

## Genetic variability within and among Hypobiotic *Haemonchus contortus* isolates from goats in Kenya

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### Abstract

*Haemonchus contortus* (order Strongylida) is a common parasitic nematode infecting small ruminants and causing significant economic losses worldwide. Knowledge of genetic variation within and among *H. contortus* populations can provide a foundation for understanding the biology and transmission patterns and might contribute to the control of haemonchosis. Infective larvae of *H. contortus* were cultured from eggs collected from goats raised on six farms located in different geographical regions in Kenya. The second internal transcribed spacer (ITS-2) of the nuclear ribosomal DNA and mitochondrial nicotinamide dehydrogenase subunit 4 gene (*nad4*) were amplified by polymerase chain reaction (PCR) and sequenced directly. The sequence variations and population genetic diversities were determined. Nucleotide sequence analyses revealed 18 genotypes (ITS-2) and 142 haplotypes (*nad4*) among the 152 worms, with nucleotide diversities of 2.6% and 0.027, respectively, consistent with previous reports from other countries. Population genetic analyses revealed that 92.4% of nucleotide variation was partitioned within populations; there was no genetic differentiation but a high gene flow among Kenyan populations; some degree of genetic differentiation was inferred between some specimens from China and those from other countries. This is the first study of genetic variation within *H. contortus* in Kenya. The results revealed high within-population variations, low genetic differentiation and high gene flow among different populations of *H. contortus* Kenya. The present results could have implications for studying the epidemiology and ecology of *H. contortus* in Kenya.

**Key words:** *Haemonchus contortus*, Genetic variation