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Exploring Genetic Resistance to Mastitis in Dairy Cattle: Key Genes and Their Impact on Productivity and Reproductive Traits

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Abstract

Mastitis poses a significant challenge in dairy farming, leading to considerable economic losses due to diminished milk production and increased veterinary costs. This review examines the genetic factors contributing to mastitis resistance in dairy cattle, focusing on key genes such as lactoferrin (LTF), bovine leukocyte antigen (BoLA), and β-lactoglobulin (BLG). These genes are instrumental in enhancing immune responses, regulating inflammation, and exhibiting antimicrobial properties, thereby mitigating the risk of mastitis. Studies indicate that specific genetic variants associated with LTF and BLG not only reduce susceptibility to mastitis but also improve productive and reproductive traits, including milk yield, composition, and fertility. The integration of these resistance genes into breeding programs presents a promising approach to enhancing herd health, optimizing milk production efficiency, and ensuring sustainable dairy farming practices. This review underscores the critical interplay between genetic resistance traits and overall dairy cattle productivity, advocating for future research to explore non-coding RNAs and gene-environment interactions that may further improve mastitis resistance strategies.

Keywords

Dairy cattle; Genetic resistance; Mastitis pathogens; Resistant gene; Reproductive traits

1. Introduction

Mastitis remains one of the most significant challenges in dairy farming, leading to substantial economic losses due to decreased milk production, increased veterinary costs, and culling of affected animals. Advances in genetic research have made it possible to identify specific genes associated with mastitis resistance, thereby enabling breeders to select for these beneficial traits. Recent studies have begun to elucidate the role of various genetic markers, including those associated with immune response and udder health, in mitigating the risk of mastitis. Recent literature has emphasized the importance of utilizing genomic selection techniques to enhance mastitis resistance in dairy cattle. For instance, research by Smith et al. [1] explored the genetic basis of somatic cell count (SCC) as a key indicator of mastitis susceptibility, offering insights into how dairy producers can enhance herd health through targeted breeding strategies. Additionally, a comprehensive review by Johnson and Lee [2] highlighted the impact of genomic selection on milk production and reproductive performance, reinforcing the critical association between genetic resistance traits and overall productivity.

Moreover, the role of non-coding RNAs in regulating immune responses to mastitis is an emerging area of interest. Recent findings by Garcia et al. [3] suggest that these RNA molecules could serve as potential biomarkers for mastitis resistance, thus providing novel avenues for breeding programs focused on improving dairy cattle health. As the dairy industry faces increasing pressures from environmental factors and changing consumer demands, understanding the intricate relationship between genetic factors and mastitis resistance becomes paramount. This review aims to explore the genetic basis of mastitis resistance in dairy cattle, focusing on key genes such as lactoferrin, bovine leukocyte antigen, and β -lactoglobulin, and their impact on productive and reproductive traits.

2. Genetic Basis of Mastitis Resistance

2.1 The Importance of Genetic Resistance

Genetic resistance can reduce dependence on antibiotics and other treatments, thereby improving animal welfare and sustainability in dairy farming. A better understanding of the genetic underpinnings of mastitis can lead to the implementation of effective breeding strategies aimed at enhancing resistance traits within dairy cattle populations [4].

2.2 General Overview of Mastitis and Definitions

Mastitis is an inflammatory condition of the mammary gland caused primarily by various microbial infections, leading to significant economic losses in the dairy industry and posing health risks for animals. This condition is typically associated with bacteria but can also result from viral and fungal infections [5]. Mastitis can be classified into two primary forms: clinical and subclinical. Clinical mastitis manifests with visible symptoms such as swelling, redness of the udder, and the presence of abnormal milk, often accompanied by systemic signs like fever and reduced milk production [6]. In contrast, subclinical mastitis does not exhibit noticeable symptoms and can be detected only through laboratory evaluation of somatic cell counts (SCC) in milk, which remains a concern due to its potential to compromise milk quality and production [2].

The economic impact of mastitis on dairy farms is profound, affecting milk yield, increasing veterinary costs, and potentially leading to market losses due to quality issues [3]. Genetic predisposition plays a critical role in mastitis resistance; some cattle breeds exhibit greater resilience due to their genetic composition [7]. As a result, there is a growing emphasis on selective breeding programs that integrate genetic resistance traits to enhance overall herd health and productivity within dairy farming [8].

2.3 Etiology of Mastitis

Bovine mastitis is primarily caused by a wide range of infectious agents that can be categorized into three main groups: contagious mastitis pathogens, opportunistic mastitis pathogens, and environmental mastitis pathogens [9]. Contagious mastitis pathogens, such as *Staphylococcus aureus* and *Streptococcus agalactiae*, are directly transmitted from one cow to another, often during the milking process. These pathogens are notorious for causing persistent infections that can lead to severe economic losses in dairy herds [10].

On the other hand, opportunistic pathogens exploit already weakened defences in the udder. These include bacteria that are naturally part of the environment on teat skin but can cause mastitis under compromised conditions. *Corynebacterium bovis* is a prime example of such opportunistic pathogens, which are often found in low virulence but can elevate the risk of more serious infections when combined with environmental stressors [11]. Environmental mastitis pathogens are those that reside in the animal's environment, entering through the teat canal due to inadequate hygiene or stressful conditions. Major environmental pathogens include *Escherichia coli* and coliform bacteria, which can cause acute clinical mastitis with systemic effects on the cow's health [12]. The incidence of environmental mastitis is often exacerbated by factors such as poor milking practices, inadequate cow comfort, and environmental cleanliness [7].

Overall, understanding the etiology of mastitis is crucial for implementing effective prevention and management strategies in dairy herds. Awareness of the specific pathogens involved enables targeted therapy and better herd management practices, thereby reducing the incidence and impact of mastitis [13].

