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Short communication

Comparison of G protein sequences of South African street rabies viruses showing distinct progression of the disease in a mouse model of experimental rabies

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Abstract

Rabies is a fatal zoonotic disease and infections generally lead to a fatal encephalomyelitis in both humans and animals. In South Africa, domestic (dogs) and the wildlife (yellow mongoose) host species maintain the canid and mongoose rabies variants respectively. In this study, pathogenicity differences of South African canid and mongoose rabies viruses were investigated in a murine model, by assessing the progression of clinical signs and survivorship. Comparison of glycoprotein gene sequences revealed amino acid differences that may underpin the observed pathogenicity differences. Cumulatively, our results suggest that the canid rabies virus may be more neurovirulent in mice than the mongoose rabies variant.

Keywords: Lyssavirus; Canid rabies; Mongoose rabies; Neurovirulent; South Africa

1. Introduction

The rabies virus (RABV) is the prototype species of the genus *Lyssavirus* (family *Rhabdoviridae*, order *Mononegavirales*). Members of the genus *Lyssavirus* are characterized by non-segmented, negative-sense RNA genome, of approximately 12 kb in size. Upon infection of a susceptible mammalian host species including humans, the highly neurotropic virus induces an acute, progressive and fatal encephalomyelitis primarily provoked by an infectious virus transmitted through bite, but also through scratches and contact with mucous membranes. The World Health Organization (WHO) estimates that as many as 60,000 human deaths occur due to rabies annually [1], approximately 98% of these are due to dog bites [2]. In South Africa, a unique situation exists because of the presence of canid and mongoose RABV biotypes within the classical rabies species. The former is maintained principally by domestic dogs in northern South Africa, KwaZulu-Natal (KZN), Mpumalanga and the Eastern Cape provinces [3], these being canine rabies endemic areas in the country. The mongoose rabies biotype (also referred to as the herpestid variant), is adapted to a variety of mongooses (small carnivores belonging to the family *Herpestidae*) and the principal vector species for the mongoose RABV biotype in South Africa is the yellow mongoose [3,4]. Spill over infection

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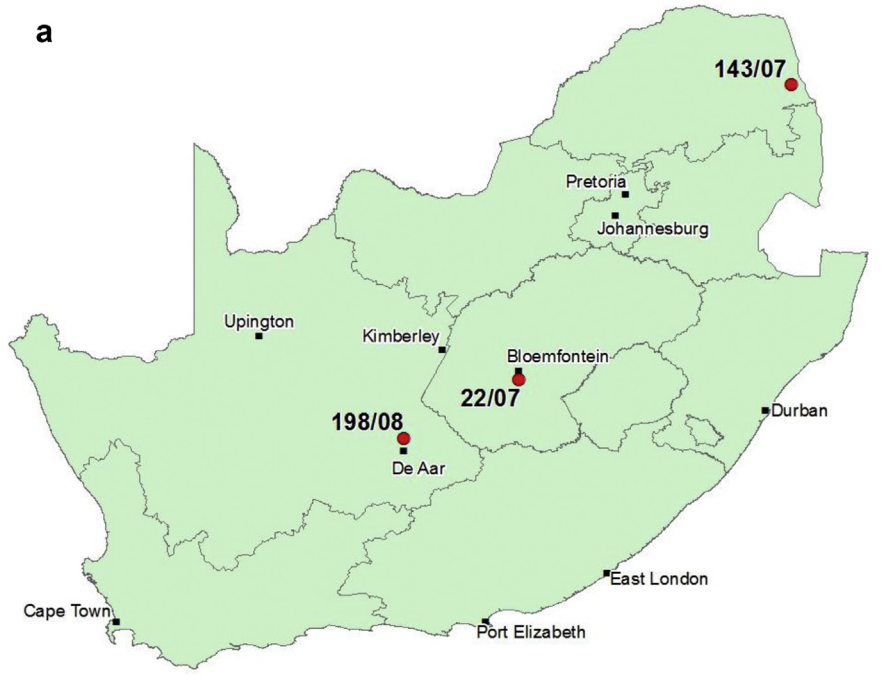
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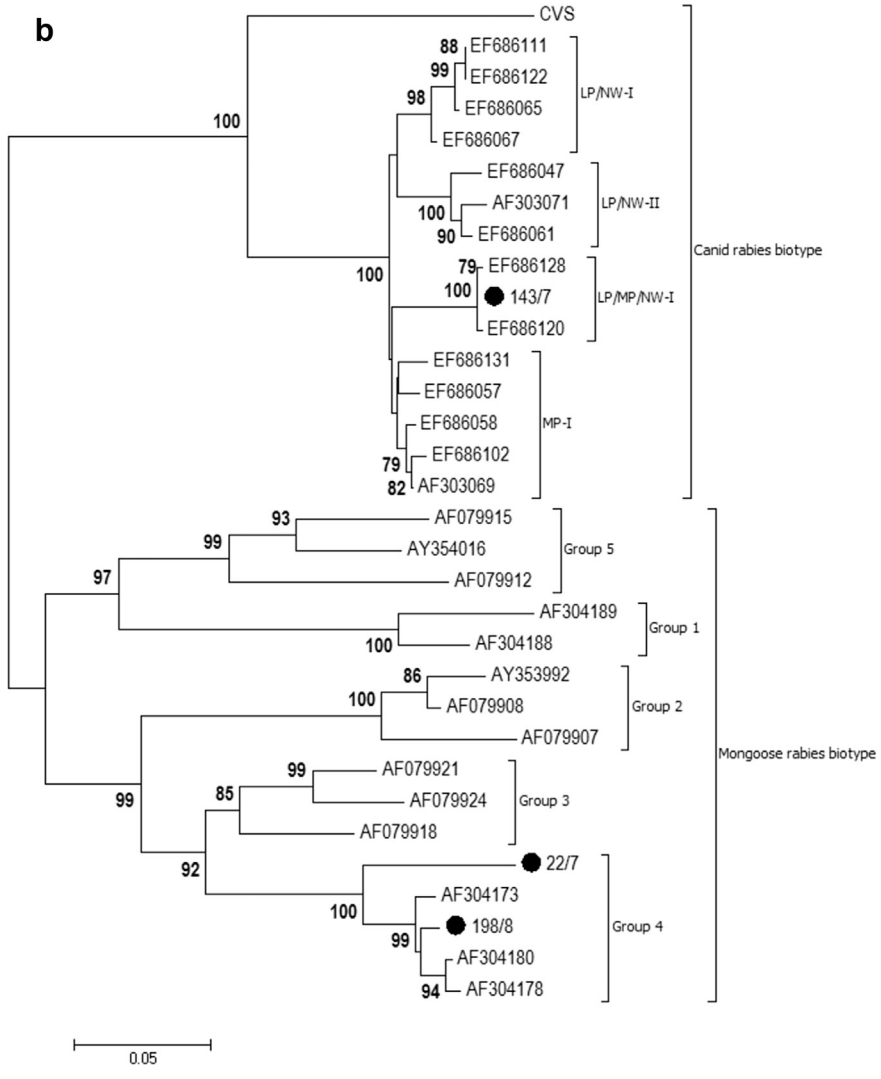
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Canid rabies biotype
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AF079912
Group 5
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AF304188
Group 1
AY353992
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Group 2
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Group 3
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198/8
AF304180
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Group 4
Mongoose rabies biotype
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