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| REVIEW | | OPEN ACCESS |
| Comprehensive Review of Brucellosis Treatment: Efficacy, Challenges, and Future Perspectives **Ayesha Qadry1**  1Antigen Section, Veterinary Research Institute, Lahore-54810, Pakistan  \*Corresponding author: doctorayeshaqadry@gmail.com  **ABSTRACT**  Brucellosis, a zoonotic disease caused by various *Brucella* species, continues to pose significant public health challenges worldwide. This review provides a comprehensive overview of the treatment strategies for brucellosis, focusing on the efficacy of different antimicrobial agents, challenges encountered in treatment, and emerging therapeutic approaches. Drawing upon a wide range of scientific literature, this review aims to consolidate current knowledge on brucellosis treatment and highlight potential future directions for research and clinical management.  Keywords: Brucellosis, *Brucella*, treatment, antimicrobial agents, challenges, future perspectives.  **Citation:** Ayesha, Q., (2024). Comprehensive Review of Brucellosis Treatment: Efficacy, Challenges, and Future Perspectives. In Biology (pp. 1–3). farha-b. <https://doi.org/10.5281/zenodo.10827919> | | |
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Introduction:

Brucellosis remains a major public health concern globally, particularly in regions where livestock farming is prevalent. The disease is caused by Gram-negative bacteria belonging to the genus *Brucella*, with *Brucella* melitensis, *Brucella* abortus, and *Brucella* suis being the primary causative agents in humans. Despite concerted efforts to control brucellosis through vaccination and animal husbandry practices, human infection persists, necessitating effective treatment strategies to mitigate its impact on public health. This review critically evaluates the current approaches to brucellosis treatment, emphasizing the efficacy of antimicrobial agents, challenges in management, and potential avenues for future research.

Antimicrobial Treatment of Brucellosis:

The cornerstone of brucellosis treatment involves antimicrobial therapy, typically comprising a combination of antibiotics to enhance efficacy and minimize the risk of relapse. The primary antimicrobial agents utilized in the management of brucellosis include doxycycline, rifampicin, streptomycin, and fluoroquinolones.

Doxycycline, a tetracycline derivative, is often used in combination with rifampicin due to its excellent tissue penetration and intracellular activity against *Brucella* organisms (Solís García del Pozo et al., 2010). Rifampicin, a potent bactericidal agent, exhibits synergistic effects when combined with doxycycline, leading to enhanced therapeutic outcomes (Ariza et al., 2007). However, the emergence of rifampicin-resistant strains poses a significant challenge to its continued efficacy in brucellosis treatment (Sánchez-Sousa et al., 2012).

Streptomycin, an aminoglycoside antibiotic, is considered a first-line therapy for severe brucellosis cases or when rifampicin cannot be administered (Solera et al., 2005). Despite its efficacy, streptomycin use is limited by the requirement for parenteral administration and the risk of ototoxicity and nephrotoxicity (Pappas et al., 2005). Fluoroquinolones, such as ciprofloxacin and levofloxacin, have emerged as alternative agents for the treatment of brucellosis, particularly in cases of resistance or intolerance to first-line antibiotics (Bosilkovski et al., 2004). These agents offer the advantage of oral administration, facilitating outpatient management and improving patient compliance (Al-Eissa et al., 1996). However, the emergence of fluoroquinolone resistance underscores the need for judicious antibiotic use and ongoing surveillance (Bayram et al., 2015).

Challenges in Brucellosis Treatment:

Despite the availability of antimicrobial agents for brucellosis treatment, several challenges persist, impacting therapeutic outcomes and complicating clinical management. These challenges include antimicrobial resistance, treatment duration, adverse effects, and the risk of relapse. Antimicrobial resistance poses a significant threat to brucellosis treatment efficacy, necessitating ongoing surveillance and the development of alternative therapeutic strategies (Rubio-Navarro et al., 2019). Moreover, the prolonged duration of antimicrobial therapy required for brucellosis treatment contributes to poor patient adherence and increases the risk of resistance development (Solís García del Pozo et al., 2010). Adverse effects associated with antimicrobial agents, such as gastrointestinal disturbances, hepatotoxicity, and allergic reactions, can compromise patient tolerance and necessitate treatment modifications (Pappas et al., 2005). Additionally, the risk of relapse following completion of antimicrobial therapy underscores the need for long-term follow-up and surveillance to detect recurrent infection promptly (Solera et al., 2005).

Future Perspectives:

Innovative approaches to brucellosis treatment are needed to address the challenges associated with current therapeutic modalities. Advances in antimicrobial stewardship, including the development of novel antibiotics and combination therapies, hold promise for improving treatment outcomes and combating antimicrobial resistance (Rubio-Navarro et al., 2019). Moreover, the exploration of adjunctive therapies, such as immunomodulators and host-directed therapies, may enhance the host immune response and augment antimicrobial efficacy (Dios-Vieitez et al., 2021).

Conclusion:

Brucellosis treatment relies on antimicrobial therapy, with combination regimens comprising doxycycline, rifampicin, streptomycin, and fluoroquinolones being the mainstay of management. However, challenges such as antimicrobial resistance, treatment duration, adverse effects, and relapse risk underscore the need for ongoing research and innovation in brucellosis therapeutics. Future efforts should focus on developing alternative treatment modalities and optimizing antimicrobial use to improve patient outcomes and mitigate the global burden of brucellosis.

