CANID RABIES IN ZIMBABWE AND SOUTH AFRICA
A REVIEW

C.T. Sabeta123 and L.H. Nel1

1 BRIEF HISTORICAL REVIEW.

Despite the advances and progress towards the control of infectious diseases made in the past century, rabies is still a disease of serious public health concern. As many as 50000 preventable deaths occur annually in the developing nations of Asia, Latin America and Africa (Meslin et al., 1994; Blan- cou, 1988).

In comparison to the other continents where rabies is endemic, the history of rabies in Africa before the 19th century, is rather fragmentary and largely anecdotal. There are no definite reports to indicate that rabies was present in Zimbabwe before 1902, although Edmonds (as cited by Foggin, 1988 and Swanepoel et al., 1993) reports anecdotal evidence from older members of the population who claimed to remember cases from before the European occupation. The first definite cases of rabies in Zimbabwe were reported in 1902 in dogs and thought to have originated from Zambia. The disease spread throughout most parts of Zimbabwe and was subsequently controlled through destruction of stray dogs, compulsory vaccination of all dogs and introduction of a dog tax. Zimbabwe remained rabies-free between 1913 and 1950, with the exception of two other dog rabies cases diagnosed in dogs that were imported from Zambia in 1938.

In South Africa, an epizootic involving domestic animals in 1893 could be traced back to an Airedale Terrier that had recently been imported from England (Hutcheon, 1894 as cited by King et al., 1994). Furthermore, traditional folklore of the Baralong tribe from the northern Cape, writings of early travelers and explorers contain accounts of rabies, are strongly suggestive of the existence of rabies before the 1900s (Snyman, 1940). From 1916 onwards, the disease occurred with more frequently in the yellow mongoose *Cynictis penicillata*. There was doubt as to whether this was indeed rabies (Cluver, 1927) and only in 1928, this doubt was removed when rabies was confirmed in two schoolboys who had died after being bitten by a tame yellow mongoose.

Canid rabies was recently introduced into southern Africa from Angola by dogs (Swanepoel et al., 1993). It then spread to Zimbabwe and South Africa in the dog population in the 1950s and in the 1960s spread into KwaZulu-Natal and has persisted ever since.

In Zimbabwe, the domestic dog *Canis familiaris*, side stripped jackal *Canis adustus* and black backed jackal *Canis mesomelas* are the principal vectors of rabies (Foggin, 1988; Bingham 1999a, 1999b, 1999d). The majority of domestic dogs live in communal lands (Brooks, 1990; Butler, 1998; Butler and Bingham, 2000) and account for approximately 50% of all confirmed rabies cases. Jackal rabies accounts for 25% of all confirmed rabies cases. In South Africa, rabies cycles in several reservoir species with specific geographical associations. These include the domestic dog in KwaZulu-Natal, black-backed jackals in the northern border areas with Zimbabwe and bat-eared foxes *Otocyon megalotis* in the western Cape region (Swanepoel et al., 1993). The geographic distribution of the principal vector species in Zimbabwe and South Africa is shown in Figure 36.
2 ANTIGENIC DATA.

Monoclonal antibodies (Mabs) can be used to detect specific epitopes on the viral proteins and presence or absence of these epitopes can define a virus taxonomically. Mab studies have demonstrated the existence of two rabies biotypes in southern Africa (King et al., 1993, 1994). The two biotypes are referred to as canid (infecting carnivores of the family Canidae) and viverrid (infecting carnivores of the subfamily Viverrinae). The demonstration of the two distinctive reaction patterns in the nucleoprotein (N) of rabies viruses isolated from species of South Africa supported Foggin’s postulation (1988) that isolates of mongoose origin differed from those that commonly circulated in domestic dogs and jackal species.

