
SHORT REPORT

An evaluation of dog rabies control in Limpopo province (South Africa)

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SUMMARY

Rabies is a prevalent and re-emerging disease in South Africa particularly in rural areas with high human densities. Outbreaks are frequently reported in the north and eastern parts of this country, probably an indication of inadequacy in the control of the disease. Following the 2005/2006 outbreak in Limpopo, we undertook an analysis of case surveillance data and genetically characterized 18 rabies viruses, all recovered from domestic dogs. Although rabies prevalence gradually declined annually from 2007, dog rabies still remains a public and veterinary health hazard in this region. Sylvatic rabies cycles are maintained by the black-backed jackal species in specific ecological conditions in the northwest of the province (Waterberg area), unlike in the north and east (Vhembe and Mopani districts, respectively), where spillover of infection between dogs and jackals is likely to predominate. Genetic analysis demonstrated that the rabies virus strain currently circulating within dog populations in Limpopo province is the same variant responsible for the 2005/2006 rabies outbreak. However, residual foci probably exist hence the observed sporadic outbreaks. These data further underline the value of continuous and sustainable dog immunization in controlling rabies.

Key words: Epidemiology, phylogeny, rabies.

Rabies virus (RABV), a member of the *Lyssavirus* genus (family Rhabdoviridae), consists of a single-stranded, negative-sense RNA genome. The virus is neuroinvasive and infection generally leads to an acute encephalitis. Epidemiologically, RABV is distributed throughout the world, with the exception of nation islands. Furthermore, RABV has a wide host range including terrestrial mammals and several bat species. In Asia and Africa, the disease is mainly diagnosed in dogs, hence most human rabies infections result from exposure to infected dogs.

Limpopo province (Fig. 1*a*), was the first entry point of rabies in the 1950s, apparently from Angola [1], and this region has experienced periodical rabies outbreaks involving domestic (dogs) and wildlife (black-backed jackals) species since then [2–4]. More recently (2005/2006), a dog rabies outbreak that occurred in this province resulted in at least 20 human deaths [5] and was subsequently traced back to southern Zimbabwe. No rabies cases were reported from Limpopo province for many years prior to the 2005/2006 outbreak. Following this outbreak, massive dog vaccination campaigns were mounted resulting in a significant reduction of human rabies cases, from 22 in 2006 to three in 2010 [5].

Dog rabies outbreaks in Limpopo province commonly occur in the north and northeastern districts

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Fig. 1. (a) Map of South Africa showing the nine provinces and the geographical location of Limpopo province. (b) Local and district municipalities of Limpopo province.

due to the presence of susceptible dog populations in rural areas (see Fig. 1*a, b*). The recent dog rabies outbreak in Limpopo was followed by comprehensive dog vaccinations by the Department of Veterinary Services.

In this investigation, dog and wildlife rabies trends in northern Limpopo between 2004 and 2009 (Fig. 2*a, b*), and genetic relationships of selected dog RABVs were established. Eighteen dog RABVs,

Table 1. *Virus isolates included in the study*

Virus number	Laboratory ref. number	Species of origin	Locality of origin	Genbank accession number
1	j45/94	Jackal	Warmbad	EF686064
2	d479/96	Dog	Thabazimbi	AF303070
3	j504/96	Jackal	Warmbad	AF177108
4	j528/97	Jackal	Thabazimbi	EF686062
5	j306/98	Jackal	Warmbad	AF177105
6	j418/99	jackal	Polokwane	EF686070
7	j549/99	Jackal	Polokwane	EF686069
8	j557/99	Jackal	Polokwane	EF686054
9	j669/99	Jackal	Polokwane	AF303062
10	j673/99	Jackal	Potgietersrus	AF303061
11	j717/99	Jackal	Polokwane	AF303064
12	j1004/99	Jackal	Polokwane	EF686052
13	j433/01	Jackal	Ellisras	EF686084
14	j307/02	Jackal	Ellisras	EF686081
15	j629/02	Jackal	Ellisras	EF686083
16	j543/03	Jackal	Ellisras	EF686088
17	d370/05	Dog	Thohoyandou	EF686082
18	d391/05	Dog	Thohoyandou	EF686089
19	d409/05	Dog	Thohoyandou	EF686091
20	d449/05	Dog	Thohoyandou	EF686095
21	d507/05	Dog	Sibasa	EF686085
22	d535/05	Dog	Sibasa	EF686093
23	d561/05	Dog	Thohoyandou	EF686094
24	d302/06	Dog	Nkomazi	FJ842746
25	d472/06	Dog	Tzaneen	HM060256
26	d992/06	Dog	Tzaneen	HM060254
27	d1033/06	Dog	Tzaneen	HM060257
28	d1034/06	Dog	Tzaneen	HM060258
29	d1088/06	Dog	Tzaneen	HM060255
30	d25/07	Dog	Tzaneen	GU808524
31	d129/07	Dog	Phalaborwa	GU808521
32	d189/07	Dog	Sibasa	GU808520
33	d377/07	Dog	Houtbosch	GU808522
34	d447/07	Dog	Giyani	GU808523
35	d120/08	Dog	Lenyenye Township	GU808519
36	d818/08	Dog	Suikervlei	GU808518
37	d1088/08	Dog	Tzaneen	GU808517
38	d1217/08	Dog	Nchakhu	GU808516
39	d169/09	Dog	Mkemané	GU808515
40	d460/09	Dog	Thohoyandou	GU808514
41	d572/09	Dog	Mukula	GU808513
42	d1305/09	Dog	Vhulaudzi Village	GU808512