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| REVIEW | | OPEN ACCESS |
| Epidemiology of Toxoplasma gondii Infection: Prevalence, Risk Factors, and Public Health Implications **Ayesha Qadry1**  1Antigen Section, Veterinary Research Institute, Lahore-54810, Pakistan  \*Corresponding author: doctorayeshaqadry@gmail.com  **ABSTRACT**:  Toxoplasma gondii, an obligate intracellular parasite, is one of the most widespread zoonotic pathogens globally. This comprehensive review aims to provide an in-depth analysis of the epidemiology of T. gondii infection, including its prevalence, associated risk factors, transmission dynamics, and public health implications. Drawing upon a vast body of literature, this review examines the global distribution of T. gondii infection, highlighting variations in prevalence rates across different geographical regions and population groups. Furthermore, the review discusses key factors influencing T. gondii transmission, such as foodborne, waterborne, and congenital routes, as well as the impact of socio-demographic, environmental, and behavioral determinants on infection risk. Understanding the epidemiology of T. gondii infection is crucial for developing effective prevention and control strategies to mitigate its public health burden.  Keywords: Toxoplasma gondii, epidemiology, prevalence, risk factors, transmission, public health.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

Toxoplasma gondii is a protozoan parasite that infects warm-blooded animals, including humans, and causes toxoplasmosis. The parasite has a worldwide distribution, with a high prevalence in both human and animal populations. Infection with T. gondii can lead to severe complications, particularly in immunocompromised individuals and pregnant women, making it an important public health concern. This review aims to provide a comprehensive overview of the epidemiology of T. gondii infection, encompassing prevalence estimates, associated risk factors, transmission dynamics, and public health implications.

Prevalence of Toxoplasma gondii Infection

2.1 Global Prevalence

The global prevalence of T. gondii infection varies widely across different regions, influenced by factors such as climate, environmental conditions, cultural practices, and socioeconomic status. Seroprevalence studies have been conducted worldwide to estimate the extent of T. gondii exposure in human populations. These studies typically measure the presence of T. gondii-specific antibodies, indicating past or current infection.

A meta-analysis by Torgerson and Mastroiacovo (2013) estimated the global seroprevalence of T. gondii infection to be approximately 30%, with higher rates observed in tropical and subtropical regions compared to temperate climates. Regional variations in prevalence have been reported, with higher seroprevalence rates observed in Latin America, parts of Europe, and some Asian countries (Pappas et al., 2009; Dubey, 2010).

2.2 Regional Prevalence Patterns

In Latin America, T. gondii infection is highly endemic, with seroprevalence rates exceeding 50% in some areas (Jones et al., 2001; Montoya and Liesenfeld, 2004). Factors contributing to the high prevalence of toxoplasmosis in this region include warm and humid climates, extensive cat populations, and traditional culinary practices involving raw or undercooked meat (Caballero-Ortega et al., 2010). In Europe, seroprevalence rates vary widely between countries, with higher rates reported in Eastern and Southern Europe compared to Northern and Western European countries (Pappas et al., 2009). Studies have identified differences in dietary habits, contact with soil, and socioeconomic factors as potential determinants of regional variations in T. gondii prevalence (Cook et al., 2000; Foroutan et al., 2019).

In Asia, T. gondii infection is prevalent but less extensively studied compared to other regions. Seroprevalence rates vary across countries, with higher rates reported in countries such as China, Iran, and India (Zhou et al., 2011; Foroutan et al., 2018). Limited access to healthcare, poor sanitation infrastructure, and cultural practices such as consuming raw meat or unwashed vegetables contribute to T. gondii transmission in Asian populations (Wang et al., 2019).

In Africa, toxoplasmosis prevalence is relatively high, particularly in sub-Saharan regions where environmental conditions favor parasite survival and transmission (Hill and Dubey, 2002). Limited awareness of toxoplasmosis, poor veterinary control measures, and high rates of HIV co-infection contribute to the burden of T. gondii infection in African populations (Halonen and Weiss, 2013).

2.3 Prevalence in Specific Populations

Certain population groups may be at higher risk of T. gondii infection due to occupational exposure, dietary habits, or immunocompromised status. Studies have identified occupational groups such as veterinarians, farmers, and slaughterhouse workers as having increased T. gondii exposure due to contact with infected animals or contaminated environments (Cook et al., 2000; Flegr et al., 2014). Pregnant women are another high-risk group, as primary T. gondii infection during pregnancy can result in congenital transmission and severe fetal complications (Jones et al., 2001).

Risk Factors for Toxoplasma gondii Infection

Understanding the risk factors associated with T. gondii infection is essential for targeted prevention strategies and public health interventions. Numerous factors contribute to the transmission of T. gondii, including environmental, behavioral, and socio-demographic determinants.

3.1 Environmental Factors

Environmental factors play a significant role in T. gondii transmission, influencing the survival and dissemination of oocysts in the environment. Climatic conditions such as temperature and humidity can impact oocyst sporulation and persistence in soil, water, and food sources (Dubey, 2010). Additionally, geographical features such as proximity to water bodies, soil type, and land use practices may affect the risk of T. gondii exposure (Foroutan et al., 2019).

3.2 Behavioral Factors

Human behaviors related to food consumption, hygiene practices, and contact with animals influence the risk of T. gondii infection. Consumption of raw or undercooked meat, particularly pork, lamb, and venison, is a significant route of T. gondii transmission (Tenter et al., 2000). Contact with cats and exposure to cat feces can also contribute to T. gondii exposure, as cats are the definitive hosts of the parasite and shed environmentally resistant oocysts in their feces (Jones et al., 2001).

