



REVIEW ARTICLE

Anthelmintic Resistance in *Haemonchus contortus* of Sheep and Goats from Asia—A Review of In Vitro and In Vivo Studies

Warda Qamar¹ and Khalid Ali Alkheraije^{2*}

¹Department of Parasitology, University of Agriculture, Faisalabad, Pakistan; ²Department of Veterinary Medicine, College of Agriculture and Veterinary Medicine, Qassim University, Buraidah, Saudi Arabia

*Corresponding author: k.alkheraije@qu.edu.sa

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ABSTRACT

The potential of *Haemonchus contortus* is quite impressive to acquire resistance to anthelmintic drugs. Asian field populations of *H. contortus* are reported to exhibit resistance to most of the anthelmintic drug families, including closantel, imidazothiazoles, macrocyclic lactones and benzimidazoles. This review paper comes up with a comprehensive overview of haemonchosis with anthelmintic resistance (AR), with particular attention to studies conducted in regions of Asia. It also confers the prevalence and mechanisms in *H. contortus* for anthelmintic resistance, indicating the necessity for alternative approaches to control the pathogen. Several SNPs identified in gene isotype-1 β -tubulin gene have been discussed that are associated with benzimidazole resistance and are prevalent in *H. contortus* populations in Asia. The methods used by *H. contortus* to withstand the effects of these medications are examined together with the history of how resistance to different anthelmintics in this species has developed. The approaches for diagnosing resistance are also compiled in this review. Such diagnosis currently largely relies on the fecal egg count reduction test, which has cost and sensitivity issues. Past and present efforts to use less expensive and time-consuming phenotypic assays with free-living life stages are also described with the developmental progress of molecular assays to provide sensitive resistance-detection tests. Overall, this paper provides valuable perception into the current understanding of AR in *Haemonchus spp.* and the challenges faced in the management of this disease in Asia.

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INTRODUCTION

Haemonchus (H.) contortus is an extremely harmful blood-feeding nematode of small ruminants, leading to Haemonchosis (Wang *et al.*, 2017; Imran and Alsayeqh, 2022). This parasite is also known as the "barber's pole worm" a major global source of mortalities (Preston *et al.*, 2016). It is transmitted through the ingestion of infective larvae present in the contaminated pasture. Grazing on pastures with high worm loads, little rainfall, high stocking density and young or immune-compromised breeds/animals are risk factors for the disease (Imran *et al.*, 2018; Khanyari *et al.*, 2021). This parasite is a major issue for cattle, leading to a variety of symptoms including anemia, weight loss, reduced production and in extreme cases, death (Nazish *et al.*, 2021; Şahin *et al.*, 2021). It is a significant threat to the profitability of the

livestock industry and therefore has a major economic impact (Besier *et al.*, 2016b; Qamar *et al.*, 2022). Haemonchosis also has implications for food security, as it reduces the amount of meat and dairy produced by infecting animals (Hoste and Chartier, 2002; Sargison, 2020). The worldwide estimated losses due to *H. contortus* can be substantial. The economic impact of *Haemonchus* infection in small ruminants is primarily due to reduced weight gain, decreased feed efficiency, decreased wool production, reduced reproduction and decreased market value (Zen *et al.*, 2014). The exact monetary losses vary depending on the region, the production system and the intensity of infection, but some estimates suggest losses of hundreds of millions of dollars globally (Mohammedsalih *et al.*, 2020; Kuiseu *et al.*, 2021). To reduce such huge economic losses control of the disease involves strategic deworming, pasture

management and the use of anthelmintic drugs. For instance, benzimidazole, levamisole, closantel and ivermectin have been extensively used in Asia and worldwide to treat worm infections. However, the extensive use of antiparasitic medications has led to significant issues with drug resistance in domestic animals around the globe (Abbas *et al.*, 2011; Kotze *et al.*, 2014; Muhammad *et al.*, 2015; Pawar *et al.*, 2019; Yuan *et al.*, 2019; Gainza *et al.*, 2021; Pinilla *et al.*, 2022; Alvi *et al.*, 2023). The emergence of resistant strains of *H. contortus* in Asia is a growing concern in livestock production. As the worm negatively affects the production of the animal, its resistance to commonly used anthelmintic drugs can lead to adverse impacts on livestock production (Saddiqi *et al.*, 2011). Effective management strategies, including targeted use of dewormers, breed resistance may help to mitigate the development of resistant strains (Imran *et al.*, 2020; Gandasegui *et al.*, 2022). Therefore, new intervention techniques must be developed in response to the rise of anthelmintic resistance in *H. contortus*. One possibility is the logical approach of developing and growing anti-parasitic medications and vaccines, based on a profound comprehension of the essential molecules in the processes of reproduction and development (Selzer and Epe, 2021). A clear understanding of the biological process at molecular level for *H. contortus* may help to identify critical molecules as potential novel therapeutic targets. This review discusses the prevalence of *H. contortus* and the current status of anthelmintic resistance in Asia. The study of key molecules in signaling pathways controlling development, the interaction between host cells and parasites, population genetics and the detection of anthelmintic resistance using conventional and molecular methods are some important areas of this study. The way these viewpoints are being brought out will help to pinpoint areas for more study and open up opportunities for new or improved control strategies.

