RESEARCH ARTICLE

Association of Candidate Gene Polymorphisms with Tick Resistance in Kankrej and Holstein-Friesian Crossbred Cattle

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Abstract

This study investigated polymorphisms in four candidate genes (CD14, SPP1, CD209, and EFR3A) previously reported to be associated with tick resistance or immune mechanisms against tick and tick-borne diseases (TTBDs). PCR-RFLP was used to genotype Kankrej and Holstein Friesian crossbred (HFCB) cattle, and associations between gene variants and tick infestation status were evaluated. CD14 and CD209 genes showed polymorphisms in crossbreds, while Kankrej cattle were monomorphic for these loci. The SPP1 and EFR3A genes were monomorphic in both breeds. Although CD14 polymorphisms were not significantly associated with tick resistance, animals with the BB genotype had reduced odds of infestation compared to AB. A significant association was observed for CD209, where the AA genotype conferred a 12.89 fold higher susceptibility to ticks than AB. These findings highlight the potential of CD209 as a genetic marker for breeding programs aimed at enhancing tick resistance, while also emphasizing the breed-specific distribution of polymorphisms in candidate immune genes.

Key words: Candidate gene, Kankrej, PCR-RFLP, Tick resistance.

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Introduction

Livestock contributes in multiple ways to the natural, financial, human, physical, and social resources within smallholder dairy, crop-livestock, and livestock-dependent production systems (Minjauw and McLeod, 2003). Earlier livestock improvement programmes largely focused on crossbreeding with exotic germplasm, which substantially enhanced the productivity of crossbred animals. However, this emphasis on milk yield inadvertently reduced their natural disease resistance (Prajapati *et al*., 2017).

Parasites are a major constraint in livestock production, and ticks, which are classified under the phylum Arthropoda, are among the most significant. They are obligate external parasites of vertebrates, feeding on the host's blood (Nava *et al*., 2009). Ticks cause economic losses through reduced milk and meat yield, devaluation of hides, transmission of diseases, increased labour and facility costs, and the need for acaricide application, which also leads to resistance against commonly used chemicals (Minjauw and McLeod, 2003; Estrada-Peña and Salman, 2013). The annual global economic loss due to tick and tick-borne diseases (TTBDs) is estimated at 20-30 billion USD (Lew-Tabor and Valle, 2016), while India alone loses about 498.7 million USD annually (Minjauw and McLeod, 2003). Although chemical control with acaricides is widely used, its limitations include high cost, residues in livestock products, the emergence of tick resistance, and the need for repeated application.

The use of naturally tick-resistant cattle in breeding and selection programmes offers a sustainable alternative for tick control (Shyma *et al*., 2015). While environmental factors significantly influence tick resistance (Adams and Templeton, 1998), genetic factors account for a substantial proportion of the variation (Burrow *et al*., 2019). This is supported by heritability estimates for tick resistance ranging from 0.05 to 0.42 (Mapholi *et al*., 2014; Porto-Neto *et al*., 2014), indicating the potential for genetic improvement through artificial selection. Advances in high-throughput sequencing and genome-wide association studies (GWAS)

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have identified numerous single nucleotide polymorphisms (SNPs) associated with host resistance to ticks (Turner *et al*., 2010). These discoveries provide opportunities for detecting genetic markers and applying marker-assisted selection (MAS) to improve resistance. Considering these factors, the present study was undertaken to detect polymorphisms in candidate genes associated with tolerance or susceptibility to tick infestation in Kankrej and HF crossbred cattle.

Materials and Methods

Experimental Animals and Tick Counting

A total of 116 cattle (27 Kankrej and 89 HF crossbred) were randomly selected from farms across different talukas of Banaskantha district. The experimental design was approved by the Institutional Animal Ethics Committee (IAEC) of the College of Veterinary Science and Animal Husbandry, Kamdhenu University, Sardarkrushinagar, Gujarat, India (Approval No. VETCOLL/IAEC/2021/18/Protocol-4) and by the CPCSEA (Approval No. VETCOLL/IAEC/ 2021/18/Protocol-5). Tick counts were recorded three times at three monthly intervals during summer (June 2021–May 2022) using the method of Wharton and Utech (1970), as applied by Kamble *et al*. (2020). Fully or partially engorged female ticks were counted on the left side of the body and multiplied by two to estimate total body counts. After each count, animals were treated with Deltamethrin 1.25% at 2 mL/L water. The mean of the three counts was calculated, and animals were classified following a modified Molento *et al*. (2013) method: tick resistant/higher tolerance (<20 average ticks) or tick susceptible/low tolerance (>20 ticks).