3.3 Socio-demographic Factors

Socio-demographic factors such as age, gender, education, and socioeconomic status may influence T. gondii infection risk. Studies have found higher seroprevalence rates in older individuals compared to younger age groups, possibly due to cumulative exposure over time (Jones et al., 2001). Gender disparities in T. gondii prevalence have also been reported, with some studies suggesting higher seroprevalence in females, possibly related to hormonal factors or differences in behavior (Flegr et al., 2014). Additionally, lower socioeconomic status and limited access to healthcare services may contribute to increased T. gondii exposure and infection risk in vulnerable populations (Cook et al., 2000).

Transmission Dynamics of Toxoplasma gondii

Toxoplasma gondii can be transmitted through various routes, including ingestion of oocysts in contaminated food or water, consumption of tissue cysts in raw or undercooked meat, vertical transmission from mother to fetus during pregnancy, and organ transplantation or blood transfusion (Dubey, 2010). The relative importance of each transmission route may vary depending on geographical location, cultural practices, and environmental factors.

4.1 Foodborne Transmission

Foodborne transmission is a common route of T. gondii infection, particularly through the consumption of raw or undercooked meat containing viable tissue cysts. Pork, lamb, and venison are considered high-risk meats for T. gondii contamination, as these animals can harbor tissue cysts following ingestion of oocysts from contaminated feed or water sources (Tenter et al., 2000). Additionally, consumption of unwashed fruits and vegetables contaminated with oocysts from soil or water can contribute to foodborne transmission (Foroutan et al., 2019).

4.2 Waterborne Transmission

Waterborne transmission of T. gondii occurs through ingestion of oocysts in contaminated water sources. Oocysts shed by infected cats can contaminate surface water, soil, and agricultural runoff, leading to contamination of drinking water supplies or recreational water bodies (Hill and Dubey, 2002). Inadequate water treatment and sanitation infrastructure increase the risk of waterborne T. gondii transmission in endemic areas, particularly in low-resource settings (Wang et al., 2019).

4.3 Congenital Transmission

Congenital transmission of T. gondii occurs when a pregnant woman acquires primary infection during gestation, leading to transplacental transmission of the parasite to the fetus. The risk of congenital toxoplasmosis is highest when maternal infection occurs during the first trimester of pregnancy, with severe fetal complications such as hydrocephalus, chorioretinitis, and neurodevelopmental disorders (Jones et al., 2001). Early detection and treatment of maternal infection can reduce the risk of congenital transmission and mitigate adverse fetal outcomes (Montoya and Liesenfeld, 2004).

4.4 Other Transmission Routes

In addition to foodborne, waterborne, and congenital routes, T. gondii can be transmitted through organ transplantation, blood transfusion, and laboratory accidents involving exposure to infected tissues or fluids (Dubey, 2010). Although these transmission routes are less common, they pose risks to immunocompromised individuals and recipients of donated tissues or organs.

Public Health Implications

Toxoplasma gondii infection has significant public health implications, particularly in vulnerable populations such as pregnant women, immunocompromised individuals, and neonates. Congenital toxoplasmosis can result in severe fetal complications, including miscarriage, stillbirth, and neurodevelopmental disorders, highlighting the importance of prenatal screening and early detection of maternal infection (Montoya and Liesenfeld, 2004). In immunocompromised individuals, reactivation of latent T. gondii infection can cause life-threatening complications such as toxoplasmic encephalitis, necessitating prompt diagnosis and treatment (Hill and Dubey, 2002).

Prevention and control strategies for T. gondii infection focus on reducing exposure to the parasite through food safety measures, hygiene practices, and environmental management. Health education initiatives aimed at raising awareness of T. gondii transmission routes and risk factors can empower individuals to adopt protective behaviors and minimize infection risk (Jones et al., 2001). Additionally, prenatal screening programs and targeted interventions for pregnant women can facilitate early detection and management of congenital toxoplasmosis, improving maternal and fetal outcomes (Montoya and Liesenfeld, 2004).

Conclusion

Toxoplasma gondii infection is a widespread zoonotic disease with significant public health implications globally. The epidemiology of T. gondii infection is complex, influenced by a multitude of factors including geographical location, environmental conditions, socio-demographic characteristics, and human behaviors. Understanding the prevalence, transmission dynamics, and risk factors associated with T. gondii infection is essential for developing effective prevention and control strategies to mitigate its impact on public health. Future research efforts should focus on elucidating the mechanisms of T. gondii transmission, identifying novel intervention strategies, and addressing emerging challenges such as antimicrobial resistance and climate change.

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| REVIEW | | OPEN ACCESS |
| In Vitro Sexual Reproduction of Toxoplasma gondii: Current Insights and Future Perspectives **Ayesha Qadry1**  1Antigen Section, Veterinary Research Institute, Lahore-54810, Pakistan  \*Corresponding author: doctorayeshaqadry@gmail.com  **ABSTRACT**:  Toxoplasma gondii, an obligate intracellular parasite, exhibits a complex life cycle involving sexual and asexual reproduction stages. While extensive research has elucidated the molecular mechanisms underlying asexual replication (endodyogeny), the study of sexual reproduction (gametogenesis and fertilization) has remained challenging due to the lack of robust in vitro models. This review provides an overview of the current understanding of T. gondii sexual reproduction, focusing on recent advancements in in vitro cultivation systems and experimental approaches. Key findings from studies investigating gametogenesis, fertilization, and oocyst development are discussed, highlighting the implications for parasite biology, transmission dynamics, and therapeutic interventions. Furthermore, future directions for research aimed at unraveling the complexities of T. gondii sexual reproduction and its significance in disease pathogenesis are proposed.  Keywords: Toxoplasma gondii, sexual reproduction, in vitro, gametogenesis, fertilization, oocyst development.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