Importance of the livestock sector in Asia: The majority of people in South Asia reside in rural regions and depend heavily on agriculture for both jobs and income. While the percentage of agriculture in total GDP varies from 12.7% in Sri Lanka to 34.7% in Nepal, the percentage of rural people in the total population spans from roughly 67% in Pakistan to over 86% in Nepal. More than 50% of the workforce in India and Nepal works in agriculture, which is a key source of employment for the enormous population in the region. Other South Asian nations have a heavy reliance on agriculture. Small farms dominate the region's agricultural production. The average size of farms in Bangladesh is 0.60, in Nepal 0.79, in Sri Lanka 0.69 and in India 1.23 hectares, respectively. In comparison to other nations in the region, Pakistan has considerably larger farms sizing 3.1 hectares (Abbas *et al.*, 2020). More than half of the world's 1 billion goats reside in Asia, which is also the region where the domestication of wild goats first started. China, India, Pakistan, Bangladesh and Mongolia have Asia's largest populations of goats and 512 million sheep and the nations with the most sheep were Turkey, Iran, Mongolia, China, India and Iran. In many low-income Asian nations, goats and sheep including dairy breeds—play important roles as producers of nourishment, food security and socioeconomic status for

their human owners. Goats are suitable for a broad variety of harsh environments (Liang and Paengkoum, 2019; Mazinani and Rude, 2020).

Infection is the dramatic drop in an infected animal's output, which includes a decline in the young animals production, a decline in output of milk in nursing animals and a decline in the production of fiber (Mehmood *et al.*, 2017; Fthenakis and Papadopoulos, 2018; Mahmoud *et al.*, 2022). All of them ultimately cause the farmer to suffer significant financial losses (Ilangopathy *et al.*, 2019). *H. contortus* damage might cost the breeding business, billions of dollars in lost revenue. The cost of *H. contortus* treatments alone is anticipated to be over 26 million USD annually in Kenya, 46 million USD annually in the Republic of South Africa and 103 million USD annually in India, demonstrating the importance of this parasite (McRae *et al.*, 2014).

Prevalence and distribution of *Haemonchus contortus* in Asia: Sequential assessments of worm burdens in grazing animals reveal connections between nematode growth and environmental variables and offer an epidemiological background. These studies consist of three types of research organized studies utilizing "tracer" animals grazing tiny pasture patches continuously contaminated with worm eggs, worm counts from flocks or herds grazing continuously contaminated pastures and slaughterhouse surveys (Besier *et al.*, 2016a; Shamim *et al.*, 2018). In the tropical and subtropical regions of Asia, studies of worm count in sheep have demonstrated their close link with rainfall patterns, where temperatures are consistently appropriate for *H. contortus* development (Chandrawathani *et al.*, 2004; Yang *et al.*, 2016). A huge population of sheep, cattle and goats also offers a favorable atmosphere for the growth and transmission of various bacteria, viruses and parasites, including *H. contortus*, a significant parasitic nematode that can cause significant financial losses to the cattle, sheep and goat breeding sector. To avoid and manage this species, it is crucial to comprehend the epidemiology of *H. contortus* (Wang *et al.*, 2017; Alvi *et al.*, 2020; Arsenopoulos *et al.*, 2021; Adduci *et al.*, 2022). The examination of *H. contortus* infection in cattle, sheep and goats in Asia has been covered in numerous reports. Diagnosis through the conventional method of Fecal Egg Count Reduction Test (FECRT) was the most frequently employed technique in the investigations (Rialch *et al.*, 2013; Chandra *et al.*, 2015; Shakya *et al.*, 2018; Yuan *et al.*, 2019) and DNA-based techniques were also applied in more recent years to investigate *H. contortus* infection in ruminants in Asia (Mohanraj *et al.*, 2017; Bihagi *et al.*, 2020; Dey *et al.*, 2020; Parvin *et al.*, 2022). In a study observed from Pakistan, the infection in goats was observed at 50-89.20% and in the sheep at 55-94% which indicates that *H. contortus* is dominant in Sheep of Pakistan (Bibi *et al.*, 2017; Khan *et al.*, 2021). In China, the opposite trend was observed, in the examined goat farms (Wang *et al.*, 2006; Ma *et al.*, 2014; Yang *et al.*, 2016), the infection rate ranged from 28 to 100% and from 0 to 92% in the analyzed sheep farms (Wang *et al.*, 2006), which show goats are more dominant to *H. contortus*. Additionally, several other studies had previously noted the high prevalence rates of gastrointestinal (GI) parasites in goats,

particularly *H. contortus* from Indonesia, India (Uttarakhand, Nagpur) was recorded as 89.4, 96 and 88.23%, respectively (Maske *et al.*, 1990; Pant *et al.*, 2009; Widiarso *et al.*, 2018). These studies have reported a high prevalence of *H. contortus* in sheep and goats which may be influenced by various factors, including the genetic makeup of both the parasite and the host and the development of resistance to commonly used anthelmintic drugs.

Anthelmintic resistance: The control of parasites relies heavily on the use of anthelmintic drugs, which are widely used in the management of GI nematodes. Anthelmintic drugs from various classes, such as benzimidazoles (albendazole), macrocyclic lactones (ivermectin), imidazothiazoles (levamisole), amino-acetonitrile derivatives (monepantel), salicylanides (closantel) and spiroindoles (derquantel) are effective against *H. contortus* (Kaminsky *et al.*, 2008a; Sager *et al.*, 2009; Malik *et al.*, 2020; Ahmad *et al.*, 2021). These chemicals may be used alone or in combination in commercially available formulations. Unfortunately, the widespread use of anthelmintic drugs has led to a significant and rapid growth of AR, particularly in the nematodes of sheep, cattle, goats and horses. (Potârniche *et al.*, 2021). An anthelmintic-susceptible parasite population may become resistant by acquiring AR, which is a heritable decrease of sensitivity. (Fissiha and Kinde, 2021).

This AR has become a growing concern in many regions of the world, including Asia. Several studies have reported the presence of AR in *H. contortus* populations in various countries of Asia, including China, India, Pakistan and Iran. Resistance to multiple classes of anthelmintic, such as benzimidazoles, levamisole and macrocyclic lactones, has been reported in these populations as mentioned in Tables 1 and 2.