Today, nucleoprotein directed Mabs are still an important diagnostic tool for differentiating lyssavirus genotypes. For instance, the Onderstepoort Veterinary Institute (OVI) is presently involved in routine typing of lyssaviruses. A case in point is a rabies virus from an African wild civet Civettictis civetta (from Zimbabwe), which gave an inconclusive result when typed in Harare but was later classified as viverrid using a polyclonal conjugate at OVI (Meredith, 1995). Rabies samples are part of a few repositories in Africa and retrospective antigenic screening can be useful in lyssavirus surveillance on the continent. In this way unusual lyssaviruses have been identified from a collection of rabies isolates (Bingham et al., 2001).

3 MOLECULAR ERA.

Although antigenic analysis of viruses has been very useful in lyssavirus epidemiology by discriminating between variants, tools of molecular biology have added dimensions of speed and precision. Sequences of genes of the nucleoprotein, phosphoprotein and the glycoprotein and G-L intergenic region have been particularly useful in determining the molecular epidemiology of rabies throughout the world (Tordo et al., 1986; Nadin-Davis et al., 1993, 2001; Sacramento et al., 1992). In southern Africa, a few molecular studies on a limited number of virus isolates were conducted (Nel et al., 1993; Von Teichman et al., 1995; Nel et al., 1997) although they were focused on the genetic distinction of the two rabies biotypes (Nel et al., 1993, 1997, 1998; Von Teichman et al., 1995).
Recently, we embarked on a comprehensive and regional comparative genetic study of viruses of the canid biotype from different host species throughout Zimbabwe and South Africa. We targeted the cytoplasmic domain of the glycoprotein and the G-L intergenic region, shown to be most divergent region of the rabies genome (Tordo *et al.*, 1986), and thus useful for short-term evolutionary studies. All the southern African virus isolates were found to lack one of the two polyadenylation sites postulated for the G genes of ERA and Pasteur Virus PV (Tordo *et al.*, 1986). The absence of this signal has been shown in street viruses from Europe, and was suggested to be of transcriptional rather than evolutionary significance (Sacramento *et al.*, 1992). Phylogenetic analysis delineated the viruses into 5 groups that had significant bootstrap support (Figure 37). The five groups corresponded to viruses from dog and jackal species from Zimbabwe and South Africa (group 1), from dogs only from northeastern Zimbabwe (group 2), a group from bat-eared fox isolates (group 3), jackal and dog viruses from central Zimbabwe (group 4) and the last one from domestic dogs and jackal species from southern Zimbabwe and northern bordering areas of South Africa (group 5).

**Figure 37: Phylogenetic tree of nucleotide sequences of the cytoplasmic domain of the glycoprotein and the G-L intergenic region of selected canid viruses from Zimbabwe and South Africa.** Principal bootstrap values are indicated at the nodes. The sequence PV was included as outgroup.

The most important finding of this investigation is that all the southern African canid viruses were closely related with an average sequence homology of 96.6% (Sabeta *et al.*, 2003) and could be distinguished from PV used as the outgroup irrespective of geographical origin. This result is suggestive of a common and recent origin, consistent with the historical emergence of canid cycles (Swanepoel *et al.*, 1993). The results from this investigation further support findings of other studies in which rabies virus isolates from both domestic dogs and jackal sp. were shown to have no antigenic distinctions, implying that they were closely related (King *et al.*, 1994; Bingham *et al.*, 1999b).
4 **FUTURE PERSPECTIVES.**

It is evident from this investigation that the canid lineage is now well established in the southern African sub-continent and is most likely to initiate future cycles. Two aspects of epidemiology, viz surveillance and knowledge of the distribution of the antigenic and genetic virus variants, are essential components of an efficient and economical rabies control program. In this regard, results from this study underscore the need for continual surveillance of lyssaviruses in the greater part of Africa, in man, domestic and wild carnivore species.

**ACKNOWLEDGEMENTS**

We are grateful to the following individuals whose work is included in this presentation:

John Bingham, Alex Wandeler, Beate von Teichman, Chris Foggin, George Bishop and Arthur King.

**REFERENCES**