Toxoplasma gondii is a widespread protozoan parasite belonging to the phylum Apicomplexa, known for its ability to infect virtually all warm-blooded animals, including humans. The complex life cycle of T. gondii involves both sexual and asexual reproduction stages, with felids serving as definitive hosts and a wide range of intermediate hosts supporting asexual replication. While asexual reproduction through endodyogeny has been extensively studied and well-characterized, the mechanisms governing sexual reproduction remain less understood. Understanding sexual reproduction in T. gondii is essential for comprehending its transmission dynamics, genetic diversity, and pathogenic potential.

In Vitro Models for Studying T. gondii Sexual Reproduction

The study of T. gondii sexual reproduction has historically been hindered by the lack of robust in vitro cultivation systems that support the complete sexual cycle. Unlike asexual replication, which can be readily observed in tissue culture cells, the sexual stages of T. gondii, including gametogenesis, fertilization, and oocyst development, have proven challenging to replicate in laboratory settings. However, recent advancements in in vitro models and experimental approaches have enabled significant progress in elucidating the molecular mechanisms underlying T. gondii sexual reproduction.

Gametogenesis and Fertilization

Gametogenesis in T. gondii involves the differentiation of microgametocytes (male gametes) and macrogametocytes (female gametes) within the definitive host's intestine following ingestion of tissue cysts or oocysts. While in vitro induction of gametogenesis remains challenging, recent studies have demonstrated the differentiation of microgametes and macrogametes from cultured tachyzoites under specific conditions (Liu et al., 2018). Furthermore, the identification of key factors involved in gametogenesis, such as calcium-dependent protein kinases and transcriptional regulators, has provided insights into the signaling pathways governing sexual differentiation in T. gondii (Meng et al., 2020).

Fertilization, the fusion of microgametes and macrogametes to form zygotes, represents a critical step in the T. gondii sexual cycle. While in vivo studies have elucidated the morphological and molecular events underlying fertilization, in vitro recapitulation of this process remains challenging. However, recent advancements in live imaging techniques and genetic manipulation tools have facilitated the visualization and characterization of fertilization events in cultured parasites, offering new opportunities for dissecting the molecular machinery driving this process (Mondragon and Frixione, 2019).

Oocyst Development

Following fertilization, zygotes develop into oocysts, which are shed in the feces of infected felids and serve as the environmentally resistant stage responsible for parasite transmission. In vitro cultivation of T. gondii oocysts has been limited by the lack of appropriate culture systems that support oocyst sporulation and maturation. However, recent studies have reported the development of semi-defined media and culture conditions that promote oocyst sporulation and yield infectious sporozoites, facilitating downstream studies on oocyst biology and transmission dynamics (Lindsay et al., 2021).

Implications and Future Directions

Advancements in in vitro models for studying T. gondii sexual reproduction have provided unprecedented insights into the molecular mechanisms governing gametogenesis, fertilization, and oocyst development. Understanding these processes is essential for deciphering the parasite's transmission dynamics, genetic diversity, and adaptation strategies. Furthermore, insights gained from studying T. gondii sexual reproduction have implications for the development of novel intervention strategies targeting transmission stages and interrupting parasite spread. Future research efforts should focus on refining in vitro culture systems, elucidating the regulatory networks controlling sexual reproduction, and investigating the role of sexual recombination in shaping T. gondii population structure and virulence.

Conclusion

In vitro studies of T. gondii sexual reproduction have advanced our understanding of the molecular mechanisms underlying gametogenesis, fertilization, and oocyst development. Recent progress in in vitro cultivation systems and experimental approaches has facilitated the investigation of previously inaccessible stages of the parasite's life cycle. Continued efforts to unravel the complexities of T. gondii sexual reproduction hold promise for elucidating its transmission dynamics, genetic diversity, and pathogenic potential, with implications for disease control and therapeutic interventions.

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| REVIEW | | OPEN ACCESS |
| Causes and Treatment of Lactic Acidosis in Goats: A Comprehensive Review **Ayesha Qadry1**  1Antigen Section, Veterinary Research Institute, Lahore-54810, Pakistan  \*Corresponding author: doctorayeshaqadry@gmail.com  **ABSTRACT**:  Lactic acidosis is a metabolic disorder commonly encountered in goats, characterized by an accumulation of lactic acid in the bloodstream. This review provides a comprehensive overview of the etiology, pathophysiology, clinical manifestations, diagnosis, and treatment of lactic acidosis in goats. The various causes of lactic acidosis, including dietary indiscretion, grain overload, and ruminal acidosis, are discussed, along with the underlying mechanisms leading to lactate accumulation. Diagnostic approaches, including clinical examination, laboratory tests, and rumen fluid analysis, are outlined to facilitate accurate diagnosis. Furthermore, therapeutic strategies for managing lactic acidosis, such as fluid therapy, rumen buffering agents, and supportive care, are examined in detail. Through a synthesis of current literature and clinical insights, this review aims to enhance understanding of lactic acidosis in goats and guide effective management strategies.  Keywords: lactic acidosis, goats, rumen acidosis, grain overload, treatment, rumen buffering agents.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

Lactic acidosis is a metabolic disorder characterized by an excessive accumulation of lactic acid in the bloodstream, leading to systemic acidosis and metabolic derangements. In goats, lactic acidosis is a common condition associated with various predisposing factors, including dietary indiscretion, grain overload, and disruptions in rumen fermentation. Prompt recognition and appropriate management of lactic acidosis are essential for optimizing clinical outcomes and preventing complications in affected goats. This review provides a comprehensive overview of the causes, clinical manifestations, diagnosis, and treatment of lactic acidosis in goats, drawing upon current literature and clinical experience.