Benzimidazole resistance: The mode of action of benzimidazole (BZ) inhibits microtubule polymerization (Rufener *et al.*, 2009), thus preventing bacterial cells from binding to tubulin monomers and causing microtubule destabilization (Mohanraj *et al.*, 2017). The cost of resistance to BZ is particularly high due to the widespread use of this drug since the 1970s and this is at least partially understood at the molecular level (Elard *et al.*, 1996). In 1986, researchers identified a link between the development of BZ resistance in *H. contortus* and the BZ target domain β -tubulin. Using the same experimental design (Lubega and Prichard, 1990), he found resistant *H. contortus* infection is associated with reduced binding of BZ to β -tubulin. (Kwa *et al.*, 1994; Kwa *et al.*, 1995) used *Caenorhabditis elegans* to explain why BZ capacity is reduced. Some mutations in the isotype-1-tubulin gene, which encodes therapeutic targets, have been shown to be associated with drug resistance. In Asia, *Haemonchus* species, isoform 1-tubulin polypeptide and *Haemophilus* sp. were found to change phenylalanine to tyrosine at codon positions 167 and 200 (F167Y and F200Y), *H. contortus* was also found to replace alanine at position 198 (E198A) with glutamate (Önder *et al.*, 2016; Ekta *et al.*, 2019; Amana and Alkhaled, 2023). Mutations in F200Y were examined in depth and all three mutations were found to be associated with the resistance phenotype.

Closantel resistance: The salicylanilide drug class includes the anthelmintic Closantel. To precisely target blood-eating parasites like *Haemonchus* species, salicylanilide binds tightly to plasma proteins. Moreover, Closantel may interfere with the parasite's pH homeostasis maintenance systems (Dixit *et al.*, 2019). The action of closantel is restricted in the larval stages of *Haemonchus* sp. Because immature and hypobiotic larval stages do not consume blood (Swan, 1999). There have been many documented cases of closantel resistance in GI nematodes including *Haemonchus* in different regions of the world, similar to other medication classes that have been accessible for several decades (Chandrawathani *et al.*, 2004; Bihaqi *et al.*, 2020). In the literature, it has also been reported that resistance to new anthelmintic can arise in a short time (Mederos *et al.*, 2014; Van den Brom *et al.*, 2015). The poor knowledge of closantel-resistant parasite strains and the pertinent mechanisms of resistance can be explained by the drug's narrow spectrum of activity in comparison to other antiparasitic drugs. Also, it was determined in many investigations that closantel resistance was caused by decreased drug intake by resistant helminths, significant albumin binding of the drug in helminth's gut and enhanced drug excretion from resistant worms (Rothwell and Sangster, 1997). The reduced concentration of drugs in Closantel resistant isolates of *Haemonchus* has not been attributed to changes in P-glycoprotein genes, according to subsequent investigation. (Kwa *et al.*, 1998; Kaminsky *et al.*, 2008b).

Imidazothiazole resistance: Imidazothiazole drugs, such as levamisole and morantel, have been used extensively for the control of *H. contortus* infections, but their efficacy has been challenged by the emergence of resistance (Muhammad *et al.*, 2015; Islam *et al.*, 2018) Imidazothiazole resistance in *H. contortus* is believed to be due to genetic mutations that alter the target site of these drugs, which is the nicotinic acetylcholine receptor (nAChR) in the parasite's neuromuscular system. The mutations can reduce the binding affinity of the drugs to the nAChR, making them less effective in killing the parasite (Fauvin *et al.*, 2010; Neveu *et al.*, 2010). With the association with imidazothiazole resistance, several mutations have been identified in the nAChR genes of *H. contortus*. For instance, different *H. contortus* populations with various degrees of resistance to morantel and levamisole have been identified to harbor the F167Y mutation in the nAChR beta subunit gene (Barrère *et al.*, 2014; Sarai *et al.*, 2015). The imidazothiazole resistance in *H. contortus* has also been linked to other mutations in the nAChR alpha subunit gene, such as the E198A and F200Y mutations. Although the precise processes by which these mutations confer resistance are not yet completely known, it is believed that they interfere with imidazothiazoles' ability to bind to the nAChR (Turnbull *et al.*, 2019; Kotze *et al.*, 2020). Nevertheless, *Haemonchus* species have evolved some mechanisms that lessen nicotinic acetylcholine receptors' sensitivity to levamisole, making it challenging to create molecular techniques for identifying anthelmintic resistance to imidazothiazoles.

Table I: Status of anthelmintic resistant haemonchosis in Asia detected through In-Vivo/Fecal Egg Count Reduction Test

