

SHORT NOTES

**Avian host DNA isolated from the feces of white-winged vampire bats  
(*Diaemus youngi*)**

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INTRODUCTION

Studies on the feeding ecology of vampire bats (Phyllostomidae: Desmodontinae) have been limited by the diagnostic techniques available for identifying host taxa. A precipitin-based test has been the standard method for determining their domestic host preferences (e.g., Cardoso, 1995). This postmortem immunological assay provides a presence or absence indication of a particular host's blood in a vampire bat's gut contents (Greenhall, 1970). However, the precipitin test has significant limitations. The bat must be sacrificed for its stomach sample, a particular difficulty for the rare species *Diaemus youngi* and *Diphylla ecaudata*. The precipitin test has low utility for identifying wild hosts (Greenhall, 1970), as it requires the harvesting of antibodies, usually in rabbits, using serum collected from all potential host organisms. For this reason, antibody techniques are generally considered too costly (time-wise and financially) for investigating a diverse potential prey

range (Symondson, 2002). Indeed, harvesting antibodies of all the potential sympatric avian host species of a vampire bat would be unfeasible. Third, cross-reactivity among related host taxa is expected, and the precipitin technique is therefore unlikely to be diagnostic at the level of families or genera.

An alternative and potentially powerful approach is to use the host DNA as a marker for host identification. Although previous studies demonstrate that prey DNA can be isolated and amplified via PCR from feces (Hoss *et al.*, 1992; Sutherland, 2000; Jarman *et al.*, 2002, 2004; Jarman and Wilson, 2004; Deagle *et al.*, 2005) and even fossilized feces (e.g., Kuch *et al.*, 2002), vampire bat fecal samples are a uniquely implausible PCR template due to the lack of robust tissue and very high concentration of PCR-inhibiting heme compounds. The resistance of prey tissue to digestion is a factor determining the extent to which the targeted fecal DNA is degraded (Jarman *et al.*, 2004). Past successful PCR-based