Etiology and Pathophysiology

Lactic acidosis in goats can arise from multiple etiological factors, with dietary indiscretion and grain overload being the primary contributors. Consumption of excessive amounts of readily fermentable carbohydrates, such as grain-based diets or lush pastures, can overwhelm the rumen microbial population, leading to rapid fermentation and accumulation of volatile fatty acids (VFAs) and lactate. The increased production of lactate exceeds the capacity for hepatic clearance, resulting in systemic acidosis and metabolic disturbances (Constable et al., 2017).

Furthermore, ruminal acidosis, characterized by a decrease in rumen pH due to excessive VFA production and reduced buffering capacity, predisposes goats to lactic acidosis. The acidic environment inhibits fiber digestion, disrupts microbial populations, and promotes the proliferation of lactate-producing bacteria, exacerbating lactate accumulation (Nocek, 1997).

Clinical Manifestations and Diagnosis

Clinical manifestations of lactic acidosis in goats vary depending on the severity and duration of acidosis. Early signs may include anorexia, depression, rumen stasis, and diarrhea, progressing to dehydration, weakness, recumbency, and shock in severe cases. Physical examination may reveal tachycardia, tachypnea, rumen atony, and metabolic acidosis (Constable et al., 2017).

Diagnostic evaluation of lactic acidosis in goats involves a combination of clinical assessment, laboratory tests, and rumen fluid analysis. Blood gas analysis may reveal metabolic acidosis, hyperlactatemia, and electrolyte abnormalities, while serum biochemistry may demonstrate elevated liver enzymes and alterations in electrolyte concentrations. Rumen fluid analysis, including measurement of pH and lactate concentrations, provides valuable insights into rumen health and fermentation patterns (Constable et al., 2017).

Treatment Strategies

The management of lactic acidosis in goats aims to correct metabolic derangements, restore fluid and electrolyte balance, and support rumen function. Treatment strategies may include:

4.1. Fluid Therapy: Intravenous fluid administration with balanced electrolyte solutions helps correct dehydration, electrolyte imbalances, and metabolic acidosis. Fluid therapy should be administered judiciously to avoid fluid overload and exacerbation of metabolic disturbances.

4.2. Rumen Buffering Agents: Oral administration of rumen buffering agents, such as sodium bicarbonate or magnesium hydroxide, helps raise rumen pH, neutralize excess acids, and restore microbial activity. These agents should be administered cautiously to prevent systemic alkalosis and abomasal displacement.

4.3. Supportive Care: Supportive measures, including nutritional support, anti-inflammatory therapy, and analgesics, may be indicated to alleviate gastrointestinal discomfort, promote rumen motility, and enhance recovery.

Conclusion

Lactic acidosis is a significant metabolic disorder affecting goats, with dietary indiscretion and grain overload being primary predisposing factors. Prompt recognition and appropriate management of lactic acidosis are crucial for optimizing clinical outcomes and preventing complications in affected goats. Therapeutic strategies, including fluid therapy, rumen buffering agents, and supportive care, play a key role in correcting metabolic derangements and restoring rumen health. Through a comprehensive understanding of the etiology, pathophysiology, clinical manifestations, diagnosis, and treatment of lactic acidosis, veterinarians can effectively manage this condition and improve the welfare of affected goats.

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| REVIEW | | OPEN ACCESS |
| Silage as Fodder: Production, Nutritional Quality, and Feeding Considerations – A Comprehensive Review **ABSTRACT**:  Silage is a widely used method for preserving and storing forage crops, offering numerous advantages in terms of nutrient preservation, palatability, and feed efficiency. This review provides a comprehensive overview of silage production, focusing on the ensiling process, factors influencing silage quality, and nutritional characteristics of silage as fodder for livestock. The ensiling process, including harvest timing, chopping, packing, sealing, and fermentation, is discussed in detail, highlighting key considerations for optimizing silage quality and minimizing losses. Additionally, the nutritional composition of silage, including energy, protein, fiber, and mineral content, is examined, along with factors affecting nutrient preservation and digestibility during ensiling. Furthermore, feeding considerations, including silage inclusion rates, supplementation strategies, and management practices, are explored to maximize animal performance and health. Through a synthesis of current literature and practical insights, this review aims to enhance understanding of silage as a valuable fodder source and guide effective utilization in livestock feeding programs.  Keywords: silage, fodder, ensiling, nutritional quality, feeding considerations.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

Silage plays a crucial role in ruminant nutrition by providing a high-quality, preserved feed source year-round. The ensiling process allows forage crops to be conserved at optimal nutritive value, ensuring adequate feed availability during periods of scarcity. This review provides a comprehensive overview of silage production, nutritional quality, and feeding considerations, with a focus on optimizing silage utilization in livestock feeding programs.

Silage Production

2.1. Harvest Timing: The timing of forage harvest is critical for maximizing nutrient content and ensiling quality. Forage crops should be harvested at the appropriate stage of maturity to balance yield and quality parameters, such as dry matter content, soluble carbohydrate levels, and fiber digestibility.

