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(Original Research)

MHC-II DRB Gene Polymorphism and its Association to Gastrointestinal Parasite Burden of Crossbred Anglo-Nubian Goats from a Single Animal Farm in Sultan Naga Dimaporo, Lanao del Norte, Philippines

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Abstract

Background: The Major Histocompatibility Complex (*MHC*), which codes for proteins essential to immune response, is frequently cited as a candidate gene associated with gastrointestinal parasite (GIP) resistance in small ruminants. This study aimed to investigate the polymorphism of the *MHC-DRB* gene in a crossbred Anglo-Nubian goat population and assess its association with GIP burden. **Methods:** Fecal analysis was conducted to estimate worm burden based on egg per gram (EPG) count. Sequence-based genotyping was used to analyze polymorphisms within the 285 bp fragment of the *MHC-DRB* gene exon 2. **Results:** The results confirmed high polymorphism of the *MHC-DRB* gene in goats, identifying 23 SNPs, 20 of which were non-synonymous mutations leading to 14 amino acid changes. Additionally, three Linkage Disequilibrium (LD) blocks and 21 closely linked SNP pairs ($r^2 > 0.9$) were identified. **Conclusion:** Association analysis revealed that individual SNPs, LD blocks, and SNP pairs were not significantly associated ($p > 0.05$) with worm burden. Thus, with the established significance of MHC in immune response mechanism it is recommended to conduct further investigation with larger sample sizes including different goat breeds. Additionally, it is recommended to explore other *MHC* loci and to associate the polymorphisms identified with other immune-related traits.

Keywords: *MHC-DRB* fragment, Non-synonymous mutations, Ruminants, Worm burden

1. Introduction

Gastrointestinal parasitism (GIP) significantly contributes to losses in goat farming worldwide [1-5]. Although anthelmintic agents are commonly used to control GIP, their indiscriminate use has led to the development of resistant parasites and the accumulation of chemical residues in the environment and animal products [4-9]. A sustainable alternative to control GIP in animal farming is selecting animals with favorable genetic markers for disease and parasite resistance [4-6, 8, 10-12].

The Major Histocompatibility Complex (*MHC*) codes for proteins that are primarily expressed on

the surface of immune cells and responsible for immune regulation [13-16]. In goats, the caprine MHC molecules are encoded on chromosome 23 by a diverse gene family [14,19,21]. The *MHC* consists of three main classes: I, II, and III [17-20], of these three, it is the *MHC-II* that received great attention especially in association studies [20]. The *MHC-II* codes for peptide-binding sites that is functionally important for the organisms' immune response [17,21]; it takes part in the antigen presentation to CD4+ T cells which help B cells to produce appropriate immunoglobulins to trigger a corresponding immune response [13,17,18,21-23]. The *MHC-II* is composed of two subtypes: DQ and DR which are mostly polymorphic among organisms and play a role in the development of MHC-specific immune response [13,14,16,19,20, 24]. Specifically, in exon 2, the *MHC-II DRB* gene codes for the first beta domain which is in close contact with foreign antigens [13,17]. This locus of *MHC* gene displays a great degree of polymorphism which is associated to the ability of the *MHC-II* molecules to recognize a wide variety of different antigen derived peptides [13-18,20].

The *MHC-DRB* locus is frequently cited in association studies of GIP resistance in sheep [23, 25-28] and in goats [4,5,19,29]. In association studies regarding endoparasite resistance the commonly used phenotypic parameter for GIP host resistance is determining the egg per gram (EPG) count of GIP per animal through fecal analysis or fecal egg counting (FEC) [2,5,10,11,23,30,31]. In different sheep breeds, different genotypes of the *MHC-DRB* were associated with resistance or susceptibility to GIP. In Ghezel sheep, the genotype 'A1A1' was observed with a lower fecal egg count [28]; in Deccani sheep, the genotype 'J' was frequently observed with a high FEC count [25] and in Southern Indian sheep breed 'bb' genotype was found to be associated with a higher EPG [26]. Notably, several polymorphism studies on the partial sequence (285bp fragment) of the *DRB* locus of *MHC* gene in exon 2 have been conducted on several goat populations [13,15,17, 20-22,32,33] using the primers that previously described [34], however association studies using this locus were limited.