Blood Collection and DNA Isolation

Following the third tick count, 5-7 mL of blood was collected from the jugular vein of each animal into sterile EDTA tubes and stored at -20 °C until DNA extraction. Genomic DNA was extracted using the QIAamp® DNA Blood Mini Kit (250) according to the manufacturer's instructions. DNA concentration, purity, and quality were assessed using a NanoDrop ND-1000 spectrophotometer.

Genotyping and Polymorphism Study

Four candidate genes were selected based on previous reports indicating their association with tick resistance or their direct or indirect roles in immune mechanisms against pathogens, *viz*., CD14 (Cluster of Differentiation 14), SPP1 (Secreted Phosphoprotein 1), CD209 (Cluster of Differentiation 209), and EFR3A (Eighty-Five Requiring 3 Homolog A). PCR conditions were optimized for each primer pair; then PCR amplification was carried out in 25 µL reactions using DreamTaq Green PCR Master Mix (Thermo Scientific). Products were verified on 1.5% agarose gels and stored at –20 °C until use. Restriction enzyme digestion was carried out according to the manufacturer's instructions in 25 µL reactions containing 2.5 µL of 10× RE buffer, one unit of enzyme, and ~22.3 µL PCR product. Digested products were resolved on 2-3% (w/v) low electroendosmosis (EEO) agarose gels for 1 h at 120 V, visualized under UV light, and documented by using gel documentation system. Details of candidate genes, targeted region, primers with annealing temperatures (AT), restriction enzymes (RE), and expected fragmentation patterns (EFP) are provided in the Table 1. Alleles, fragment sizes, and genotype frequencies for the entire population were determined from gel images.

Statistical Analysis

Genotype counts were obtained by direct counting (Falconer and Mackay, 1996), and gene and genotype frequencies were calculated. The Polymorphism Information Content (PIC) and heterozygosity (H) were calculated using standard methods described by Botstein *et al*. (1980) and Nei and Roychoudhary (1974), respectively. The Chi-square test was used to assess Hardy–Weinberg equilibrium (HWE). The effect of variables on tick infestation status was evaluated using univariate logistic regression in R software (R Core Team, 2020), with the model:

$$ln\left(\frac{\hat{p}}{(1-\hat{p})}\right) = \theta_0 + \theta_1 x_1 + \theta_2 x_2 + \cdots + \theta_n x_n$$

Where, $\hat{p}$ is the expected probability of infestation, x_1 through x_p denotes independent variables, and θ the regression

Table 1: Details of candidate genes, targeted regions, primers, and PCR-RFLP conditions

Gene name	Targeted region	Allele	Sequences of primers	AT (°C)	SAF (bp)	RE	EFP
CD14	Chr7: 51764442-51765266	C/T	F: GGGTACTCTCGTCTCAAGGAAC R: CTGAGCCAATTCATTCCTCTTC	60.0	825	*HpyCH4*IV	113, 712, 825
SPP1	Chr6: 36698979-36699463	A/C	F: CCCAAGAGGCAGAAGCAAATC R: CATGTTGGAAAATGGAGACAGC	59.5	485	*Dde*I	85, 400, 485
CD209	Chr7: 16586921-16587218	G/A	F: CTGTAACACATCTGCCATCATTC R: GGGAAGCCCACATTTAACTTTC	60.0	298	*Alu*I	92, 206, 298
EFR3A	Chr14: 9138970-9139189	C/T	F: GCTGAAATGCTCAGAATTCTTCTA R: TGCTCTACCTTCCCCATAGC	59.5	220	*Dde*I	10, 210, 220

AT: Annealing Temperatures; SAF: Size of Amplified Fragment; RE: Restriction Enzymes; and EFP: Expected fragmentation Patterns (EFP)

coefficients. Relative risk among genotypes was also calculated.