Country	Anthelmintic involved	Dosage as per Body weight	Animal species	Age of the animal in months	No of animals	FECR%	Testing Day	Reference	
Pakistan	Oxfendazole	1 ml/8 kg (2.265% w/v)	Dera din panah Goat	15-25	10	61	FECRT at 14 TH day	(Jabbar <i>et al.</i> , 2008)	
			Angora Goat	15-25	10	83			
			Beetal Goat	15-20	10	82			
	Ivermectin	1 ml/50 kg (1% w/v)	Dera din panah Goat	15-25	10	99	FECRT on the 14th day		
			Angora Goat	15-25	10	97			
			Beetal Goat	15-20	10	100			
	Levamisole	1 ml/2 kg (HCl 1.5% w/v)	Dera din panah Goat	15-25	10	95	FECRT on the 14th day		
			Angora Goat	15-25	10	94			
	Oxfendazole	2.83 mg/kg (2.265% w/v)	Beetal Goat	15-20	10	88	FECRT on the 14th day	(Saeed <i>et al.</i> , 2010)	
				6-9	40	94			
	Levamisole	7.5 mg/kg (1.5% w/v)	Beetal Goat	6-9	40	90			
	Ivermectin	0.2 mg/kg (1% w/v)	Beetal Goat	6-9	40	98			
	Oxfendazole	2.83 mg/kg (2.265% w/v)	Beetal Goat	9-12	40	87	FECRT on the 14th day		
	Levamisole	7.5 mg/kg (1.5% w/v)	Beetal Goat	9-12	40	95			
	Ivermectin	0.2 mg/kg (1% w/v)	Beetal Goat	9-12	40	96			
	Oxfendazole	2.83 mg/kg (2.265% w/v)	Beetal Goat	12-15	40	89	FECRT on the 14th day		
	Levamisole	1.5% w/v, dose 7.5 mg/kg	Beetal Goat	12-15	40	75			
	Ivermectin	1% w/v, dose 0.2 mg/kg		12-15	40	99			
	Oxfendazole	2.265% w/v, dose 2.83 mg/kg	Beetal Goat	12-24	40	82	FECRT on the 14th day		
	Levamisole	1.5% w/v, dose 7.5 mg/kg	Beetal Goat	12-24	40	52			
	Ivermectin	1% w/v, dose 0.2 mg/kg		12-24	40	99			
	Albendazole	N/A	Salt range Sheep	3-4	10	88	FECRT on the 14th day	(Muhammad <i>et al.</i> , 2015)	
Levamisole				10	89				
Ivermectin				10	99				
Albendazole	N/A	Pak karakul Sheep	3-4	10	91				
Levamisole				10	90				
Ivermectin				10	97				
Albendazole	N/A	Jattal Goat	3-4	10	91				
Levamisole				10	91				
Ivermectin				10	98				
Albendazole	1 ml/5kg	Goat	N/a	20	93.4	FECRT on the 30 th day	(Rehman <i>et al.</i> , 2020)		
Oxfendazole	1 ml/5kg	Goat	N/a	20	94.7				
Bangladesh	Albendazole	7.5 mg/kg	Sheep	N/A	10	90	FECRT on the 14th day	(Islam <i>et al.</i> , 2018)	
					10	98			
	Ivermectin	2.5 mg/kg				10	96		
						10	100		
	Albendazole	7.5 mg/kg	Goat	N/A		10	100		
						10	97		
	Levamisole	7.5 mg/kg				10	97		
						10	100		
	Ivermectin	2.5 mg/kg				10	100		
						10	100		
	Albendazole	7.5 mg/kg	Goat	N/A		10	93.46	FECRT on the 14th day	(Dey <i>et al.</i> , 2020)
						10	90.44		
	Levamisole	7.5 mg/kg				10	85.62		
						10	94.05		
	Ivermectin	0.2 mg/kg	Sheep	N/A		10	94.05		
						10	100		
	Albendazole	7.5 mg/kg				10	87.44		
						10	87.44		
	Levamisole	7.5 mg/kg				10	87.44		
						10	87.44		
	Ivermectin	0.2 mg/kg	Goat	N/A		10	90.57		
						10	90.57		
Albendazole	7.5 mg/kg				10	93.12			
					10	93.12			
Levamisole	7.5 mg/kg				10	96.39			
					10	96.39			
Ivermectin	0.2 mg/kg	Goat	N/A		10	99.11			
					10	99.11			
Albendazole	7.5 mg/kg				10	99.11			
					10	99.11			
Levamisole	7.5 mg/kg				10	74.11			
					10	74.11			
Ivermectin	0.2 mg/kg	Goat	N/A		10	67.55			
					10	67.55			
Albendazole	7.5 mg/kg				10	93.81			
					10	93.81			
Levamisole	7.5 mg/kg				10	99.32			
					10	99.32			
Ivermectin	0.2 mg/kg	Goat	N/A		10	94.06			
					10	94.06			
Albendazole	7.5 mg/kg				10	91.17			
					10	91.17			
Levamisole	7.5 mg/kg				10	93.86			
					10	93.86			
Ivermectin	0.2 mg/kg	Boer and Bakerwal cross-	N/A		31	62	FECRT on the 14th day	(Bihagi <i>et al.</i> , 2020)	
					31	86			

Country	Anthelmintic involved	Dosage as per Body weight	Animal species	Age of the animal in months	No of animals	FECR%	Testing Day	Reference
China	Ivermectin	0.2 mg/kg	bred Goats		31	90		
	Ivermectin	0.2 mg/kg	Goat	N/A	N/A	48	FECRT on the 14th day	(Yuan et al., 2019)
	Ivermectin + Albendazole	7.5 mg/kg	Goat	N/A	N/A	86.96		
India	Benzimidazole group	N/A	Sheep and goat	N/A	22 flocks (3 farm and 19 field flocks)	genotype (96.58%) in flocks exhibiting <50% efficacy	FECRT on the 14th day	(Maharshi et al., 2011)
	Fenbendazole	5mg/kg	Sheep	N/A	4 flocks (20 animals from each)	54-100% (2 Resistant 2 susceptible)	FECRT on 10 th day	(Rialch et al., 2013)
	Fenbendazole	10mg/kg	Goat	N/A	10 flocks (20 animals from each)	59-100% (6 resistant 4 Susceptible)		
	Albendazole	5mg/kg	Goat	N/A	N/A	60-100% in different regions	FECRT on the 14th day	(Chandra et al., 2015)
	Albendazole	10 mg/kg	Goat	15 months	N/A	83.94	FECRT on the 14th day	(Shakya et al., 2018)
	Levamisole	7.5 mg/kg		15 months		89.09		
	Ivermectin	200µg/kg		15 months		100		
	Fenbendazole	2.25% w/v	Goat	8-30 months	10	84	FECRT on the 14th day	(Pawar et al., 2019)
	Ivermectin	0.08% w/v			10	85		
	Levamisole	30%w/w			10	88		
Fenbendazole	2.25% w/v	Sheep	10-36 months	10	51			
Malaysia	Ivermectin	0.08% w/v			10	26		
	Levamisole	30%w/w			10	87		
	Oxfendazole	5 mg/kg	Sheep and Goat	4-12 months of age	10 animals	22	September 2002- February 2003	(Chandrawathani et al., 2004)
	Levamisole	7.5 mg/kg				75		
	Ivermectin	200 µg/kg				72		
	Closantel	5 mg/kg				76		
	Oxfendazole	5 mg/kg	Sheep and Goat	4-12 months of age	10 animals	68		
	Levamisole	7.5 mg/kg				66		
	Ivermectin	200 µg/kg				40		
	Closantel	5 mg/kg				62		
	Oxfendazole	5 mg/kg	Sheep and Goat	4-12 months of age	10 animals	61		
	Levamisole	7.5 mg/kg				91		
	Ivermectin	200 µg/kg				77		
	Closantel	5 mg/kg				78		
	Oxfendazole	5 mg/kg	Sheep and Goat	4-12 months of age	6 Animals	72		
Levamisole	7.5 mg/kg				96			
Ivermectin	200 µg/kg				85			
Closantel	5mg/kg				78			
Oxfendazole	5mg/kg	Sheep and Goat	4-12 months of age	10 Animals	68			
Levamisole	7.5mg/kg				66			
Ivermectin	200µg/kg				40			
Closantel	5mg/kg				62			

