Molecular identification of different Trichostrongylus species infecting sheep and goats from Dakahlia governorate, Egypt

Rana Elseadawy1 • Ibrahim Abbas1 • Moustafa Al-Araby1 • Salah Abu-Elwafa1
[b]Department of Parasitology, Faculty of Veterinary Medicine, Mansoura University, Mansoura 35516, Egypt.

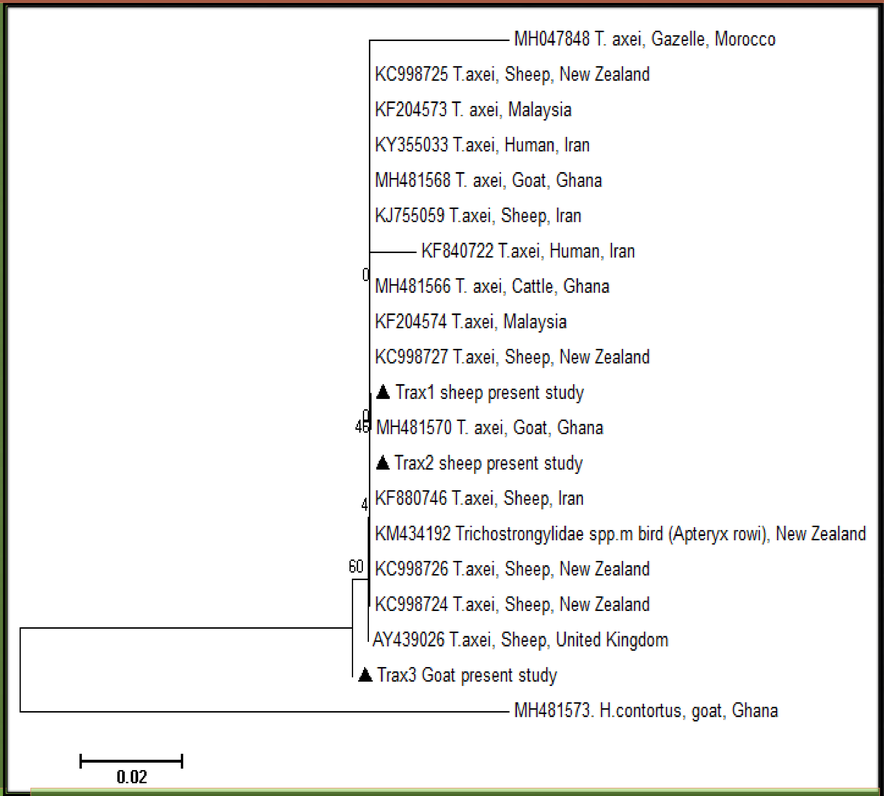
Introduction

- Nematodes of the family Trichostrongylidae are common causes of parasitic gastroenteritis,
  - ✓ Serious diahrrea
  - ✓ Decrease weight gain
  - ✓ Recumbancy
  - ✓ Increase morbidity
    - Several *Trichostrongylus* species (e.g. T*. colubriformis, T. axei, T. orientalis, T. vitrinus and T. capricola*) have been identified in infected humans
    - However, *T. colubriformis* is associated with many reported cases worldwide and isolates of this parasite from humans are molecularly identical to those from animals in the same area.
- Thus, accurate identification of different *Trichostrongylus spp*. in animal hosts would reflect the species that can infect humans in the same area.
- Reports on human trichostrongylosis in Egypt are scarce.
- The present study aimed at accurate identification of different *Trichostrongylus spp.* infecting small ruminants from Dakahlia governorate, employing the molecular characters of this parasite and amplifying the ITS2 rDNA .

Materials and Methods

Sample collection

- Rectal fecal samples were collected from 340 sheep and 115 goat samples in rural areas of 3 cities in Dakahlia governorate (Talkha, Dekernse and Nabrouah) and 2 cities (ElMahala ElKubra and Biyala) at the borders of Dakahlia.
- **Faecal examination**
- using the modified Wisconsin sucrose flotation method.
- **DNA extraction**
- using the DNeasy plant kits (Qiagen, Valencia, CA, USA) .
- **PCR amplification**
- The isolated DNA was amplified in conventional PCR reactions targeting the ITS2 region of the ribosomal DNA for 3 different *Trichostrongylus spp*. using species-specific primers; *T. axei, T. colubriformis* and *T. vitrinus*.
- **Sequencing**
- The positive bands were incised, purified using QIA quick PCR purification kits (Qiagen, Valencia, Ca, USA) and commercially sequenced (Colors lab, Cairo, Egypt).
- **Data analysis**
- The phylogenetic analysis was conducted using the Neighbor-joining method with Kimura 2-parameter of evolution in Mega6 software.



Results

- Microscopic examination revealed strongyle-type eggs in 33.2% (113/340) of sheep and 14.7% (17/115) of goat samples.
- In the PCR-tested samples, 2 *Trichostrongylus species* were identified; *T. axei* (186 bp) and *T. colubriformis* (232 bp).
- No *T. vitrinus* was noted in any sheep or goat sample.
- *Trichostrongylus axei* was the most prevalent species
- *Trichostrongylus colubriformis* was detected in 2 samples but in a combination with *T. axei*
- sequence analysis of the revealed ITS2 partial nucleotide sections of *T. axei* isolates displayed 3 different haplotypes, 2 from sheep (Trax1 and Trax2) and one from goats (Trax3).

Legend

- ❑ Neighbor-joining phylogenetic tree constructed using partial ITS2 rDNA nucleotide sections of *Trichostrongylus axei* isolates from different hosts and geographical regions.
- ❑ *Haemonchus contortus* was used as an out group.
- ❑ Scale bar indicates the proportion of sites changing along each branch.