Results and Discussion

Details of genotype and allele frequencies of the candidate genes, along with the corresponding polymorphism information content (PIC), heterozygosity (H), and chi-square (χ^2) values are presented in Table 2. Details of the association between candidate gene genotypes and tick infestation in Kankrej and HF crossbred cattle, including AIC, BIC, odds ratio (OR), and p-values, are presented in Table 3.

CD14 Gene

PCR-RFLP analysis revealed a polymorphic pattern for the CD14 gene in the studied cattle population (Fig. 1A, 2A). In HF crossbreds, two genotypes, AB and BB, were observed, whereas the gene exhibited a monomorphic pattern in Kankrej cattle. Chi-square analysis indicated that both Kankrej and crossbred populations significantly deviated from HWE (Table 2). This suggests that the Kankrej population may be under selection pressure or not representative of the broader population. Population sub-structuring in the field samples used in this study may also explain the significant departure from HWE. The CD14 gene encodes a membrane glycoprotein found on the surface of monocytes and macrophages, playing a pivotal role in innate immunity, particularly in pathogen recognition and mediation of inflammatory responses. In cattle, higher CD14 expression, both at the gene transcription level in skin and at the protein level in blood, has been associated with tick-susceptible phenotypes (Piper *et al*., 2009; Piper *et al*., 2010). This gene is also recognized as a marker for monocytes and macrophages and can therefore be involved in numerous immune response mechanisms (Ziegler-Heitbrock and Ulevitch, 1993).

Association analysis with tick infestation status showed that the genotypes identified were not significantly associated with tick resistance or susceptibility. However, the odds of being tick-susceptible in the BB genotype were only 0.35 times those of the AB genotype (Table 3). No direct studies linking CD14 polymorphisms with tick resistance have been reported in the literature; however, there is ample evidence suggesting a possible role of this gene in tick infestation status. Piper *et al*. (2009) reported significantly higher levels of CD14+ monocytes and MHC II-presenting cells in tick-susceptible cattle. deAraujo *et al*. (2019) observed a significant increase in CD14 expression at days 9 and 21 compared to days 0 and 1 following artificial tick infestation. Marima *et al*. (2020) reported increased CD14 expression levels after tick infestation across all breeds and tick species treatment groups.

SPP1 Gene

Secreted phosphoprotein 1 (SPP1), also known as Osteopontin (OPN), acts as a mediator between the innate and adaptive immune mechanisms (Clemente *et al*., 2016). Macrophages