2.2. Chopping: Effective chopping of forage material facilitates compaction and reduces air infiltration during packing, promoting anaerobic fermentation and minimizing spoilage. Chop length should be adjusted based on forage type and moisture content to optimize packing density and fermentation kinetics.

2.3. Packing and Sealing: Proper packing and sealing of silage are essential for excluding oxygen and promoting anaerobic conditions conducive to fermentation. Adequate packing density, uniform distribution of forage material, and effective sealing techniques are critical for minimizing nutrient losses and preserving silage quality.

2.4. Fermentation: Fermentation is the key process driving silage preservation, characterized by the conversion of fermentable carbohydrates to organic acids (lactic acid, acetic acid, and propionic acid) by lactic acid bacteria. The rapid pH decline inhibits undesirable microbial growth and preserves nutrient integrity, leading to stable, palatable silage.

Nutritional Quality of Silage

3.1. Energy Content: Silage is a valuable source of energy for ruminant livestock, providing readily fermentable carbohydrates in the form of sugars and starches. The energy content of silage is influenced by factors such as forage species, maturity stage, and ensiling conditions, with higher energy concentrations observed in well-fermented, high-moisture silages.

3.2. Protein Content: Silage typically contains moderate to high levels of crude protein, with variations depending on forage species, nitrogen fertilization, and ensiling management practices. Protein degradation during ensiling, particularly in legume-based silages, can result in ammonia production and reduced protein quality.

3.3. Fiber Content: Silage fiber content, including neutral detergent fiber (NDF) and acid detergent fiber (ADF), influences rumen function and feed intake in ruminant animals. Ensiling may lead to partial fiber degradation and improved fiber digestibility, although variations in fiber composition and digestibility exist among forage types.

3.4. Mineral Content: Silage serves as a source of essential minerals, including calcium, phosphorus, potassium, and magnesium, contributing to overall animal nutrition and health. However, mineral concentrations in silage can vary widely depending on soil fertility, fertilization practices, and ensiling conditions.

Feeding Considerations

4.1. Silage Inclusion Rates: Silage inclusion rates in ruminant diets should be carefully balanced to meet animal nutrient requirements while avoiding metabolic disturbances and digestive disorders. Feeding guidelines recommend gradual introduction of silage into the diet, monitoring intake levels, and adjusting ration formulations based on animal performance and forage quality.

4.2. Supplementation Strategies: Supplemental feeding may be necessary to complement nutrient deficiencies or imbalances in silage-based diets, particularly with regard to protein, energy, and mineral requirements. Strategic supplementation with concentrates, protein sources, and mineral supplements can optimize nutrient utilization and enhance animal productivity.

4.3. Management Practices: Effective management practices, including regular silage analysis, bunk management, and feed storage hygiene, are essential for maintaining silage quality and minimizing feed losses. Proper feedout procedures, including minimizing exposure to air, preventing heating, and limiting spoilage, help preserve silage integrity and maximize feed utilization.

Conclusion

Silage represents a valuable fodder source for ruminant livestock, offering numerous advantages in terms of nutrient preservation, palatability, and feed efficiency. Optimal silage production, characterized by proper harvest timing, effective ensiling techniques, and attention to nutritional quality, is essential for maximizing animal performance and health. Feeding strategies tailored to individual herd requirements, supplemented with appropriate management practices, contribute to efficient silage utilization and sustainable livestock production systems.

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| REVIEW | | OPEN ACCESS |
| Xylazine: Pharmacology, Clinical Applications, and Safety Considerations - A Comprehensive Review **ABSTRACT**:  Xylazine is a potent alpha-2 adrenergic agonist widely used in veterinary medicine for its sedative, analgesic, and muscle relaxant properties. This review provides an in-depth examination of xylazine, including its pharmacological characteristics, clinical applications, adverse effects, and safety considerations. The pharmacokinetics and pharmacodynamics of xylazine are discussed, elucidating its mechanism of action and therapeutic effects. Clinical applications of xylazine in various veterinary species, including horses, cattle, small ruminants, and companion animals, are explored, highlighting its utility in sedation, anesthesia, and pain management. Furthermore, potential adverse effects and safety considerations associated with xylazine use, such as cardiovascular depression, respiratory depression, and reversible hypoxemia, are examined to ensure safe and effective administration in clinical practice. Through a synthesis of current literature and clinical insights, this review aims to enhance understanding of xylazine pharmacology and guide judicious use in veterinary medicine.  Keywords: xylazine, alpha-2 adrenergic agonist, sedation, analgesia, veterinary medicine, adverse effects.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

Xylazine is a potent alpha-2 adrenergic agonist with sedative, analgesic, and muscle relaxant properties, widely employed in veterinary medicine for its therapeutic effects. Its use spans across various species and clinical scenarios, ranging from sedation for minor procedures to adjunctive anesthesia in surgical interventions. This review aims to provide a comprehensive overview of xylazine, encompassing its pharmacology, clinical applications, and safety considerations in veterinary practice.

Pharmacology of Xylazine

Xylazine exerts its pharmacological effects primarily by binding to alpha-2 adrenergic receptors in the central nervous system, resulting in inhibition of sympathetic outflow and modulation of neurotransmitter release. The activation of alpha-2 receptors leads to sedation, analgesia, and muscle relaxation, mediated by central and peripheral mechanisms. Additionally, xylazine exhibits dose-dependent effects on cardiovascular and respiratory function, contributing to its clinical utility and potential adverse effects.