In connection to the information presented, in the Philippines where goat industry is predominantly composed of backyard raisers [35], GIP infestation is among the top three concerns for animal farms [36] and although goat farming is considered as a sunrise industry in the country [36, 37], studies to control GIP infestation in goats through sustainable methods such as the use of possible genetic markers are scarce. Thus, this study was conducted as a preliminary investigation on the polymorphism of the 285 bp fragment of the *MHC-DRB* exon 2 gene and its association with the gastrointestinal parasite burden of crossbred Anglo-Nubian goats reared on an animal farm located in Sultan Naga Dimaporo, Lanao del Norte, Philippines. It also aims to contribute to improving marker-assisted breeding practices in the country and the data on possible markers for selection candidates in goat breeding, which will ultimately improve livestock quality and survivability.

2. Materials and Methods

2.1 Animals

Crossbred Anglo-Nubian X Native goats reared at the *SaGoat Kita* Farm, located at Mindanao State University – Lanao del Norte Agricultural College in Sultan Naga Dimaporo, Lanao del Norte, Philippines, were utilized as the sample population for this study. The animal house, established in 2001, initially had a buck-to-doe ratio of 3:40. During sample collection, the population consist of 117 goats, of which 34 were males and the remaining were females. A total of thirty goats were included in the study, excluding those younger than four months [5, 28], as this age threshold ensures the presence of a mature immune response [38]. Does were also excluded from the study due to the possibility of pregnancy, thus avoiding potential stress to the animals during sampling period. The goats were raised in a cut-and-carry system with *ad libitum* access to water. The dry season in the region occurs from January to June, while the rainy season spans from late June to early January. The goats were dewormed alternately with Fenbendazole and Ivermectin every 60 days. Additionally, supplements were provided, including Vitamin B complex for goats under one year of age and Vitamin ADE for those over one year of age.

2.2 Fecal Sampling and Fecal Analysis

Sample collection was performed by collecting an estimated five grams of feces directly from the rectum of the animals using sterile gloves [28].

Samples were placed separately inside labeled clean, sealable plastics, transported to the laboratory, and refrigerated at 4°C. The collection was conducted 30 days post-deworming and performed thrice at one-week intervals [28, 39]. Fecal analysis was performed immediately within 48 h after the collection [40].

The McMaster flotation technique was used for fecal analysis to determine the EPG count for each animal [41]. Fecal samples from each animal were homogenized individually to ensure thorough mixing. Two grams of fecal matter were then weighed and combined with 28 mL of a concentrated NaCl solution, which was prepared by dissolving 180 grams of NaCl in 500 mL of distilled water. The mixture was filtered through a mesh sieve, and the resulting suspension was pipetted into the chambers of a McMaster slide (Eggzamin® McMaster Microscope Slides), with each chamber filled separately. The slide was left to stand for five minutes to allow the parasite eggs to float then examined under a compound microscope at 10x magnification to count parasite eggs. To prevent crystal formation, the counting was completed within 60 minutes. Only eggs larger than 60–80 microns [41,42] were included in the count and reported as EPG using the formula: (Chamber 1 + Chamber 2) × 50. A single EPG value was used for each animal by calculating the average EPG from the three collections.

2.3 Amplification of *MHC-DRB* Gene

Hair follicles were collected in the rump area of the animals and were stored in a resealable plastic. Genomic DNA was extracted using a QIAGEN DNEASY kit with some minor modifications. The 285 bp fragment in Exon 2 of the *MHC-DRB* sequence was amplified using the primers previously described: F: 5' - TATCCCGTCTCTGCAGCACATTTC-3'; R: 5'-TCGCCGCTGCACACTGAAACTCTC-3' [5,34,43]. A 30 uL PCR mixture was used consisting of 1 X buffer, 1.5 uM of each primers, 0.2 uM dNTPs, 0.5 U/uL Taq Polymerase and 4 uL genomic DNA. The thermocycler (35x) was set at 95°C for 15 min for initial denaturation, 95°C for 30 sec for denaturation, 67°C for 30 sec for annealing, 72°C for 1 min for extension, and a final extension of 72°C for 5 min. Amplicons were confirmed and assessed via AGE and were sent to Biofact Co., Ltd, South Korea, for PCR purification and sequencing.

2.4 Sequence Analysis

Multiple sequence alignments with the reference sequence (NC_030830.1) [44] from NCBI were performed using MEGA11 [45]. Genotyping and SNP confirmation were then performed using the chromatograms [27] of each sequence through Geneious Prime [46] at the default setting (minimum variant coverage of 1 and at a minimum variant frequency of 0.15).

