Molecular epidemiology and diagnosis of SAT-type foot-and-mouth disease in southern Africa

By

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Summary

Foot-and-mouth disease (FMD) is an economically devastating picornaviral disease affecting over 40 species of cloven-hoofed animals. The virus occurs as seven immunologically distinct serotypes which are characterized by high levels of intra- and intertypic variation. The three South African Territories (SAT) serotypes 1-3 are endemic to sub-Saharan Africa, a region where the epidemiology of the disease is particularly complex due to the presence of six of the seven serotypes, the role of wildlife in virus maintenance and the apparently higher levels of variation in the endemic serotypes. These factors make it imperative to establish methods suited to elucidating the regional epidemiology. One of the integral parts of this process is the genetic characterization of regionally representative viruses in order to assess the variation in the field and to clarify the role of wildlife. Nucleotide sequence data and methods suited to studying the SAT-types are however limited. A first priority was therefore to establish a PCR-based nucleotide sequencing technique targeting the highly immunogenic and phylogenetically informative 1D genome region encoding the VP1 protein. The screening of multiple serotypes and subtypes prevalent on the African continent confirmed that this method was robust and well-suited to molecular epidemiological studies in the southern Africa region. The method was first applied in the characterization of FMD virus recovered from the reproductive tract of free-living

African buffalo in the Kruger National Park. Nucleotide sequencing assisted in authentication of the results and indicated that carrier status was likely, but it was not possible to unequivocally demonstrate persistent infection of FMDV. In a separate study, the role of impala antelope (*Aepyceros melampus*) in the epidemiology of the disease in South Africa was assessed. Genetic characterization of impala and African buffalo (*Syncerus caffer*) viruses collected over an eleven year period confirmed that inter-species transmission occurred on several occasions and that virus can persist in impala populations for more than 12 months. Inter-species transmission and investigation of the possible mechanisms facilitating virus transmission from persistently infected buffalo focussed on the Kruger National Park in South Africa. In order to ensure regional relevance the study was broadened to incorporate buffalo populations throughout southern Africa. Viruses of the three SAT-types recovered from diverse African buffalo populations were therefore characterized. The results reveal that independently evolving viral lineages occur in distinct geographical regions for each of the SAT-types examined and that the levels of intratypic variation are in the order of 52 - 55 % on nucleotide level across the genome region characterized. Given the strict locality-specific grouping of buffalo viruses the likely usefulness of this database for tracing the origin and course of contemporary and historical SAT-type outbreaks was investigated. Molecular epidemiological studies conclusively show that buffalo are indeed the ultimate source of infection for susceptible cloven-hoofed animals occurring in close proximity, that interspecies transmission occurs between cattle and antelope and that trans-boundary transmission of virus remains a threat to disease security in southern African countries.

SCIENTIFIC PRESENTATION OF RESULTS

Scientific publications emanating directly from this thesis

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2. **Bastos, A.D.S**, Bertschinger, H.J., Cordel, C., van Vuuren, C. de W.J., Keet, D., Bengis, R.G., Grobler, D.G. & Thomson, G.R. 1999. The possibility of sexual transmission of foot-and-mouth disease from African buffalo to cattle. *Veterinary Record* **145**: 77-79.

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* Indicates presenting author

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aa	amino acid
ANG	Angola
BEC	Becuanaland
BOT	Botswana
BUN	Burundi
BVI	Botswana Vaccine Institute
bp	base pairs
CD	Corridor disease
CPE	cytopathic effect
ERI	Eritrea
FMD	foot-and-mouth disease virus
ICTV	International Committee for the Taxonomy of Viruses
KEN	Kenya
KNP	Kruger National Park
MAL	Malawi
MOZ	Mozambique
NAM	Namibia
NCR	non-coding region
nt	nucleotide
OIE	Office International des Epizooties
OP	oesophageo-pharyngeal
OVI	Onderstepoort Veterinary Institute
PAL	Phalaborwa
PCR	polymerase chain reaction
PFU	plaque forming units
p.i.	post-infection
POT	Potgietersrus
RHO	Rhodesia
RWA	Rwanda
SAR	South African Republic
SAT	South African Territories
SAU	Saudi Arabia
SWA	South West Africa
SWL	Swaziland
TAN	Tanzania
TB	tuberculosis
UGA	Uganda
VP	Virus protein
WRL	World Reference Laboratory
ZAI	Zaire
ZAM	Zambia
ZIM	Zimbabwe