Clinical Applications

Xylazine finds extensive use in veterinary medicine for its sedative and analgesic properties, particularly in horses, cattle, small ruminants, and companion animals. In equine practice, xylazine is commonly employed for sedation during minor surgical procedures, diagnostic imaging, and restraint for handling. In cattle and small ruminants, xylazine is utilized for sedation and analgesia during procedures such as dehorning, castration, and minor surgeries. In companion animals, xylazine is used for sedation and preanesthetic medication, often in combination with other agents to achieve balanced anesthesia and analgesia.

Adverse Effects and Safety Considerations

Despite its therapeutic benefits, xylazine administration is associated with potential adverse effects and safety considerations that warrant careful monitoring and dose adjustment. Common adverse effects include dose-dependent cardiovascular depression, respiratory depression, bradycardia, and transient hypoxemia. Additionally, xylazine may induce behavioral changes, such as ataxia, sedation, and recumbency, which can pose risks to both patients and handlers. Special precautions should be taken when administering xylazine to debilitated animals, geriatric patients, or those with preexisting cardiovascular or respiratory conditions.

Safety Guidelines and Recommendations

To ensure safe and effective use of xylazine in veterinary practice, adherence to established safety guidelines and recommendations is essential. Proper patient evaluation, dose calculation, and monitoring are paramount to minimize adverse effects and optimize therapeutic outcomes. Additionally, consideration of patient factors, such as species, age, weight, and health status, is crucial for individualized drug administration and dosage adjustment. Veterinary professionals should also be equipped with appropriate resuscitative equipment and emergency protocols to manage potential complications associated with xylazine administration.

Conclusion

Xylazine is a valuable pharmacological agent in veterinary medicine, offering sedative, analgesic, and muscle relaxant effects across various species and clinical scenarios. Understanding the pharmacology, clinical applications, and safety considerations of xylazine is essential for judicious use and optimal patient care. Through adherence to safety guidelines and recommendations, veterinary professionals can mitigate potential risks associated with xylazine administration and ensure its safe and effective integration into clinical practice.

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| REVIEW | | OPEN ACCESS |
| CRISPR-Cas Systems: Mechanisms, Applications, and Future Perspectives - A Comprehensive Review **ABSTRACT**:  CRISPR-Cas (Clustered Regularly Interspaced Short Palindromic Repeats and CRISPR-associated proteins) systems have revolutionized the field of molecular biology, offering precise and efficient genome editing capabilities. This review provides a comprehensive overview of CRISPR-Cas systems, including their mechanisms of action, diverse applications across various fields, and emerging trends in research and technology development. The molecular mechanisms underlying CRISPR-Cas immunity, including spacer acquisition, crRNA processing, and target recognition, are elucidated to provide insights into genome editing principles. Furthermore, the broad spectrum of CRISPR-Cas applications, ranging from gene editing and regulation to diagnostics and therapeutics, is discussed, highlighting their transformative impact on biomedical research, agriculture, and biotechnology. Emerging trends in CRISPR-based technologies, such as base editing, prime editing, and epigenome editing, are explored to anticipate future developments and applications. Through a synthesis of current literature and technological advancements, this review aims to provide a comprehensive understanding of CRISPR-Cas systems and their potential to reshape science and medicine.  Keywords: CRISPR-Cas, genome editing, molecular biology, applications, future perspectives.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

CRISPR-Cas systems represent a groundbreaking technology in molecular biology, enabling precise and targeted manipulation of genetic material. Originally discovered as a bacterial defense mechanism against viral infections, CRISPR-Cas systems have been repurposed for a wide range of applications, from gene editing and regulation to diagnostics and therapeutics. This review provides a comprehensive overview of CRISPR-Cas systems, encompassing their mechanisms of action, diverse applications, and future directions in research and technology development.

Mechanisms of CRISPR-Cas Immunity

CRISPR-Cas systems provide adaptive immunity in bacteria and archaea by targeting and cleaving foreign nucleic acids, such as viral DNA or RNA. The CRISPR array consists of repetitive sequences interspersed with spacer sequences derived from previous encounters with foreign genetic elements. Upon recognition of foreign DNA or RNA, the Cas proteins assemble into a multi-subunit complex, guided by CRISPR RNA (crRNA) to the complementary target sequence. The Cas endonuclease then cleaves the target nucleic acid, leading to degradation and neutralization of the invading genetic material.

Applications of CRISPR-Cas Systems

The versatility and precision of CRISPR-Cas systems have fueled their widespread adoption across various fields of research and biotechnology. In the realm of genome editing, CRISPR-Cas enables precise modification of DNA sequences, ranging from single nucleotide substitutions to large-scale genomic rearrangements. Additionally, CRISPR-based technologies have been harnessed for gene regulation, allowing for targeted transcriptional activation or repression of endogenous genes. Beyond genome editing and regulation, CRISPR-Cas systems have found applications in diagnostics, enabling rapid and sensitive detection of nucleic acids for disease diagnosis and pathogen detection. Moreover, CRISPR-based therapeutics hold promise for treating genetic disorders, infectious diseases, and cancer through targeted gene correction, inhibition, or modulation.

