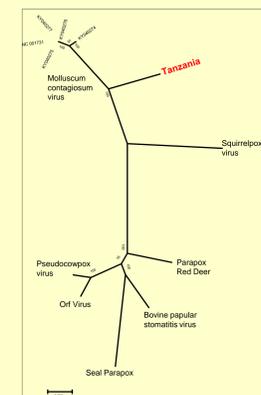


Fig. 6: Maximum Likelihood Tree using the most similar Ref-Seq genomes of the *Chorodopoxvirinae*. Whole genomes were aligned using software "mafft". Conserved blocks were extracted using software "Gblocks". The final dataset is based on a total of 93839 aligned nucleotides. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The value next to the nodes show bootstrap values from 500 replicates.



Fig. 7: Sequencing coverage plot of the whole genome sequence showing an average of 8,500-fold (max 20,000-fold) continuous coverage of the determined sequence.

## Results:

Histopathologically the mass corresponded with a sharply delimited epidermal hyperplasia, consisting of an enlarged stratum spinosum with numerous large, eosinophilic, intracytoplasmic inclusion bodies within the keratinocytes (Fig. 2, 3). Electron microscopy demonstrated brick-shaped virions with core structures characteristic for Molluscum contagiosum virus (MCV) (Fig. 4). PCR targeting the DNA-dependent RNA polymerase gene followed by sequencing of 550 base pairs demonstrated sequence identity of 99% with a MCV-like poxvirus derived from a horse and a lower identity (92%) with MCVs derived from humans.

By *in-situ*-hybridisation using a 300 bp digoxigenin labelled probe starting from purified MCV-like poxviral DNA and Bovine Papular Stomatitis Virus (BPSV) DNA it was possible to detect hybridisation signals within the intracytoplasmic inclusions of the hyperplastic epidermis of the horse (Fig. 5), but not within tissues of bovine papular stomatitis. However, cross hybridisation of the probe was assessed with samples of human MCV which led to an identical staining pattern (Fig. 5 insert).

Whole genome sequencing with de novo assembly showed 91% nucleotide sequence homology to published human MCV genome sequences over a single 163.400 bp contig localized mainly in the conserved genome region (Fig. 6, 7).

## Discussion:

Based on pathohistological and molecularbiological results extensive skin lesions in a Tanzanian horse were caused by a MCV-like poxvirus. Partial genome sequencing revealed sufficient nucleotide sequence homology to suggest this virus is a new member of the genus *Molluscipoxvirus*. Like human molluscum contagiosum clinical presentation is more severe in immunocompromised horses. Transmission to humans (farm workers or guests) was not observed.

## Literature:

1. van Rensburg I.B.J. et al. 1991; Molluscum contagiosum in a horse. Tydskr.S.Afr.vet.Ver. 62(2):72-74.