all previously shown to contain RABV antigen [6], were selected from the archive at the Onderstepoort Veterinary Institute (OVI), Pretoria, and included in this study. Total viral RNA was extracted and the cytoplasmic domain of the glycoprotein and the G–L intergenic region of each virus isolate was amplified and sequenced as described previously [4, 5] (BigDye[®] Terminator v. 3.1, Applied Biosystems, USA) and the G(+) and L(–) primers.

Nucleotide sequences were analysed using standard software packages for multiple alignments [7, 8] and phylogenetic analysis was based on an alignment of a 592-nt sequence region for the construction of the Neighbour-joining tree [7]. The phylogenetic analyses demonstrated that the RABVs recently recovered from domestic dogs in eastern Limpopo clustered together with RABVs responsible for the 2005/2006 outbreak [(1i);

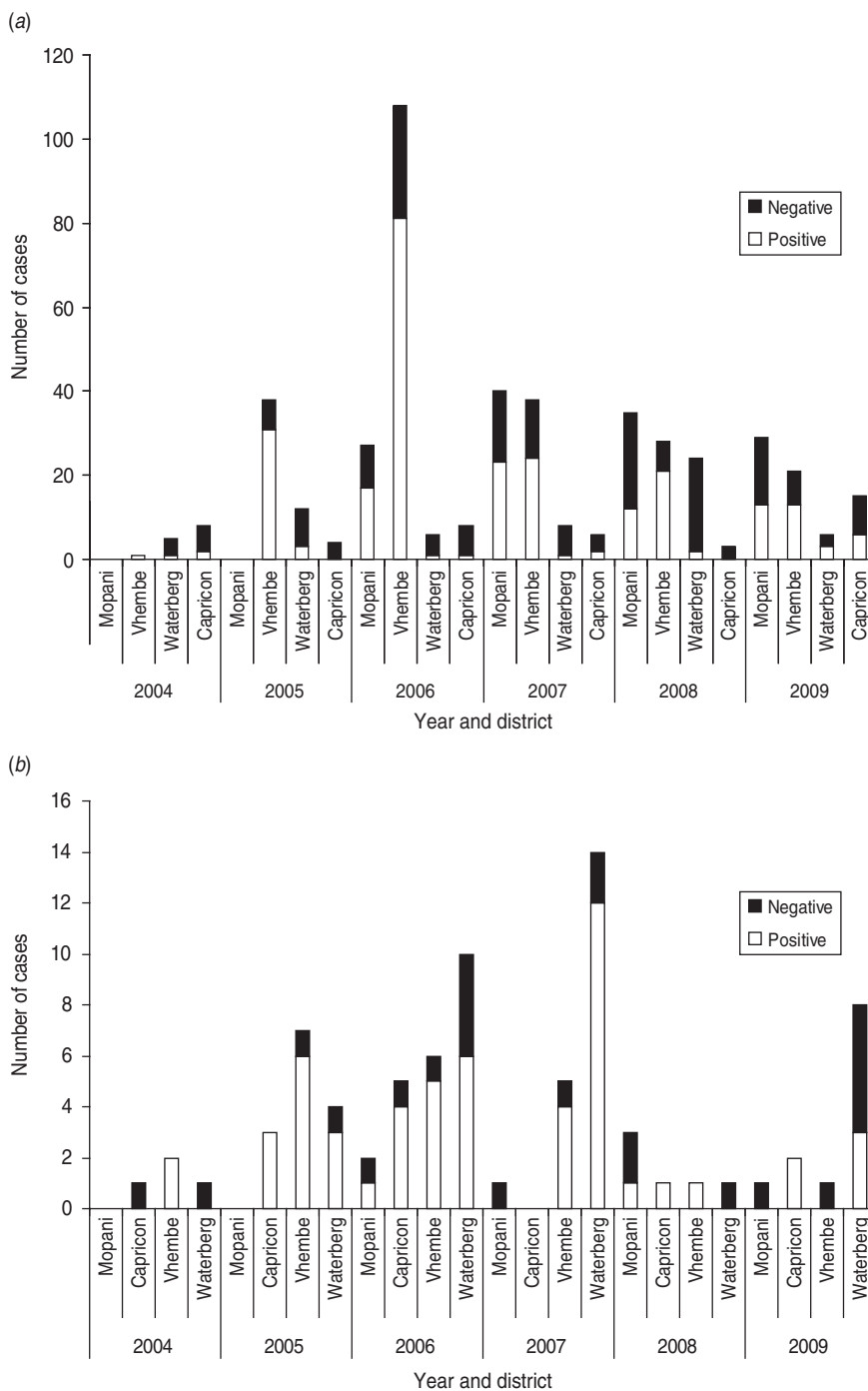


Fig. 2. Number of (a) positive dog rabies cases and (b) positive jackal rabies cases in Limpopo, 2004–2009, according to municipal district (data obtained from the Records of Onderstepoort Veterinary Institute, Pretoria, South Africa).