FECR % = Fecal Egg Count Reduction Percentage, FECRT= Fecal Egg Count Reduction Test.

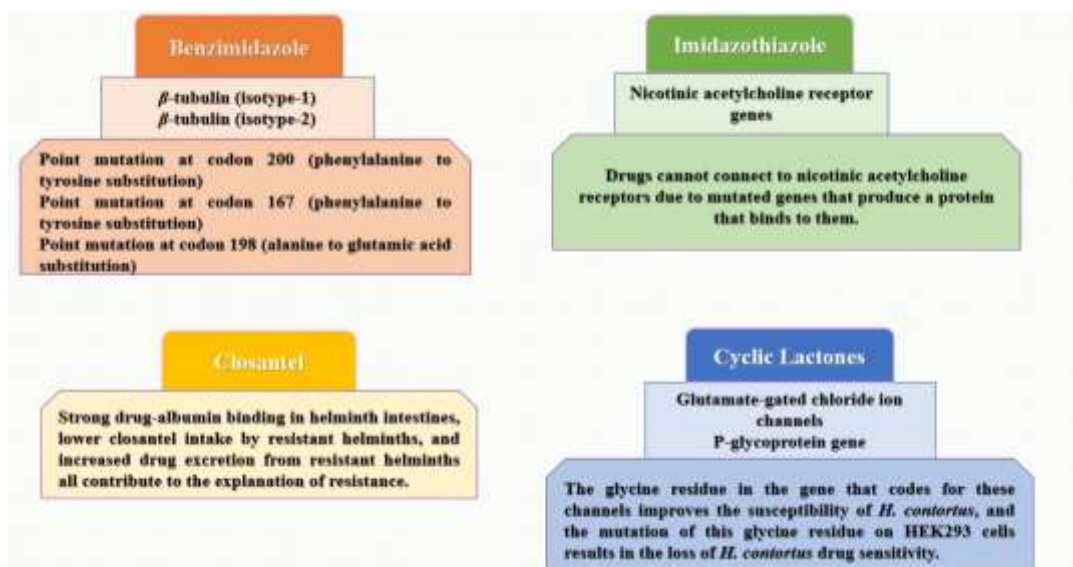


Fig. 1: Summary of resistance by different anthelmintic groups.

Table 2: Status of anthelmintic resistance in Asia specific to Benzimidazole resistance using Molecular Methods

Country	Region	No. of Haemonchus Worms/Larvae	Test Used	Drug Used	Polymorphism in the β -tubulin isotype I gene.	Results	Source of Sample Collection	Reference
Iraq	Bareilly	40 adult worms	AS- PCR	BZ	F200Y	8% RR, 30% RS and 62% SS	Sheep	(Amana and Alkhaled, 2023)
Bangladesh	Mymensingh, Tangail, Sirajgonj, Dinajpur, Barishal, Khulna, Sylhet and Rangamati	160 Adult Worms	AS- PCR	BZ	F200Y	9.4% RR (TAC), 61.2% RS (TAC/TTC) and 29.4% SS (TTC)	Slaughtered Sheep and goat	(Parvin et al., 2022)
Thailand	Chiang Mai	20 adult worms	AS- PCR	BZ	F200Y	0% RR, 60% RS and 40% SS	Goat	(Pitaksakulrat et al., 2021)
	Tak	17 adult worms	AS- PCR	BZ	F200Y	11.8% RR, 52.9% RS and 35.3% SS	Goat	
	Nakhon Ratchasima	20 adult worms	AS- PCR	BZ	F200Y	25% RR, 50% RS and 25% SS	Goat	
	Lopburi	20 adult worms	AS- PCR	BZ	F200Y	15% RR, 30% RS and 55% SS	Goat	
	Nakhon Sawan	3 adult worms	AS- PCR	BZ	F200Y	33% RR, 0% RS and 66% SS	Goat	
	Surat Thani	9 adult worms	AS- PCR	BZ	F200Y	88.9% RR, 11.1% RS and 0% SS	Goat	
	Nakhon Si Thammarat	15 adult worms	AS- PCR	BZ	F200Y	33.3% RR, 46.7% RS and 20% SS	Goat	
	Krabi	17 adult worms	AS- PCR	BZ	F200Y	43.9% RR, 41.5% RS and 14.6% SS	Goat	
Bangladesh	7 topographical zones	195 adult worms	AS- PCR	BZ	F200Y	6% RR (TAC), 59% RS (TAC/TTC) and 35% SS (TTC)	Slaughtered sheep and goat	(Dey et al., 2020)
Kashmir	Srinagar	200 Larvae	AS-PCR followed by nested PCR	BZ	N/A	52% RR on day 0 (Pre-treatment) and 100% RR (TAC/TAC) On day 7 th (Post Treatment), 31% SS (TTC/TTC) and 17% RS (TAC/TTC)	Fecal sample and larval culture	(Bihagi et al., 2020)
India	Ludhiana	50 Adult worms	AS-PCR	BZ	F200Y	(RR) showing 100% prevalence of resistant allele (r)	Slaughtered sheep	(Ekta et al., 2019)
	The western zone of Punjab	138 larvae	AS PCR	BZ	F200Y	49.28% RR, 3.62% SS and 46.37% RS population	Slaughtered sheep	
	Sattur, Pottaneri, Ooty and Hosur	673 larvae	AS- PCR	BZ	N/A	80.08 RR and 19.91 RS	Sheep	(Mohanraj et al., 2017)
	Northern Punjab	(23 population) 830 worms	Pyrosequencing followed by PCR	BZ	F200Y	Detected in 18 populations with allele frequency between 9–84%	Sheep and goat	(Chaudhry et al., 2015)
	Northern Punjab	(23 population) 830 worms	Pyrosequencing followed by PCR	BZ	E198A	Detected in 8 populations with allele frequency between 8–18%	Sheep and goat	
	Uttar Pradesh	300 larvae	AS- PCR	BZ	N/A	10-21% SS, 5-24% RS and 55–85% RR	Goat	(Chandra et al., 2015)
	Uttar Pradesh	300 larvae	AS- PCR	BZ	N/A	67–87.5% RR and 12.5–33% SS	Goat	
	Rohilkhand	30 larvae	AS-PCR followed by RFLP PCR	BZ	N/A	63% RR, 20% SS and 17% RS	Sheep	(Chandra et al., 2014)
	Bundelkhand	40 larvae	AS-PCR followed by RFLP PCR	BZ	N/A	85% RR, 10% SS and 5% RS	Sheep	
	Jaunpur	30 larvae	AS-PCR followed by RFLP PCR	BZ	N/A	53% RR, 27% SS and 20% RS	Sheep	
	Varanasi	30 larvae	AS-PCR followed by RFLP PCR	BZ	N/A	57% RR, 17% SS and 26% RS.	Sheep	
	North-eastern region and Eastern region farm areas	691 Larvae	AS- PCR	BZ	F200Y	RR 72.22% (north-eastern region) to RR 96.87% (eastern region) in farm flocks	Sheep and goat	(Maharshi et al., 2011)