2.5 Data Analysis

The final EPG value for each goat was distributed among the worm burden categories: Low/mild worm burden (EPG < 500), moderate worm burden (EPG 501-1500), heavy/high worm burden (EPG 1501-3000), and fatal worm burden (>3000) [36]. The mean EPG for each category was computed by adding all EPG values within the category and then dividing by the total number of animals within that category.

On the other hand, identified SNPs were examined for their diversity indices, including allele and genotypic frequencies, observed heterozygosity (Ho), expected heterozygosity (He), deviation from Hardy-Weinberg equilibrium (HWE), and polymorphism information content (PIC). SNP blocks and linkage disequilibrium (LD) coefficient (r^2) of the SNPs were also determined. These analyses were performed using R studio [47], employing the following packages: 'genetics' [48], 'BioManager' [49], 'ggplot2' [50], and 'reshape2' [51]. The associations of the individual SNPs, LD blocks, and linked SNP pairs to the EPG and worm burden categories were determined using the Chi-square test. All association tests were conducted using Jamovi Software [51, 53]. All statistical analyses were performed with 95% confidence interval.

3. Results

3.1 Distribution of Worm Burden of crossbred Anglo-Nubian goats

Descriptive statistics for each worm burden category are presented in Table 1. Goats with low EPG counts (<500) are generally considered GIP-resistant, whereas those with EPG counts greater

Table 1. Descriptive statistics for the worm burden categories of the thirty crossbred Anglo-Nubian goats

Categories	N*	Mean EPG**
Low/mild (EPG of <500)	4	359
Moderate (EPG of 501-1500)	16	900
Heavy/high (EPG of 1501-3000)	4	1929
Fatal (>3,000)	6	3936

*number of animals; **mean egg per gram per category.

than 500 are classified as GIP-susceptible (Khobra *et al.*, 2012; Pratap *et al.*, 2024). In this study, only four animals fell into the GIP-resistant category, while the rest were classified as GIP-susceptible. Sixteen goats had moderate worm burdens, while four had high EPG counts and six were classified with fatal EPG counts. The animals that displayed moderate worm burdens had a mean EPG value of 900, which is approaching the upper limit of the moderate category, indicating that animals within this group were more likely to have higher EPG counts. Supplementary Table 1 presents the individual EPG count of animals.

3.2 Detection of Polymorphism and Diversity Indices of *MHC-DRB* gene

Genotyping analysis of the DNA sequence of the *MHC-DRB* gene revealed 23 SNPs. Based on the findings, heterozygosity was observed to be low (He>Ho) in the samples. HWE analysis revealed 15 SNP loci that have significantly deviated ($p<0.05$) from the HWE, and only eight SNP loci revealed no significant deviation ($p\geq0.05$). Alignment of the translated sequence of this fragment of the MHC gene containing the 23 SNPs revealed 14 amino acid changes. The complete summary of the SNPs and the diversity indices is presented in Supplementary Table 2.

On the other hand, Table 2 presents four SNPs out of twenty-three which include two non-biallelic loci (DRB9489A>C/T and DRB9546G>T/A) whose allele and genotype frequencies were highly varied, resulting with the PIC values of 0.460 and 0.504, indicating that these loci are moderate informative. Twelve biallelic loci were also observed to obtain moderately informative PIC values (0.250<PIC<0.460) [19,32].

For a clear illustration, Fig. 1 exhibits the *MHC-DRB* gene of the goats found on the exon 2

Table 2. Diversity indices of SNP in *MHC-DRB* gene of crossbred Anglo-Nubian goats.

SNP No*	SNP ID**	Type of Mutation	Amino Acid Change	Allele	Allele Frequency	Genotype	Genotype Frequency	Ho	He	HWE (*p* value)	PIC
12	DRB9489A>C/T	N[12,13]	I>L/F	A	0.63	AA	0.53	0.300	0.526	0.076	0.460****
				C	0.25	AT	0.07				
				T	0.12	AC	0.13				
						CC	0.13				
						CT	0.10				
						TT	0.03				
13	DRB9491T>C			T	0.05	TT	0.03	0.033	0.095	0.002***	0.090
				C	0.95	TC	0.03				
						CC	0.93				
22	DRB9546G>T/A	N[22,23]	G>F/I/V	G	0.55	GG	0.47	0.300	0.578	0.000***	0.504****
				T	0.32	GT	0.10				
				A	0.13	TT	0.23				
						TA	0.07				
						AA	0.07				
						GA	0.07				
23	DRB9547G>T			G	0.52	GG	0.40	0.233	0.499	0.014***	0.375****
				T	0.48	GT	0.23				
						TT	0.37				

