Table S1. Prevalence of GI parasites among 276 meat goats in Nakhon Si Thammarat province, southern Thailand.

GI parasite	Stage	No. of positives	Prevalence (%)	Zoonotic status
Nematode				
Strongyles	Egg	186	67.4	Zoonotic (some species)
Strongyloides papillosus	Egg	15	5.4	Non-zoonotic
Trichuris spp.	Egg	61	22.1	Non-zoonotic
Capillaria spp.	Egg	3	1.1	Non-zoonotic
Cestode				
Moniezia spp.	Egg	5	1.8	Non-zoonotic
Trematode				
Rumen flukes	Egg	52	18.8	Non-zoonotic
Fasciola spp.	Egg	9	3.3	Zoonotic
Protozoa				
Eimeria spp.	Oocyst	201	72.8	Non-zoonotic
Giardia spp.	Cyst	1	0.4	Zoonotic

GI: Gastrointestinal

Table S2. Prevalence of single infection and co-infection of GI parasites of meat goats (*n* = 245) detected by microscopic examination.

Parasite infection	No. of positive samples (%)
Single infection	
Eimeria spp.	43 (17.6)
Strongyles	20 (8.2)
Trichuris spp.	4 (1.6)
Rumen flukes	1 (0.4)
Total	68 (27.8)
Double infection	
Strongyles + *Eimeria* spp.	70 (28.6)
Strongyles + *Trichuris* spp.	7 (2.9)
Strongyles + Rumen flukes	9 (3.7)
Strongyles + *Fasciola* spp.	1 (0.4)
Trichuris spp. + *Eimeria* spp.	4 (1.6)
Capillaria spp. + *Eimeria* spp.	1 (0.4)
Rumen flukes + *Eimeria* spp.	2 (0.8)
Total	94 (38.4)
Triple infection	
Strongyles + *Strongyloides papillosus* + *Eimeria* spp.	2 (0.8)
Strongyles + *Trichuris* spp. + *Eimeria* spp.	26 (10.6)
Strongyles + *Capillaria* spp. + *Eimeria* spp.	2 (0.8)
Strongyles + *Moniezia* spp. + *Eimeria* spp.	2 (0.8)
Strongyles + Rumen flukes + *Eimeria* spp.	21 (8.6)
Strongyles + *Fasciola* spp. + *Eimeria* spp.	1 (0.4)
Trichuris spp. + Rumen flukes + *Eimeria* spp.	1 (0.4)
Strongyles + Rumen flukes + *Fasciola* spp.	1 (0.4)
Rumen flukes + *Fasciola* spp. + *Eimeria* spp.	2 (0.8)
Total	58 (23.7)
Quadruple infection	
Strongyles + *Strongyloides papillosus* + *Trichuris* spp. + *Eimeria* spp.	8 (3.3)
Strongyles + *Strongyloides papillosus* + Rumen flukes + *Eimeria* spp.	2 (0.8)
Strongyles + *Strongyloides papillosus* + *Giardia* spp. + *Eimeria* spp.	1 (0.4)
Strongyles + *Trichuris* spp. + *Moniezia* spp. + *Eimeria* spp.	1 (0.4)
Strongyles + *Trichuris* spp. + Rumen flukes + *Eimeria* spp.	7 (2.9)
Strongyles + Rumen flukes + *Fasciola* spp. + *Eimeria* spp.	1 (0.4)
Strongyloides papillosus + *Trichuris* spp. + Rumen flukes + *Fasciola* spp.	1 (0.4)
Total	21 (8.6)
Quintuple infection	
Strongyles + *Strongyloides papillosus* + Rumen flukes + *Fasciola* spp. + *Eimeria* spp.	1 (0.4)
Strongyles + *Trichuris* spp. + *Moniezia* spp. + Rumen flukes + *Eimeria* spp.	2 (0.8)
Strongyles + *Trichuris* spp. + Rumen flukes + *Fasciola* spp. + *Eimeria* spp.	1 (0.4)
Total	4 (1.6)

GI: Gastrointestinal; *n*: No. of samples.

Table S3. Strongyle genera identified from pooled fecal positive samples of individual farms detected by microscopic examination of L3 and semi-nested PCR of strongyle nematode eggs during the wet and dry seasons.

Strongyle infection	No. of strongyle detected (%)		
	Wet season (*n* = 20)	Dry season (*n* = 16)	Total (*n* = 36)
Microscopic examination of L3 larvae			
Trichostrongylus spp. + *Haemonchus* spp.	14 (70.0%)	9 (56.3%)	23 (63.9%)
Trichostrongylus spp. + *Haemonchus* spp. + *Oesophagostomum* spp.	6 (30.0%)	7 (43.7%)	13 (36.1%)
Semi-nested PCR of strongyle nematode eggs			
Trichostrongylus spp. + *Haemonchus* spp.	—	1 (6.3%)	1 (2.8%)
Trichostrongylus spp. + *Haemonchus* spp. + *Oesophagostomum* spp.	20 (100.0%)	15 (93.7%)	35 (97.2%)

L3: Third-stage larvae; PCR: Polymerase chain reaction; *n*: number of samples

Table S4. BLAST searches of strongyle sequences from representatives of known genera of L3.