Country	Region	No. of Haemonchus Worms/Larvae	Test Used	Drug Used	Polymorphism in the β -tubulin isotype I gene.	Results	Source of Sample Collection	Reference
	North-eastern region and Eastern region field areas	691 Larvae	AS- PCR	BZ	F200Y	61.79% RR (north-eastern region) to 95.83% RR (eastern region) in field flocks	Sheep and goat	
	Mukteshwar	40 adult worms	AS- PCR	BZ	F200Y	3% RR, 10% RS and 87% SS	Sheep	
	Pantnagar	40 adult worms	AS- PCR	BZ	F200Y	23% RR, 67% RS and 10% SS	Sheep	(Garg and Yadav, 2009)
	Rajasthan, India	160 adult worms	AS- PCR	BZ	F200Y	81.25% RR, 13.75% RS and 6.25% SS	Sheep	(Tiwari et al., 2007)
	Rajasthan, India	160 adult worms	AS- PCR	BZ	F200Y	81.25% RR, 13.75% RS and 6.25% SS	Sheep	
	Rajasthan, India	160 adult worms	AS- PCR	BZ	F200Y	81.25% RR, 13.75% RS and 6.25% SS	Sheep	
	Bikaner region	54 Adult worms	RFLP-PCR	BZ	F200Y	54% RR, 33% RS and 17% SS	Sheep	(Tiwari et al., 2006)
	Avikanagar	54 Adult worms	RFLP-PCR	BZ	F200Y	93% RR, 2% RS and 5% SS	Sheep	
	Mukteshwar	40 adult worms	AS- PCR	BZ	F200Y	3% RR, 10% RS and 87% SS	Sheep	
	Bikaner region	54 Adult worms	RFLP-PCR	BZ	F200Y	54% RR, 33% RS and 17% SS	Sheep	
	Avikanagar	54 Adult worms	RFLP-PCR	BZ	F200Y	93% RR, 2% RS and 5% SS	Sheep	
China	Qingyang Ravine and Xiazi Ravine	27 adult worms	Nested PCR	BZ	E198A	RR 11.11%, and SS 88.89%	Wild blue sheep	(Shen et al., 2019)
	Helan Mountain	20 adult worms	Nested PCR	BZ	E198A	RR 7.50% and SS 92.50%	Domestic sheep	
	Hubei	24 adult worms	PCR coupled sequencing	BZ	E198A	SS 83% and RR 17%	Sheep	(Zhang et al., 2016)
	Hubei	24 adult worms	PCR coupled sequencing	BZ	F200Y	SS 96% and RR 4%	Sheep	
	Inner Mongolia	24 adult worms	PCR coupled sequencing	BZ	E198A	SS 30% and RR 70%	Sheep	
	Inner Mongolia	24 adult worms	PCR coupled sequencing	BZ	F200Y	SS 81% and RR 19%	Sheep	
	Liangning	24 adult worms	PCR coupled sequencing	BZ	E198A	SS 60% and RR 40%	Sheep	
	Liangning	24 adult worms	PCR coupled sequencing	BZ	F200Y	SS 87.5% and RR 12.5%	Sheep	
	Heilongjiang	24 adult worms	PCR coupled sequencing	BZ	E198A	SS 96% and RR 4%	Sheep	
	Heilongjiang	24 adult worms	PCR coupled sequencing	BZ	F200Y	SS 92% and RR 8%	Sheep	
	Hebei	24 adult worms	PCR coupled sequencing	BZ	E198A	SS 90% and RR 10%	Goat	
	Hebei	24 adult worms	PCR coupled sequencing	BZ	F200Y	SS 98% and RR 2%	Goat	
	Yunnan	24 adult worms	PCR coupled sequencing	BZ	E198A	SS 54% and RR 46%	Goat	
	Yunnan	24 adult worms	PCR coupled sequencing	BZ	F200Y	SS 69% and RR 31%	Goat	
	Shaanxi	24 adult worms	PCR coupled sequencing	BZ	E198A	SS 100% and RR 0%	Goat	
	Shaanxi	24 adult worms	PCR coupled sequencing	BZ	F200Y	SS 100% and RR 0%	Goat	
	Guangxi	24 adult worms	PCR coupled sequencing	BZ	E198A	SS 65% and RR 35%	Goat	
	Guangxi	24 adult worms	PCR coupled sequencing	BZ	F200Y	SS 75% and RR 25%	Goat	
Pakistan	North-east Punjab	50 Adult worms	Purification and Sequencing	BZ	F200Y	74% SS and 26% RR	Sheep	(Irum et al., 2014)