* SNP location within the 23 SNP array, ** SNP ID ware based on NCBI reference no NC_030830.1, ***significantly deviated from Hardy-Weinberg Equilibrium (HWE) ($p<0.05$), **** moderately informative polymorphism information content (PIC), Non-synonymous mutation (N), Observed heterozygosity (Ho), Expected heterozygosity (He), Phenylalanine (F), Glycine (G), Isoleucine (I),

in chromosome 23. Out of 23 SNPs detected in this study, four SNPs were previously reported by other researchers [16, 19, 43].

Furthermore, the twenty-one biallelic SNPs of the *MHC-DRB* gene were subjected to linkage disequilibrium analysis. LD plays a crucial role in mapping and identifying r^2>0.9000 (Fig. 2), indicating close to complete linked genetic variants [56]. The closest pair, with 1 bp apart, exhibited a complete linkage (r^2=1) (DRB(*BsaHI*)9459 and DRB(*BasHI*)9460), and the farthest in these selected SNP is with only 157 bp (DRB9367T>A and DRB(*PstI*)9524) (r^2=0.9022).

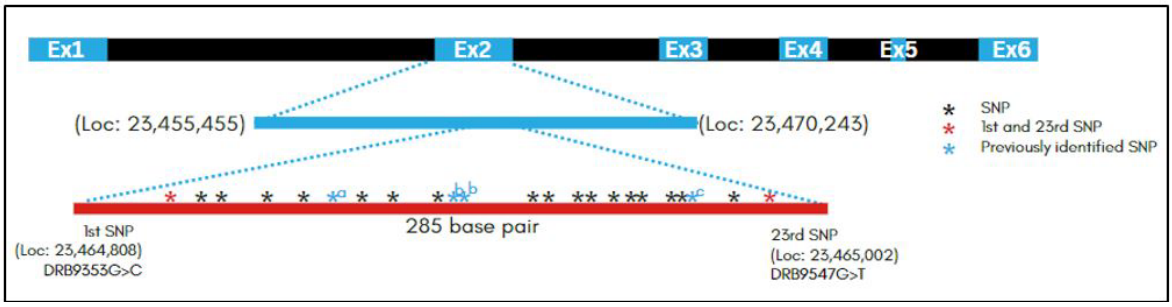

Figure 1. Illustration of the 285bp fragment of *MHC-DRB* gene showing: *locations of the single nucleotide polymorphisms within the fragment, a [19], b [16, 19], c [43].

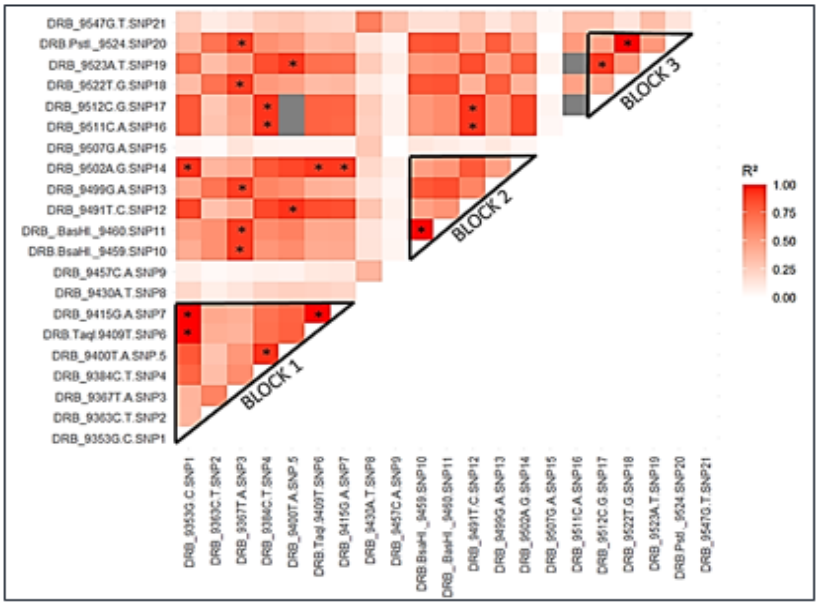

Figure 2. Heatmap-generated blocks based on the Linkage disequilibrium (r^2) values of 21 balletic SNPs in MHC-DRB gene in crossbred Anglo-Nubian goats. Dark red (high r^2 value) indicate that SNPs are most likely to be inherited together. *SNP pairs with r2> 0.9000.