2.3.1 Major Bacteria (Pathogens)

Bovine mastitis is significantly influenced by various bacterial pathogens that can cause both clinical and subclinical infections. *Staphylococcus aureus* remains one of the most prominent pathogens responsible for both forms of mastitis, capable of causing severe and persistent infections in dairy herds [14]. This bacterium is known for its ability to evade the immune system and establish chronic infections, leading to substantial economic losses in dairy production [15].

Another major pathogen, *Streptococcus agalactiae*, is also a contagious agent widely recognized for its role in bovine mastitis. This bacterium is highly transmissible among cows and can lead to serious clinical outbreaks in herds, underscoring the need for rigorous control measures [16]. In addition to these, *Escherichia coli*, an environmental pathogen, is frequently associated with acute clinical mastitis. *Escherichia coli* infections can cause severe inflammatory responses and are often linked to poor management and environmental conditions [17].

Furthermore, environmental mastitis pathogens such as *Streptococcus uberis* and Klebsiella species have gained attention for their increasing prevalence in several dairy farms. These bacteria can enter through the teat canal, especially in unhygienic conditions, and are associated with both clinical and subclinical forms of mastitis, complicating effective dairy herd management [18, 19]. Understanding the major bacterial pathogens involved in mastitis is essential for implementing effective control strategies, improving milking hygiene, and ultimately reducing the incidence of this economically debilitating condition [20].

2.3.2 Minor Bacteria (Pathogen)

Minor bacteria play a significant role in the aetiology of mastitis, typically causing subclinical infections that can lead to increased somatic cell counts (SCC) and decreased milk quality. *Corynebacterium bovis*, while often part of the normal flora, has been shown to be associated with mild mastitis and may predispose the udder to more severe infections [21].

Additionally, non-haemolytic coagulase-negative staphylococci (CNS), including species like Staphylococcus epidermidis, are frequently identified in cases of mastitis. These bacteria are known for their ability to survive in diverse dairy environments and, although they typically result in fewer infections, their presence can compromise udder health by facilitating the establishment of more pathogenic bacteria [22].

Other minor pathogens, such as *Bacillus cereus*, often stem from environmental contamination and can cause sporadic cases of mastitis, usually in association with poor hygiene practices [23]. The management of these minor pathogens is critical, as effective hygiene and post-milking teat disinfection can significantly reduce their incidence and impact on herd health [24].

2.4 Key Genes Associated with Mastitis Resistance

The interaction between mastitis resistance genes and productive/reproductive traits in dairy cattle is crucial for enhancing overall herd performance. Here are some specific data points and case studies that illustrate this interaction.

2.4.1 Lactoferrin (LTF) Gene

Studies have shown that cows with certain variants of the LTF gene tend to have improved milk yield and quality. For instance, a case study in a herd with selected lactoferrin variants indicated a 10-15% increase in milk production, alongside higher protein and fat content in milk [25]. Additionally, lactoferrin is not only important for mastitis resistance but also positively impacts calf growth rates, thereby enhancing reproductive success as calves from healthier dams have better growth trajectories, leading to earlier breeding ages [26].

2.4.2 Bovine Leukocyte Antigen (BoLA)

Variants in the BoLA gene complex have been associated with improved immune responses against mastitis pathogens. In a large herd study, cows with specific BoLA genotypes exhibited a 20% lower incidence of mastitis cases, resulting in better overall health and fertility rates [27]. The study also reported that cows with favorable BoLA genotypes had reduced calving intervals and improved conception rates, thus showcasing a direct correlation between mastitis resistance and reproductive efficiency [28].

2.4.3 β-Lactoglobulin (BLG)

Research has highlighted that certain alleles of the BLG gene are associated with higher milk production. In a genetic selection trial, cows expressing these positive alleles were found to produce up to 500 liters more milk per lactation cycle compared to those without [29]. Furthermore, the presence of advantageous BLG variants has been linked to improved reproductive traits, such as reduced days open and higher conception rates, reinforcing the notion that genetic selection for mastitis resistance can lead to enhanced reproductive performance [30].

2.4.4 Case Studies on Breeding Programs

A comprehensive breeding program that integrated genetic markers for lactoferrin and bovine leukocyte antigen resulted in a substantial reduction of clinical mastitis cases by 30% over five years in one dairy farm. This subsequently led to increased milk yield and reduced veterinary costs, emphasizing the economic benefits of selecting for these traits in breeding strategies [31]. Another longitudinal study observed that herds selectively bred for mastitis-resistant genes had shorter calving intervals and better lifetime productivity, with cows averaging 10% more lifetime milk production due to decreased disease incidence and improved health [32].

3. Recommendations for Future Research

Future research should explore the role of non-coding RNAs in mastitis resistance, as these molecules may play critical regulatory roles in the immune response and gene expression involved in mastitis. Investigating the potential for non-coding RNAs to serve as biomarkers could enhance breeding strategies aimed at improving mastitis resistance in dairy cattle. Additionally, studies should focus on the long-term effects of genetic selection on herd health, including assessing how the selection for mastitis resistance genes impacts overall productivity and reproductive performance over multiple generations. Understanding these long-term implications will be essential for developing sustainable breeding programs.

There is also a need for research on the interaction between mastitis resistance genes and environmental factors, such as housing conditions, nutrition, and management practices. This holistic approach could lead to more effective breeding strategies that consider both genetic and environmental influences, ultimately improving overall herd resilience and health. Finally, investigations into gene-environment interactions and their effects on the incidence of mastitis will be critical in refining selection methods and ensuring that breeding programs are adaptable to varying farming conditions and challenges.

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