Fig. 3] [5], and are of the canid-associated Africa 1b variant [9].

A case surveillance data analysis (for 2004–2009) from the study region (Fig. 2a) demonstrated an initial increase in the number of dog rabies cases in the Vhembe district reaching a peak in 2006 which coincided with the human rabies outbreak [5, 10].

No samples were submitted from Mopani district in 2004 and 2005, but in 2006 ($n = 17$) and 2007 ($n = 23$) rabies cases were recorded, and a marked reduction was noted in 2008 and 2009 (in Mopani district) parallel to observations in neighbouring Vhembe district. Whether these rabies cases in Mopani district were due to spillover from Vhembe is not clear. Although

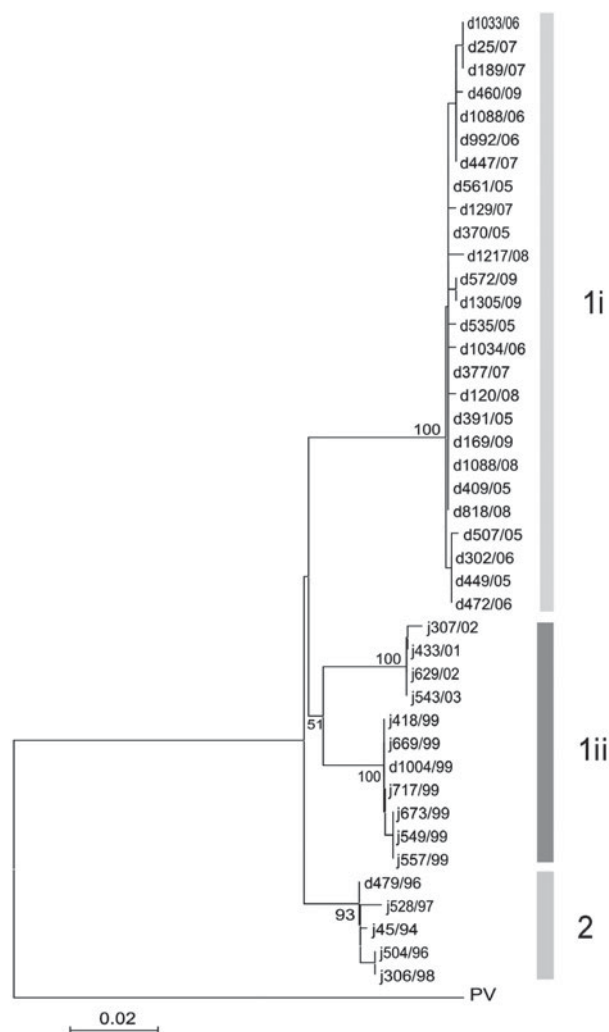


Fig. 3. Phylogenetic tree based on an alignment of a 592-bp region of the G–L intergenic region of 42 RABV isolates obtained from domestic dog (d) and jackal (j) species from Limpopo province. The Pasteur Virus (PV) strain was used to root the tree.