Homozygous resistant =RR, Homozygous susceptible = SS, Heterozygous = RS, ALLELE-SPECIFIC=AS, PCR= Polymerase Chain Reaction, RFLP= Restriction Fragment Length Polymorphism, BZ= Benzimidazole

Macrocyclic lactones resistance: Genetic modifications that induce a lower sensitivity of the parasite to the treatment are the main source of resistance to macrocyclic lactones (MLs), which include moxidectin, doramectin

and ivermectin in *H. contortus*. Due to the recurrent use of MLs, which gives parasites with resistant alleles a survival advantage, these genetic alterations may be brought on by selection pressure (Lespine et al., 2012;

Prichard *et al.*, 2012). Numerous researchers have inspected the mechanisms that lead to the development of resistance against macrocyclic lactones in *H. contortus*. Some reports concluded that the increased drug efflux, reduced drug uptake, metabolic degradation of the drug and altered drug targets are the reasons behind resistance (McKellar and Gokbulut, 2012). Target site mutation, which results in genetic alterations in the parasite's glutamate-gated chloride channel (GluCl), is the most often described cause of MLs resistance (Kerboeuf *et al.*, 2003).

While some studies have failed to find a correlation between these mutations and resistance (Williamson *et al.*, 2011). Additionally, mutations in the genes encoding γ -aminobutyric acid receptors and polymorphisms in the P-glycoprotein genes have also been associated with resistance. P-glycoprotein inhibitors have been shown to increase the efficacy of macrocyclic lactones against resistant *H. contortus* strains both in vitro and in vivo (Xu *et al.*, 1998; Sangster *et al.*, 1999; Mani, 2016). Overall, there is evidence of multiple mechanisms for the development of resistance to these drugs. Hence, to develop and manage appropriate antiparasitic control programs, all parties concerned should be aware of the possibility of interactions leading to multi-drug resistance. A summary of AR has been shown in Fig.1.

To address this issue, AR in *H. contortus* has been studied and reported in many parts of the world. The examination of resistant *Haemonchus* in the studies observed was through FECRT (Jabbar *et al.*, 2008; Saeed *et al.*, 2010; Islam *et al.*, 2018). Molecular techniques were also used to identify benzimidazole resistance and single nucleotide polymorphism (SNP) analysis in isotype-1 β tubulin-resistant *H. contortus* in addition to conventional methods. As a consequence, we examined the research findings on anthelmintic resistance in *H. contortus* in Asia.

In-Vivo/ Fecal egg count reduction test: By comparing the animal's pre- and post-treatment worm egg counts, one may assess a chemical's anthelmintic effectiveness. This test has undergone extensive standardization, enabling its widespread usage. FECRT states that resistance is present when both of the following conditions are satisfied: the reduction in egg count is less than 95% and the lower limit of the 95% confidence interval is equal to or less than 90% (Levecke *et al.*, 2018; Salgado *et al.*, 2019). Many studies have been reported from Asia in which the AR in sheep and goats was observed using the test fecal egg count reduction as mentioned in Table 1. In a study from Pakistan the anthelmintic efficacy of three commonly used anthelmintic, viz., oxfendazole, levamisole and ivermectin was observed in three breeds of dairy goats, i.e. Dera Din Panah, Pak Angora and Beetal kept at Government Livestock Farm. The result showed resistance to oxfendazole formulation. Whereas levamisole in two breeds and ivermectin in all breeds resulted in a decrease (P 0.05) in *H. contortus* (Jabbar *et al.*, 2008). Whereas, From Bangladesh (Dey *et al.*, 2020) reported *H. contortus* to be resistant to albendazole, levamisole and ivermectin in FECRT, as shown by the percentage decrease and 95% confidence intervals. Small ruminant farms in Malaysia were also examined to check

the status of anthelmintic drug efficacy but unfortunately, all the anthelmintic groups showed a total failure to control *H. contortus* (Chandrawathani *et al.*, 2004).

In-Vivo/ Molecular test to detect benzimidazole resistance: Several benzimidazoles (BZ) resistance SNPs in parasitic worms have been detected utilizing molecular diagnostic testing employing a variety of techniques, including allele-specific (AS)-PCR, restriction fragment length polymorphism (RFLP) and pyrosequencing (Winterrowd *et al.*, 2003; von Samson-Himmelstjerna *et al.*, 2009; Mohanraj *et al.*, 2017). Additionally, alternative molecular techniques, such as restriction fragment length polymorphism-PCR, have been published for the identification and/or quantification of this SNP as well as the other two linked to BZ resistance (F167Y, E198A) (Tiwari *et al.*, 2006; Chandra *et al.*, 2014), Real-time PCR and Pyrosequencing (Chaudhry *et al.*, 2015). The molecular test was not always connected with the level of resistance, but it was able to distinguish well between resistant and susceptible isolates, according to a comparison of molecular data with other tests. As shown in Table 2. Several countries in Asia were observed to detect resistance through molecular means. Tiwari *et al.* (2007) diagnosed benzimidazole (BZ) resistance in *H. contortus* using Allele-specific PCR and observed 87 % of *Haemonchus* had the BZ resistant allele (R), compared to 13% who had the BZ susceptible allele (S). In another study from Kashmir, Allele-specific PCR was used resulting in 52% homozygous resistance on day 0 (Pre-treatment) and 100% Homozygous resistance (RR, TAC/TAC) On day 7th (Post Treatment), 31% homozygous susceptible (SS, TTC/TTC) and 17% heterozygous (RS, TAC/TTC) (Bihaqi *et al.*, 2020). In Turkey, qPCR along with sequencing was used and Point mutation (replacement of phenylalanine (TTC) to tyrosine (TAC) only at codon 200 was observed (Önder *et al.*, 2016). It has been demonstrated that molecular techniques might be utilized as a diagnostic tool to find BZ resistance in a population, even if they are unable to quantify the resistance to the same extent as FECRT (Kotze and Prichard, 2016). In reality, a mix of molecular and biological assays should be employed in the field. The use of genetic assays to identify BZ resistance in field samples made up of numerous worm species has not yet been thoroughly evaluated. In addition, fecal samples directly containing nematode eggs have not been subjected to molecular analyses, which might save time (Roeber *et al.*, 2013).