haplotype blocks. It is frequently utilized to quantify the association between two genetic loci [29] and is utilized as a fundamental tool for investigating economically important traits, degree of diversity among animal breeds; r^2 represent correlation between two bi-allelic loci [29, 54, 55]. LD analysis revealed three haplotype blocks and 21 linked SNP pairs with

3.3 Association of *MHC-DRB* Gene Polymorphism with Animal's Worm Burden Category based on EPG

Goats were distributed based on EPG categories which are: Low/mild worm burden (EPG of <500), Moderate worm burden (EPG of 501-1500), Heavy worm burden (EPG of 1501-

3000), and (>3000) [36]. The 23 SNPs were found to be non-significant ($p \geq 0.05$) associated with worm burden even with the locus having the highest PIC value (DRB9546G>T/A) which might be due to the limited number of samples used in the study. The complete summary of the association of the 23 SNPs with the worm burden is presented in Supplementary Table 3.

Furthermore, Table 3 shows the association of the SNPs with high PIC values (DRB9489A>C/T and DRB9546G>T/A) and a locus (DRB9491T>C) which obtained a *p*-value of 0.03. However, the distribution of individual EPG values among the genotypes of locus DRB9491T>C was inconclusive. Specifically, 16 animals with the CC genotype exhibited moderate worm burdens, while animals with the TT and TC genotypes displayed varying worm burdens. This variability among the genotypes in terms of worm burden does not provide a clear, consistent pattern linking genetic variations specific genetic variations at the investigated loci. The diverse range of EPG values within each genotype group weakens any potential correlation between genotype and worm burden category.

The discrepancy in EPG distribution raises concerns about the statistical power of the analysis, particularly considering the small sample size used in the study. The limited sample size may have reduced the ability to detect meaningful associations, resulting in inconclusive findings. Therefore, increasing the sample size in future studies is crucial for enhancing the robustness of the analysis and more accurately assessing genetic factors influencing worm burden susceptibility.

Furthermore, LD blocks and pairs were analyzed separately to assess their association with worm burden in the animals. Consistent with the individual SNP analyses, the association analysis revealed no significant correlations between the three LD blocks (Table 4) or the 21 SNP pairs (Table 5) and EPG values ($p > 0.05$). However, one SNP pair (pair No. 10) yielded a p-value of 0.03, which is statistically significant at the 0.05 threshold. Despite this, it is important to note that one of the SNPs in this pair (DRB9491T>C) had already shown a significant p-value in the individual SNP analysis of worm burden, which was deemed inconclusive due to inconsistent EPG distribution across genotypes, with no distinct

Table 3. Association of the SNPs in the *MHC-DRB* gene of crossbred Anglo-Nubian goats with worm burden categories.

SNP ID	Genotype	Number of goats in Worm Burden Category				x^2	*p*-value
		Low	Moderate	High	Fatal		
DRB9489A>C/T	AA	3	7	2	4	13.7	0.548
	AT	0	2	0	0		
	AC	1	2	0	1		
	CC	0	2	1	1		
	CT	0	3	0	0		
	TT	0	0	1	0		
DRB9491T>C	TT	1	0	0	0	13.9	0.030*
	TC	1	0	0	0		
	CC	2	16	4	6		
DRB9546G>T/A	GG	1	7	2	4	14.6	0.481
	GT	2	1	0	0		
	TT	1	4	1	1		
	TA	0	2	0	0		
	AA	0	1	1	0		
	GA	0	1	0	1		

*significance based on *p*-value is dismissed as the distribution of genotypes per worm burden is inconclusive.

Table 4. Association of the Heatmap-generated LD blocks of the SNPs in the *MHC-DRB* gene of crossbred Anglo-Nubian goats with worm burden categories using chi-square test.