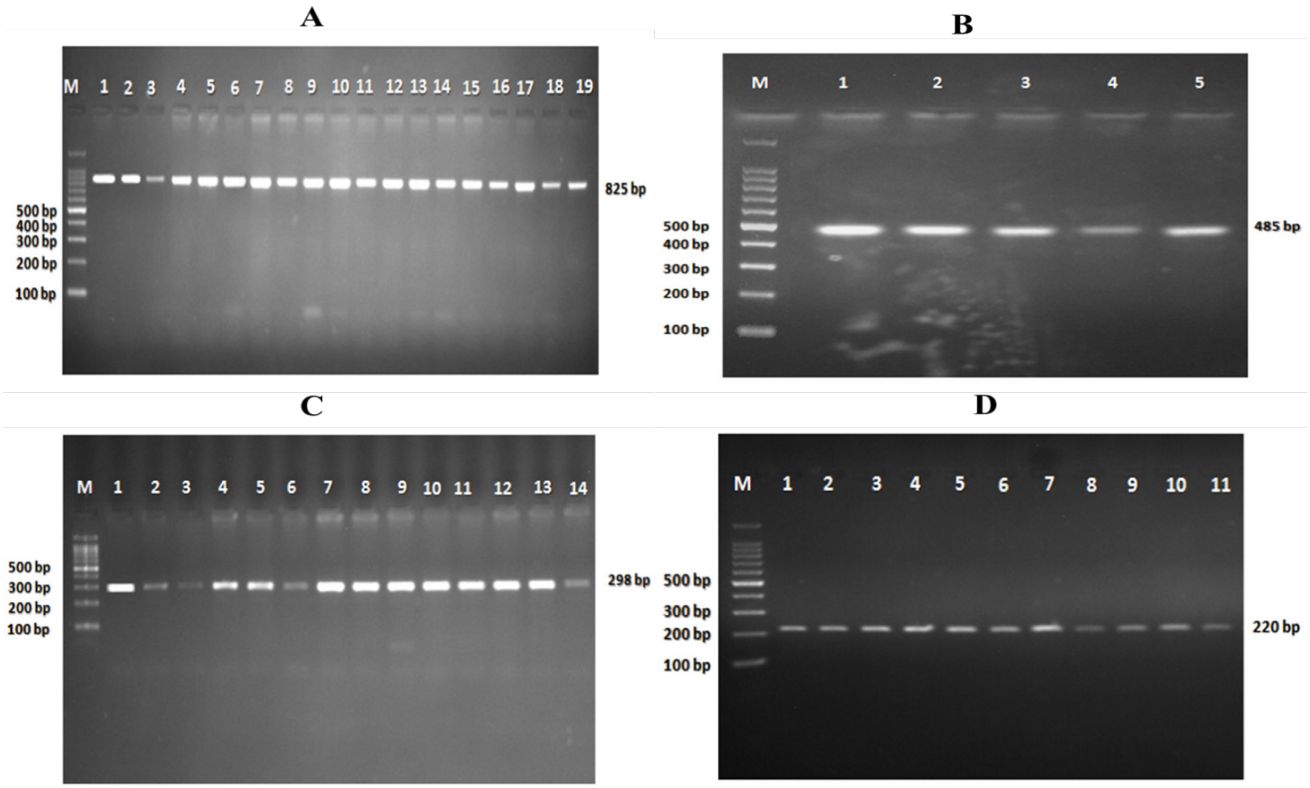

Fig. 1: Representative gel image of PCR amplification products using primers targeting: **A.** CD14 gene; **B.** SPP1 gene; **C.** CD209 gene; **D.** EFR3A gene; all with Marker-100bp.

and activated T cells are the main producers of the cytokine OPN (Patarca *et al*., 1989). In T cell activation, OPN is considered one of the early factors. SPP1 plays important roles in inflammation and immunity against infectious diseases (O'Regan and Berman, 2000). In the present study, no mutation was detected in the targeted region of the SPP1 gene; therefore, no association analysis with tick resistance or susceptibility was carried out in either Kankrej or crossbred cattle populations (Fig 1B, Fig 2B). However, there is sufficient evidence supporting the involvement of the SPP1 gene in immunity related to tick infestation and other diseases.

CD209 (DC-SIGN) Gene

CD209 (Cluster of Differentiation 209) encodes a C-type lectin receptor known as DC-SIGN, which is expressed on the surface of immune cells, primarily dendritic cells

