

Detection of *Vibrio cholerae* O1 in animal stools collected in rural areas of the Limpopo Province

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Abstract

Vibrio cholerae (*V. cholerae*), the causative agent of cholera, has been responsible for various outbreaks worldwide and may be associated with animal faeces. In an attempt to understand the occurrence of this organism in the environment, 230 faecal samples were collected from pigs, chickens, goats, donkeys, cows and pigeons in rural areas of the Limpopo Province. Bacterial DNA was extracted from the faecal samples using a guanidium thiocyanate-based method. The DNA was screened for the presence of the *sodB*, *rfb*, *FlaE*, 16S rRNA and *ctxA* genes associated with *V. cholerae*, *V. cholerae* O1, *V. cholerae* O139 using 2 multiplex polymerase chain reactions (m-PCR). The *V. cholerae sodB* gene was detected in 74 of the 230 samples tested. Detection rates for the faecal samples obtained from individual species were as follows: cows (55/74), chickens (8/74), goats (2/74), donkeys (4/74), pigs (3/74) and pigeons (2/74). *V. cholerae* O1 was detected in (17/74) cow and (3/74) chicken samples, of which (9/17) cow samples and (3/3) chicken samples tested positive for toxigenic *V. cholerae* O1. The presence of this organism in faecal samples, taken close to water sources used by the villagers, raises the possibility that the causative *V. cholerae* O1 strain of the most recent outbreak in South Africa was present in the area 6 months prior to the outbreak.

Keywords: *Vibrio cholerae*, PCR, animal faeces, cholera toxin