Block No.	SNPs	x^2	*p*-value
Heat Map Block 1	DRB_9353G>C DRB_9363C>T DRB_9367T>A DRB_9384C>T DRB_9400T>A DRB(*TaqI*)9409* DRB_9415G>A	28.1	0.707
Heat Map Block 2	DRB(*BsaHI*)9459* DRB(*BasHI*) 9460* DRB_9491T>C DRB_ 9499G>A DRB_9502A>G	23.6	0.788
Heat Map Block 3	DRB_9512C>G DRB_9522T>G DRB_9523A>T DRB(*PstI*)9524*	8.86	0.963

*SNPs that were previously detected in other studies.

pattern linking genotypes to worm burden categories.

4. Discussion

The *MHC II –DRB* gene in exon 2 of chromosome 23 investigated in this study code for proteins that are found on the surface of B cells and antigen-presenting cells such as macrophages, dendritic, and Langerhans cells; these molecules take part in the antigen presentation to CD4+ T cells which help B cells to produce appropriate immunoglobulins against infection [13,17,18,21-23]. This locus exhibits the most polymorphism in the *MHC* gene [4,5,13-17,19-22,29,33,43] as confirmed by the 23 SNPs identified in this study.

Table 5. Association of the linked SNP pairs based on LD of crossbred Anglo-Nubian goats with worm burden categories using chi-square test.

No.	SNP Pairs		r^2*	x^2	*p*-value
1	DRB_9353G>C	DRB(*TaqI*)9409	1.0000	7.62	0.267
2	DRB(*BsaHI*)9459	DRB(*BasHI*)9460	1.0000	5.28	0.809
3	DRB_9353G>C	DRB_9415G>A	1.0000	6.25	0.395
4	DRB(*TaqI*)9409	DRB_9415G>A	1.0000	9.22	0.417
5	DRB_9522T>G	DRB(*PstI*)9524	1.0000	5.53	0.786
6	DRB_9384C>T	DRB_9400T>A	0.9333	1.88	0.931
7	DRB_9353G>C	DRB_9502A>G	0.9329	10.3	0.326
8	DRB_9400T>A	DRB_9491T>C	0.9310	14.7	0.099
9	DRB_9384C>T	DRB_9511C>A	0.9286	4.76	0.855
10	DRB_9491T>C	DRB_9511C>A	0.9286	18.4	0.03**
11	DRB_9384C>T	DRB_9512C>G	0.9286	4.04	0.909
12	DRB_9491T>C	DRB_9512C>G	0.9286	15.6	0.076
13	DRB_9400T>A	DRB_9523A>T	0.9200	8.29	0.505
14	DRB_9512C>G	DRB_9523A>T	0.9200	9.29	0.678
15	DRB(*TaqI*)9409	DRB_9502A>G	0.9192	14.9	0.245
16	DRB_9415G>A	DRB_9502A>G	0.9158	14.1	0.297
17	DRB_9367T>A	DRB(*BsaHI*)9459	0.9073	7.44	0.944
18	DRB_9367T>A	DRB(*BasHI*)9460	0.9073	7.44	0.944
19	DRB_9367T>A	DRB_9522T>G	0.9042	13.2	0.591
20	DRB_9367T>A	DRB(*PstI*)9524	0.9022	13.5	0.76
21	DRB_9367T>A	DRB_9499G>A	0.9000	19.5	0.363

*Only pairs with r^2> 0.9000, **significance is dismissed.

Notably, four SNPs detected in the current study were also identified in previous studies [16,19,43]. These include the DRB(*TaqI*)9409 restriction site recognized by *TaqI* at 163bp/122bp, coding for the allele B/T restriction pattern or the undigested fragment allele A/t pattern [19]; DRB(*BsaHI*)9459 and DRB(*BsaHI*)9460 at 174bp/112bp, which code for allele B [16,19]; and DRB(*PstI*)_9524C>G at the site of 241bp/44bp, also coding for allele B [43]. In these studies, DNA amplification utilized similar forward and reverse primers for the *MHC-DRB* locus [34]. Subsequently, it was determined that the goat population under investigation were undergoing inbreeding, as supported by the higher He values compared to Ho and deviation from HWE [57,58] of the SNPs.

Although SNPs were determined to be moderately informative for association study, as indicated by the PIC values [19,32,59], association results revealed otherwise. The high degree of polymorphism in this gene is generally associated with the ability of the MHC-DRB molecule to recognize a wide variety of antigen-derived peptides [13-18,20]. The 14 amino acid substitutions caused by the non-synonymous SNPs found in these loci of the *MHC-DRB* gene may alter the functionality of the MHC-DRB molecule [29,60] by changing the three-dimensional conformation of the protein and affecting its ability to interact with antigenic peptides [60,61].

