4. FUTURE PROSPECTS

The genetic diversity observed in parasitic populations is not solely influenced by their own reproductive and transmission patterns, but also by the host's genetics and behaviour (Höglund *et al.* 2012). The connectivity between sampled regions is contributed to by the movement of domestic/ companion animals (Belanger *et al.* 2011), also known as anthropogenic mediation (Jung *et al.* 2010). It is therefore necessary to further explore the potentially important role of human-induced dispersal in shaping genetic structure. The result of such a study may well find that limiting the movement of hosts in order to create barriers to gene flow may be an effective control strategy (Johnson *et al.* 2006).

Future studies may have to rely on samples of offspring in the egg stage (Gilabert & Wasmuth 2013) that can be obtained from the faeces of infested dogs since the collection of adult parasites is impractical – adult worms can only be obtained from deceased dogs (personal communication with veterinary parasitologists).

The study of genetic variation in parasitic populations has implications for vaccine development and anthelminthic efficacy trials. In the case of vaccine development, it is essential to know whether parasitic populations differ at targeted loci so that one can predict the geographical scale at which potential vaccines will be effective (Anderson *et al.* 1998; Hawdon *et al.* 2001). The use of anthelminthics to control infestation with a parasite remains the most widely used method since it is easy to implement. However, when treating spirocercosis it is important to keep in mind that symptoms only become visible once the disease has progressed to advanced stages, at which point treatment is considered ineffective. Also, the high costs associated with preventative treatments most likely discourage pet owners from implementing them (personal communication with local veterinarians).

Mating systems can affect the distribution of genetic variation within and among populations (Charlesworth 2003; Steinauer *et al.* 2010). Uncovering mating systems are essential to determine which individuals are mating with each other. Like many other internal parasites, *S. lupi* adult worms are confined to their final hosts, e.g. dogs. Adult worms are limited to mating with other adult worms within the same host or nodule. Yet, the results of the present study indicate that the worms within dogs are outbred, suggesting that the worms inside the nodules already have a high amount of genetic variation and will give rise to highly varied offspring. Thus further investigation into the mating system of *S. lupi* would be beneficial to further understanding the dynamics of the populations.

For future studies it may also be of value to explore the role of sex-specific structure in order to determine whether male and female parasites induce differences in transmission patterns (Gorton *et al.* 2012). Sex-specific genetic structure has been demonstrated in *Schistosoma mansoni* (Prugnolle *et al.* 2002) and will indeed be beneficial for furthering the study of host-parasite interactions. Host-parasite systems need to be explored in order to determine the effects of parasite genetic diversity on host biology regarding aspects such as host immunity and pathology (Theron *et al.* 2004).

Landscape genetics can be used as a tool to reconstruct parasite movement and improve epidemiological estimates of the geographical origin of a parasite species (Archie *et al.* 2008). Population genetics, landscape ecology and spatial statistics are combined to determine how landscape and environmental variables influence individual movement and microevolutionary processes such as gene flow, genetic drift and local adaptation (Archie *et al.* 2009; Guillot *et al.* 2005). It allows one to determine where and why parasites are moving on the landscape. The analysis is conducted by detecting and locating genetic discontinuities between populations (Guillot *et al.* 2005) and correlating these discontinuities with landscape and environmental features (e.g., mountains, rivers, roads, degree of humidity, and deforested areas). Such a study would be useful since certain landscape features are known to increase or decrease disease spread.

The findings of this study have important implications for the further study of molecular epidemiology in *Spirocerca lupi* and possibly controlling the spread of spirocercosis in South Africa.

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