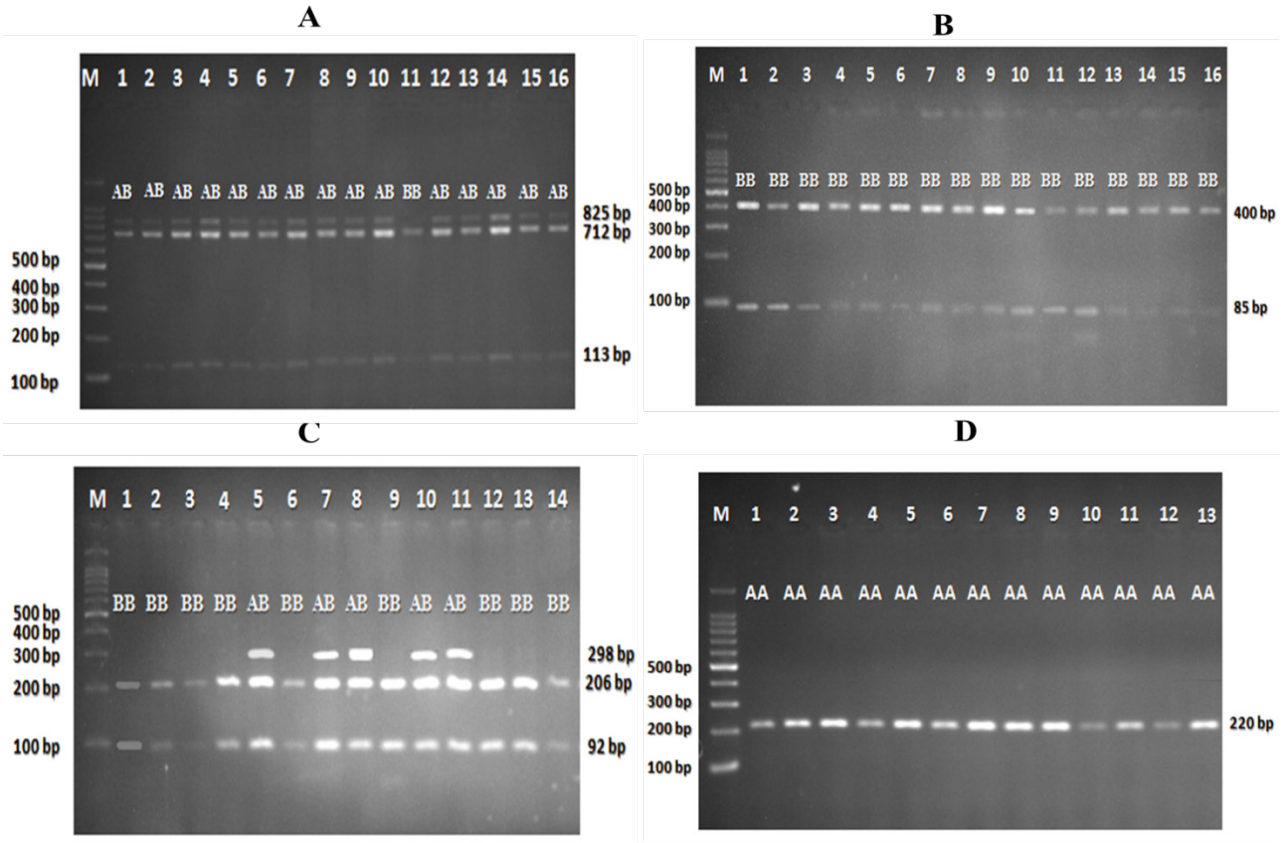

Fig. 2: Representative gel image of the PCR-RFLP profile generated using primers targeting: **A.** CD14 gene; RE enzyme- *HpyCH4*IV (lane 11 displayed BB genotype, while all other lane displayed AB genotype); **B.** SPP1 gene; RE enzyme- *Dde*I; **C.** CD209 gene; RE enzyme- *Alu*I (lane no 5,7, 8, 10 and 11 displayed AB genotype, while other lane displayed BB genotype); **D.** EFR3A gene; RE enzyme- *Dde*I; all with Marker-100bp

Table 2: Genotype and allele frequencies, polymorphism information content (PIC), heterozygosity (H), and chi-square (χ^2) of candidate genes

Gene name	Genotype	Genotype frequency (GF)			Allelic frequency		PIC value	H value	χ^2 (HWE)	p-value
		Kankrej N (GF)	HF crossbred N (GF)	Polled population N (GF)	A	B				
CD14	AA	00 (0.00)	00 (0.00)	0 (0.00)	0.47	0.53	0.12	0.13	88.00**	0.00
	AB	27 (1.00)	81 (0.91)	108 (0.93)						
	BB	00 (0.00)	08 (0.09)	08 (0.07)						
CD209	AA	27 (1.00)	81 (0.91)	108 (0.93)	0.97	0.03	0.12	0.13	0.15^{ns}	0.93
	AB	00 (0.00)	08 (0.09)	08 (0.09)						
	BB	00 (0.00)	00 (0.00)	00 (0.00)						

N: Number of animal having particular genotype. *Significant at 5%, **Significant at 1%, ^{ns}non-significant.