However, the results of this study suggest that these changes in amino acids did not significantly impact the worm burden in goats, which aligns with findings from other studies that similarly find no significant association between *MHC-DRB* polymorphisms and parasitic infections [5,19]. The lack of association may be due to various factors, including the limitations of the current study, such as a small sample size and inbreeding within the goat population. These factors highlight the need for larger and a diverse sample sizes in future studies, as well as the importance of considering population genetics and breeding practices. Such improvements could provide clearer insights into whether the *MHC-DRB* gene fragment plays a role in GIP resistance or susceptibility.

As mentioned by various researchers, *MHC* genes have great potential as a marker for selection programs in livestock breeding [24,30, 38,62]. However, studies using the fragment sequenced in the current study, primarily focus on polymorphism analysis [13,15,17,20-22,32,33] and those that explored its role in parasite infection did not find association [5,19]. In contrast, two studies sequenced two different loci of *MHC-DRB* gene using two different sets of primers. One study found allele C, based on *HaeIII* restriction enzyme pattern, to be highly expressed with high EPG counts of goats [4]. Another study associated haplotypes CCC and GCT of *MHC-DRB* with GIP infected goats [29].

Thus, given the established function of the *MHC-DRB* gene and its role in interacting with various antigens, alterations in this gene in the form of polymorphisms and changes in amino acids are expected to influence an animal's immune response. However, these changes may not be associated with GIP resistance or susceptibility. Instead, the *MHC-DRB* locus examined in this study may be linked to other economically significant traits, or the association with GIP may involve a different locus within the *MHC-DRB* gene.

5. Conclusion

Research on the correlation between gene polymorphism and GIP resistance in goats is scarce in the Philippines. With this study, the *MHC-DRB* of the crossbred Anglo-Nubian goats was confirmed to be highly polymorphic, of which the majority were non-synonymous mutations resulting in amino acid changes. Three LD blocks and eleven closely linked genetic variants were identified. However, the association analysis revealed that the individual SNP, LD blocks, and linked SNPs are not associated with the worm burden of the goats. Nevertheless, the highly polymorphic fragment investigated in this study may be utilized as a potential marker for other association studies. With these, further investigation of the SNPs, LD blocks, and linked variants identified in this study, using a larger sample size, additional goat breeds, and goats from different farms, is recommended. Such studies should focus on associating these possible markers with immune-related and other economically important traits, which would significantly contribute to the development of genetic-based strategies for animal farming, particularly in the Philippines. Additionally, the authors also recommend exploring polymorphisms in other *MHC* loci.

Availability of Data and Materials

All data are available in this study.

Author Contributions

Conceptualization, A.N.N.S., J.M.D.D., S.R.M.T., N.H.N.S., E.T.A., K.S.K., and C.S.O.M.; Methodology, A.N.N.S., J.M.D.D., S.R.M.T., N.H.N.S., E.T.A., K.S.K., and C.S.O.M.; Software, A.N.N.S., and J.M.D.D.; Validation, A.N.N.S., J.M.D.D., S.R.M.T., N.H.N.S., E.T.A., K.S.K., and C.S.O.M.; Formal Analysis, A.N.N.S., J.M.D.D., K.S.K., and C.S.O.M.; Investigation, A.N.N.S., J.M.D.D., S.R.M.T., N.H.N.S., E.T.A., K.S.K., and C.S.O.M.; Resources, A.N.N.S., J.M.D.D., E.T.A., K.S.K., and C.S.O.M.; Data Curation, A.N.N.S., J.M.D.D., K.S.K., and C.S.O.M.; Writing, A.N.N.S., J.M.D.D., S.R.M.T., N.H.N.S., E.T.A., K.S.K., and C.S.O.M.; Visualization, A.N.N.S., J.M.D.D., and C.S.O.M.; and Supervision, A.N.N.S., J.M.D.D., S.R.M.T., N.H.N.S., E.T.A., K.S.K., and C.S.O.M.

Ethics Approval and Consent to Participate

The study was conducted with the approval of the Research Integrity and Compliance Office, Institutional Animal Care and Use Committee of the Mindanao State University Iligan Institute of Technology with the IACUC Protocol Approval No.: 2024A02.

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Conflict of Interest

The authors declare no conflict of interest.

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