Strategies to delay resistance: Many management measures, including pasture management and refugia, are used to either avoid parasite infection or to maintain low infection pressure. This would lessen the need for anthelmintic, which might help to postpone the onset of AR (Shalaby, 2013). A farm can prevent the spread of resistance by treating newly purchased stock upon arrival and putting it into a quarantine period (Hosie and Clark, 2007). It can also prevent the spread of resistance by maintaining a population of worms that are susceptible to anthelmintic and by regularly testing for AR (Sarai *et al.*, 2014; Mehnaz *et al.*, 2023). Here are some strategies that can help delay anthelmintic resistance in *H. contortus*.

Targeted treatments: When helminth parasite populations are exposed to an anthelmintic medication, there is thought to be a risk of resistance development. Surprisingly, when using anthelmintic belonging to the same class often and at low doses, the chance of resistance development increases (Sargison, 2011). The development of resistance may be slowed by switching up the anthelmintic classes. The strategic use of anthelmintic should be based on the results of fecal egg count monitoring and targeted towards individual animals that have a high worm burden, rather than blanket treatment of the entire flock/herd. This helps to reduce the selection pressure for AR (Berk *et al.*, 2016).

Combination therapy: Using combination of anthelmintic with different modes of action can help prevent the development of resistance. This approach is particularly effective when combined with targeted treatment, as it helps to minimize the selection pressure for resistance (Leathwick *et al.*, 2012). Combinations lower the number of resistant genotypes that survive treatment and hence prevent the development of a resistant parasite population since several alleles conferring resistance to each of the various anthelmintic classes must be present in the same parasite for survival. Less people carry several resistance alleles than just one resistant allele (Van Wyk, 2001). Its increased effectiveness causes the unselected parasites in refugia to contaminate more resistant genotypes, decreasing the number of resistant parasites that can mate with other resistant adults that have endured treatment (Bartram *et al.*, 2012).

Pasture management and rotational grazing

The purpose of rotational grazing is to establish safe pastures for grazing. In order for a pasture to be considered safe, sheep or goats must not have been permitted to graze there for three months during hot, dry weather or six months during cool or cold weather. In order to lessen the possibility that delicate animals may come into touch with numerous infectious larvae, it is recommended to wean sheep and goats at two months of age and transfer them among pastures before the adults (Barger, 1999). The division of pastures into smaller lots will enable longer intervals between regrazing. Mismanaged pastures that have become severely polluted can be tilled and reseeded. As it impacts exposure to infectious larvae and pasture contamination, the stocking rate is a crucial factor in the management of parasites. Regularly rotating animals to different pastures can help to break the parasite life cycle and reduce the overall worm burden (Barger, 1999; Athanasiadou *et al.*, 2001; Niezen *et al.*, 2002). In addition, multispecies grazing also results in reducing the parasite burden, but there is limited information available on equine parasitology and most of the guidelines are acquired from ruminant studies (Nielsen *et al.*, 2018). This strategy can also help to reduce the selection pressure for resistance, as it reduces the exposure of parasites to the same anthelmintic repeatedly. Using biological control is another excellent way to cut back on anthelmintic. The fundamental idea behind biological control is to reduce the amount of infection in pastures by employing natural enemies that may consume

or destroy parasites (Larsen, 2006). Entomopathogenic fungi, such as the species in the genus *Hirsutiella*, can infect and kill *Haemonchus* larvae. These fungi are used as a biological control agent to reduce parasite burdens in pastures. These therapies aim to reduce free-living larval stages to a level where their clinical or subclinical effects are minor while enhancing an acquired immune response, rather than to completely eradicate them (Waller *et al.*, 2004). It's important to note that while these strategies can help delay AR, they are not a guarantee. A comprehensive parasite management plan should be developed in consultation with a veterinarian or animal health professional.

Conclusions: *Haemonchus contortus* infection in small ruminants leads to substantial economic losses. This parasite is well-known to rapidly develop resistance towards routinely used classes of anthelmintics. The anticipated rise in prevalence in various countries and the severity of resistance in *H. contortus* to the available drugs make it hard for small ruminant farmers to control *H. contortus*. Keeping in view the rising trend of AR in *H. contortus*, in conclusion, our comprehensive review highlights the prevalence of resistance to major classes of anthelmintic with special emphasis on benzimidazole resistance-associated SNPs in the isotype-1 β -tubulin gene of *H. contortus* populations in small ruminants in Asia. This information can help inform the development of more effective strategies for the control of parasitic infections in small ruminants, to mitigate the impact of anthelmintic resistance on animal health and welfare, as well as on food security and livelihoods in rural communities. It is the need of the hour to develop better diagnostic methods, which will enable the producers to choose drugs or drug combinations that remain efficacious to prevent Haemonchosis. Furthermore, to curtail the resistance development, it is suggested to gain a deep insight into the mechanisms and genetics of AR.

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