Table 3: Association of candidate gene genotypes with tick infestation in Kankrej and HF crossbred cattle

Candidate gene	Genotype	AIC; BIC	Odds ratio (OR)	p-value
CD14	AB	156.96;	1 (reference)	0.17
	BB	162.46	0.35	
CD209	AB	150.12;	1 (reference)	0.02*
	AA	155.63	12.89	

*Significant at 5%.

and some macrophages (Park *et al*., 2016). Several studies have examined this gene and concluded that CD209 is an important immune gene in cattle, functioning both as a pattern recognition receptor and as a pathogen entry point, with its polymorphisms influencing disease resistance (Kumar *et al*., 2020; Gopi *et al*., 2020). In the present study, we targeted a specific region of CD209 gene to investigate polymorphisms and their association with tick resistance. PCR-RFLP analysis revealed a polymorphic pattern in HF crossbred cattle with two genotypes (AA and AB), whereas Kankrej cattle showed a monomorphic pattern (Fig. 1C, 2C). The population under study was found to be in HWE (Table 2). A significant association was observed between the CD209 gene and tick infestation, where animals with the AA genotype were 12.89 times more susceptible to ticks than those with the AB genotype (Table 3). Although no direct association studies between CD209 polymorphisms and tick resistance have been reported in the literature, sufficient evidence exists to suggest a potential role of this gene in tick infestation status. Franzin *et al*. (2017) reported downregulation of CD209 expression in skin infested with larvae in resistant hosts compared to stressed skin, and upregulation in skin infested with larvae in susceptible hosts, as well as in skin infested with nymphs in both host breeds. Gopi *et al*. (2020) and Kumar *et al*. (2020) also explored the association of the CD209 gene with paratuberculosis (PTB) in cattle.

EFR3A Gene

In the Kankrej and HF crossbred cattle population studied here, PCR-RFLP analysis revealed a monomorphic pattern for this gene (Fig. 1D, 2D). Consequently, no association analysis with tick infestation was carried out. EFR3A encodes a protein component of the plasma membrane in eukaryotes, including cattle. Recent studies suggest that EFR3A interacts with proteins such as flotillin-2, contributing to the organization and regulation of cholesterol-rich membrane rafts, which serve as critical platforms for signaling and pathogen responses (Trybus *et al*., 2025). Previous studies have highlighted EFR3A as a candidate gene for tick resistance. Mapholi *et al*. (2016) examined 586 Nguni cattle, collecting tick counts at eight anatomical locations, and identified EFR3A as a potential candidate associated with tick resistance. Conversely, Gouveia *et al*. (2021) investigated host resistance to ticks, gastrointestinal nematodes and *Eimeria* spp. under natural infestation. While they did not find an association between EFR3A and tick resistance, they observed a link between this gene and host resilience to gastrointestinal nematodes.

Conclusion

This study revealed distinct genetic patterns in key immune-related genes between Kankrej and HF crossbred cattle. Among the four genes examined, CD209 showed a strong association with tick susceptibility, where the AA genotype markedly increased the risk of infestation. Although CD14 polymorphism did not reach statistical significance, the BB genotype indicated a possible protective trend. The absence of variability in SPP1 and EFR3A suggests limited potential for these loci in the studied populations. Overall, the findings underscore the role of CD209 as a promising marker for selective breeding programs targeting enhanced tick resistance, particularly in crossbreds. Integrating such genetic markers into breeding strategies could reduce reliance on chemical acaricides, improve animal health, and support sustainable livestock production in tick-endemic regions.

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References

Adams, L.G., & Templeton, J.W. (1998). Genetic resistance to bacterial diseases of animals. *Revue Scientifiqueet Technique (International Office of Epizootics)*, *17*(1), 200-219.

Botstein, D., White, R. L., Skolnick, M., & Davis, R.W. (1980). Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *American Journal of Human Genetics*, *32*(3), 314.

Burrow, H.M., Mans, B.J., Cardoso, F.F., Birkett, M.A., Kotze, A.C., Hayes, B.J., Mapholi, N., Dzama, K., Marufu, M.C., Githaka, N.W., & Djikeng, A. (2019). Towards a new phenotype for tick resistance in beef and dairy cattle: A review. *Animal Production Science*, *59*(8), 1401-1427.

Clemente, N., Raineri, D., Cappellano, G., Boggio, E., Favero, F., Soluri, M.F., Dianzani, C., Comi, C., Dianzani, U., & Chiocchetti, A. (2016). Osteopontin bridging innate and adaptive immunity in autoimmune diseases. *Journal of Immunology Research*, *2016*(1), 7675437.

deAraujo, F.F., Ronda, J.B., Bittar, E.R., Venturini, G.C., Garcia, G.C., Martins-Filho, O.A., Araújo, M.S.S., & Bittar, J.F.F. (2019). Distinct immune response profile during *Rhipicephalus (Boophilus) microplus* infestations of Guzerat dairy herd according to the maternal lineage ancestry (mitochondrial DNA). *Veterinary Parasitology*, *273*, 36-44.