the Waterberg and Capricorn districts generally had fewer reported cases of dog rabies ($n=5$) during the same period under review, an increase in submissions was noted in 2008 (Waterberg, $n=24$) and 2009 (Capricorn, $n=15$). These two districts are generally associated with game ranches and less human settlements compared to Vhembe and Mopani districts hence the reduced number of dog rabies cases.

Case surveillance data confirmed RABV infection in the black-backed jackal (BBJ) species *C. mesomelas* in Vhembe, Mopani, Capricorn and Waterberg districts. Capricorn district also recorded positive cases in this species in 2005, 2006 and 2009. Rabies in BBJ is commonly reported in the Waterberg district and is independent of dog rabies. This observation is

consistent with ecological conditions that exist here and are believed to be conducive to the proliferation of the BBJ species. No parallel decrease in rabies cases was observed in BBJ as seen in dogs (2005–2007), a possible indication that spatial factors influence rabies dynamics in this wild carnivore species [4, 11].

The reduction in the number of rabies-positive cases is most likely a result of vaccination campaigns that were mounted in response to the 2005/2006 rabies outbreak. This situation is likely to persist for some years in future, provided that vaccination campaigns are appropriately targeted and performed annually. Based on the surveillance data presented here (Fig. 2*a*) it is possible that an increase in vaccination coverage levels and sustainability of vaccination campaigns could eliminate or control rabies.

In many developing nations of Africa and Asia, vaccination coverage levels are often quite low, and range from 4% to 60% [5] depending on accessibility to dogs for these programmes. However, in order to achieve herd immunity against rabies, the World Health Organization (WHO) recommends that at least 70% of a population should be vaccinated annually. Nonetheless, the efficacy of vaccination campaigns are rarely evaluated by means of monitoring herd immunity in South Africa and the rest of Africa. Similarly, in the Eastern Cape province (South Africa), although vaccination of dogs and cats has been implemented since 1996, the practice has neither curbed the spread nor prevented the number of domestic rabies cases [12] and this underscores the challenge that rabies control is facing not only in Limpopo, but in many other parts of the country. Although rabies prevalence appears to be in gradual decline, it could be that residual foci may still persist in some isolated areas and could potentially serve as sources of subsequent outbreaks in the presence of susceptible dog populations [13].

It is true that parenteral vaccination still remains the most effective approach in reducing the spread of canine rabies in Africa [14]. It should be further emphasized that only well coordinated and comprehensive vaccination campaigns are capable of eliminating dog rabies in the sub-region and these approaches will greatly assist in preventing future rabies outbreaks in dogs. Naturally, ongoing surveillance is required to detect residual foci or re-infection, particularly in those areas where rabies has been or is believed to have been eliminated [13].

Phylogenetic data presented here demonstrate an expansion of a cluster of viruses previously shown to

have originated from Zimbabwe and further underline the maintenance of the same variant in dog populations in Limpopo province. There is a definite potential of rabies to spillover to wildlife species (cluster Iii) and the opportunistic nature of the RABV strain enhances the ability of RABV to cross species barriers fairly easily, making it very difficult to eliminate rabies in this region.

Domestic and wildlife species in communal areas clearly remain the major sources for rabies outbreaks. The inconsistency and infrequency of vaccination campaigns and lack of evaluation of their effectiveness thereof makes it more difficult to eliminate or control rabies foci in these regions. Furthermore, the lack of awareness in communities about rabies compounds the problem, resulting in small numbers of animals being presented for vaccination. Biannual vaccinations with campaigns repeated every 6–8 months, particularly in areas with high dog populations, should be considered but the practicality of such approaches present potential problems given the cost limitations associated with these approaches.

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DECLARATION OF INTEREST

None.

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