Voucher code	Result of sequencing		GenBank ID	Host animal	Country	Reference
	Species from BLAST top hit	% identity to BLAST top hit				
PAH	*Haemonchus contortus*	98.82	MT193663	Goat	China	[35]
MUH	*Haemonchus contortus*	100.00	MT193663	Goat	China	[35]
CYH	*Haemonchus contortus*	100.00	MT193663	Goat	China	[35]
RPH	*Haemonchus contortus*	99.70	MT193663	Goat	China	[35]
SCH	*Haemonchus contortus*	99.70	MT193663	Goat	China	[35]
PKH	*Haemonchus contortus*	99.41	MT193663	Goat	China	[35]
TYH	*Haemonchus contortus*	98.82	JF680983	Sheep	Africa	Unpublished
TSH	*Haemonchus contortus*	99.70	MT193663	Goat	China	[35]
PAT	*Trichostrongylus colubriformis*	100.00	AB908960	Goat	Laos	[36]
CYT1	*Trichostrongylus colubriformis*	100.00	AB908960	Goat	Laos	[36]
CYT2	*Trichostrongylus colubriformis*	100.00	AB908960	Goat	Laos	[36]
CLT1	*Trichostrongylus colubriformis*	100.00	AB908960	Goat	Laos	[36]
CLT2	*Trichostrongylus colubriformis*	100.00	AB908960	Goat	Laos	[36]
RPT	*Trichostrongylus colubriformis*	99.42	AB908960	Goat	Laos	[36]
SCT	*Trichostrongylus colubriformis*	99.71	AB908960	Goat	Laos	[36]
CKT	*Trichostrongylus colubriformis*	100.00	AB908960	Goat	Laos	[36]
TYT	*Trichostrongylus colubriformis*	100.00	AB908960	Goat	Laos	[36]
TST	*Trichostrongylus colubriformis*	100.00	AB908960	Goat	Laos	[36]
CYO	*Oesophagostomum asperum*	100.00	KM200805	Goat	China	[37]
CLO1	*Oesophagostomum asperum*	100.00	KM200805	Goat	China	[37]
CLO2	*Oesophagostomum asperum*	99.72	KM200805	Goat	China	[37]

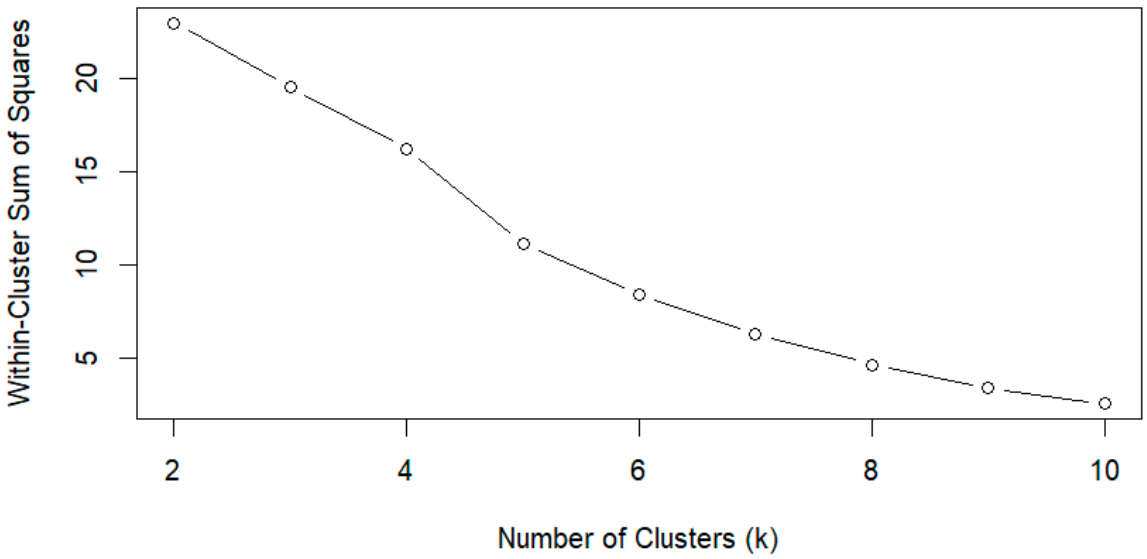


Figure S1. Determination of the optimal number of clusters for the prevalence patterns of parasitic infections using the elbow. The elbow plot illustrates the total within-cluster sum of squares (WSS) as a function of the number of clusters (k). The elbow at k = 4 indicates that four clusters effectively minimize within-cluster variability.