Estrada-Peña, A., & Salman, M. (2013). Current limitations in the control and spread of ticks that affect livestock: A review. *Agriculture*, *3*(2), 221-235.

Falconer, D.S., & Mackay, T.F.C. (1996). Introduction to quantitative genetics, Longman. *Essex, England*, p. 254-256.

Franzin, A.M., Maruyama, S.R., Garcia, G.R., Oliveira, R.P., Ribeiro, J.M.C., Bishop, R., Maia, A.A.M., Moré, D.D., Ferreira, B.R., & Santos, I.K.F.D.M. (2017). Immune and biochemical responses in skin differ between bovine hosts genetically susceptible and resistant to the cattle tick *Rhipicephalus microplus*. *Parasites & Vectors*, *10*(1), 51.

Gopi, B., Singh, R.V., Kumar, S., Kumar, S., Chauhan, A., Kumar, A., & Singh, S.V. (2020). Single-nucleotide polymorphisms in CLEC7A, CD209 and TLR4 gene and their association with susceptibility to paratuberculosis in Indian cattle. *Journal of Genetics*, *99*(1), 14.

Gouveia, G.C., Ribeiro, V.M.P., Fortes, M.R.S., Raidan, F.S.S., Reverter, A., de Moraes, M.M., de Araújo, A.E.M., Gonçalves, D.R., da Silva, M.V.G.B., & Toral, F.L.B. (2021). Unraveling the genetic variability of host resilience to endo and ectoparasites under natural infestation, in Nellore cattle. *Genetics of Selection & Evolution*, *55*, 81.

Kamble, B.M., Dinesh, C.N., Ravindran, R., Chopade, M., Bindu, K.A., Rojan, P.M., & Asaf, V.M. (2020). Identification of single nucleotide polymorphism in the selected quantitative trait loci associated with resistance/susceptibility to tick infestation in Vechur cattle. *The Pharma Innovation Journal*, *9*(4), 03-07.

Kumar, S., Kumar, S., Singh, R.V., Chauhan, A., Kumar, A., Bharati, J., & Singh, S.V. (2022). Association of genetic variability in CD209 gene with bovine paratuberculosis disease: A case–control study in the Indian cattle population. *Animal Biotechnology*, *33*(4), 664-671.

Lew-Tabor, A.E., & Valle, M.R. (2016). A review of reverse vaccinology approaches for the development of vaccines against ticks and tick borne diseases. *Ticks and Tick-Borne Diseases*, *7*(4), 573-585.

Mapholi, N.O., Maiwashe, A., Matika, O., Riggio, V., Bishop, S.C., MacNeil, M.D., Banga, C., Taylor, J.F., & Dzama, K. (2016). Genome-wide association study of tick resistance in South African Nguni cattle. *Ticks and Tick-Borne Diseases*, *7*(3), 487-497.

Mapholi, N.O., Marufu, M.C., Maiwashe, A., Banga, C.B., Muchenje, V., MacNeil, M.D., Chimonyo, M., & Dzama, K. (2014). Towards a genomics approach to tick (Acari: Ixodidae) control in cattle: A review. *Ticks and Tick-Borne Diseases*, *5*(5), 475-483.

Marima, J.K., Nel, C.L., Marufu, M.C., Jonsson, N.N., Dube, B., & Dzama, K. (2020). A genetic and immunological comparison of tick-resistance in beef cattle following artificial infestation with Rhipicephalus ticks. *Experimental and Applied Acarology*, *80*(4), 569-590.

Minjauw, B., & Mcleod, B.A. (2003). Tick-borne diseases and poverty. The impact of ticks and tick- borne diseases on the livelihood of small-scale and marginal livestock owners in India and eastern and southern Africa. *Research report, DFID Animal Health Programme*. p. 124.

Molento, M.B., Fortes, F.S., Buzatti, A., Kloster, F.S., Sprenger, L.K., Coimbra, E., & Soares, L.D. (2013). Partial selective treatment of Rhipicephalusmicroplus and breed resistance variation in beef cows in Rio Grande doSul, Brazil. *Veterinary Parasitology*, *192*(1-3), 234-239.

Nava, S., Guglielmone, A.A., & Mangold, A.J. (2009). An overview of systematics and evolution of ticks. *Frontier in Bioscience*, *14*(8), 2857-77.

Nei, M., & Roychoudhury, A.K. (1974). Sampling variances of heterozygosity and genetic distance. *Genetics*, *76*(2), 379-390.

O'Regan, A., & Berman, J.S. (2000). Osteopontin: A key cytokine in cell-mediated and granulomatous inflammation. *International Journal of Experimental Pathology*, *81*(6), 373-390.

Park, K.T., ElNaggar, M.M., Abdellrazeq, G.S., Bannantine, J.P., Mack, V., Fry, L.M., & Davis, W.C. (2016). Phenotype and function of CD209+ bovine blood dendritic cells, monocyte-derived-dendritic cells and monocyte-derived macrophages. *PloS One*, *11*(10), p.e0165247.

Patarca, R., Freeman, G.J., Singh, R.P., Wei, F.Y., Durfee, T., Blattner, F., Regnier, D.C., Kozak, C.A., Mock, B.A., & Morse, H.C. (1989). Structural and functional studies of the early T lymphocyte activation 1 (Eta-1) gene. Definition of a novel T cell-dependent response associated with genetic resistance to bacterial infection. *The Journal of Experimental Medicine*, *170*(1), 145-161.

Piper, E.K., Jackson, L.A., Bielefeldt-Ohmann, H., Gondro, C., Lew-Tabor, A.E., & Jonsson, N.N. (2010). Tick-susceptible *Bos taurus* cattle display an increased cellular response at the site of larval *Rhipicephalus (Boophilus) microplus* attachment, compared with tick-resistant *Bos indicus* cattle. *International Journal for Parasitology*, *40*(4), 431-441.

Piper, E.K., Jonsson, N.N., Gondro, C., Lew-Tabor, A.E., Moolhuijzen, P., Vance, M.E., & Jackson, L.A. (2009). Immunological profiles of *Bos taurus* and *Bos indicus* cattle infested with the cattle tick, *Rhipicephalus (Boophilus) microplus*. *Clinical and Vaccine Immunology*, *16*(7), 1074-1086.

Porto-Neto, L.R., Reverter, A., Prayaga, K.C., Chan, E.K., Johnston, D.J., Hawken, R.J., Fordyce, G., Garcia, J.F., Sonstegard, T.S., Bolormaa, S., & Goddard, M.E. (2014). The genetic architecture of climatic adaptation of tropical cattle. *Plos One*, *9*(11), p.e113284.

Prajapati, B.M., Gupta, J.P., Pandey, D.P., Parmar, G.A., & Chaudhari, J.D. (2017). Molecular markers for resistance against infectious diseases of economic importance. *Veterinary World*, *10*(1), 112.

R Core Team (2016). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. *http://www. R-project. org/.*

Shyma, K.P., Gupta, J.P., & Singh, V. (2015). Breeding strategies for tick resistance in tropical cattle: a sustainable approach for tick control. *Journal of Parasitic Diseases*, *39*(1), 1-6.

Trybus, M., Hryniewicz-Jankowska, A., Czogalla, A., & Sikorski, A.F. (2025). EFR3A, an intriguing gene, and protein with a scaffolding function. *Cells*, *14*(6), 445.

Turner, L.B., Harrison, B.E., Bunch, R.J., Neto, L.R.P., Li, Y., & Barendse, W. (2010). A genome-wide association study of tick burden and milk composition in cattle. *Animal Production Science*, *50*(4), 235-245.

Wharton, R.H., & Utech, K.B.W. (1970). The relation between engorgement and dropping of *Boophilus microplus* (Canestrini) (Ixodidae) to the assessment of tick numbers on cattle. *Australian Journal of Entomology*, *9*(3), 171-182.

Ziegler-Heitbrock, H.W.L., & Ulevitch, R.J., (1993). CD14: Cell surface receptor and differentiation marker. *Immunology Today*, *14*(3), 121-125.