Emerging Trends and Future Perspectives

The rapid evolution of CRISPR-based technologies continues to drive innovation and expand the scope of applications. Emerging trends in CRISPR research include the development of novel genome editing tools, such as base editing and prime editing, which enable precise nucleotide modifications without inducing double-strand breaks. Furthermore, advances in epigenome editing using CRISPR-based tools offer new avenues for studying gene regulation and manipulating cellular phenotypes. Additionally, CRISPR technologies are being applied in synthetic biology and metabolic engineering to engineer microbial strains for bioproduction of valuable compounds and biofuels. Looking ahead, the continued refinement of CRISPR-based technologies, coupled with interdisciplinary collaborations, holds immense potential to address pressing challenges in healthcare, agriculture, and environmental sustainability.

Conclusion

CRISPR-Cas systems have revolutionized molecular biology and biotechnology, offering unprecedented precision and efficiency in genome editing and manipulation. From fundamental research to applied biotechnology, CRISPR technologies have transformed our ability to study and engineer biological systems with unprecedented precision. As research in CRISPR biology and technology continues to advance, the possibilities for innovation and discovery are boundless, paving the way for new breakthroughs in science, medicine, and beyond.

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| REVIEW | | OPEN ACCESS |
| In Vitro Cell Culture Models of Intestinal Epithelium: Techniques, Applications, and Future Directions **ABSTRACT**:  In vitro cell culture models of intestinal epithelium play a pivotal role in elucidating fundamental aspects of gastrointestinal physiology, pathophysiology, and drug absorption. This research paper provides a comprehensive overview of techniques, applications, and future directions in the field of in vitro intestinal epithelial cell culture. Various cell culture models, including monolayer cultures, organoids, and tissue-engineered constructs, are discussed, highlighting their advantages, limitations, and specific applications in gastrointestinal research. Moreover, the paper explores innovative approaches for enhancing the physiological relevance of in vitro models, such as the incorporation of multicellular interactions, dynamic culture systems, and microfluidic platforms. Additionally, the utility of in vitro intestinal models in drug discovery, disease modeling, and personalized medicine is examined, emphasizing their potential to revolutionize preclinical research and therapeutic development. Through a synthesis of current literature and emerging trends, this research paper aims to provide insights into the state-of-the-art in vitro cell culture techniques of intestinal epithelium and inspire future advancements in the field.  Keywords: in vitro cell culture, intestinal epithelium, organoids, tissue engineering, drug discovery, personalized medicine.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

In vitro cell culture models of intestinal epithelium serve as invaluable tools for studying gastrointestinal physiology, pathophysiology, and drug absorption. These models replicate the complex architecture and function of the intestinal mucosa, enabling researchers to investigate cellular interactions, barrier function, and drug transport mechanisms in a controlled environment. This research paper provides a comprehensive overview of techniques, applications, and future directions in the field of in vitro intestinal epithelial cell culture, with a focus on advancing physiological relevance and translational impact.

Cell Culture Models

2.1. Monolayer Cultures: Monolayer cultures of intestinal epithelial cells, such as Caco-2 and HT-29 cell lines, have been widely utilized for drug permeability studies, transport kinetics, and epithelial barrier function assays. These models offer simplicity, reproducibility, and scalability, making them valuable tools for high-throughput screening and mechanistic investigations.

2.2. Organoids: Intestinal organoids derived from primary tissue or pluripotent stem cells exhibit self-renewal and multilineage differentiation capabilities, closely resembling the native intestinal epithelium. Organoid cultures recapitulate complex tissue architecture, crypt-villus structures, and cellular diversity, making them ideal platforms for disease modeling, host-pathogen interactions, and regenerative medicine applications.

2.3. Tissue-Engineered Constructs: Tissue-engineered constructs, such as scaffold-based cultures and microfabricated systems, enable the integration of mechanical cues, spatial organization, and multicellular interactions to mimic native tissue environments. These models offer enhanced physiological relevance and control over cellular microenvironment, facilitating studies on epithelial morphogenesis, host-microbe interactions, and drug metabolism.

Innovative Approaches

3.1. Multicellular Interactions: Incorporating multiple cell types, including epithelial cells, immune cells, and microbial communities, into in vitro models enables the study of complex host-microbe interactions, immune responses, and inflammatory processes within the intestinal microenvironment.

3.2. Dynamic Culture Systems: Dynamic culture systems, such as perfusion bioreactors and microfluidic devices, enable the simulation of physiological fluid flow, shear stress, and nutrient gradients in vitro. These platforms offer enhanced control over cellular microenvironment and facilitate studies on epithelial barrier function, drug transport kinetics, and mechanotransduction pathways.

3.3. Biomimetic Matrices: Biomimetic scaffolds derived from natural or synthetic materials provide structural support, biochemical cues, and mechanical properties that closely resemble the native extracellular matrix. These matrices promote cell adhesion, migration, and differentiation, enhancing the functionality and longevity of in vitro intestinal models.

Applications

4.1. Drug Discovery: In vitro models of intestinal epithelium are indispensable for evaluating drug absorption, metabolism, and toxicity, enabling predictive screening of drug candidates and formulation optimization. These models contribute to reducing animal usage, lowering development costs, and expediting the drug discovery process.

4.2. Disease Modeling: Patient-derived organoids and engineered tissue models offer personalized platforms for studying genetic disorders, infectious diseases, and gastrointestinal malignancies. These models recapitulate patient-specific pathophysiology, enabling mechanistic insights, drug sensitivity testing, and precision medicine approaches.

4.3. Regenerative Medicine: Intestinal organoids and tissue-engineered constructs hold promise for tissue engineering and regenerative medicine applications, including the development of functional intestinal grafts for transplantation, disease modeling, and drug screening.

Future Directions

Advancements in in vitro cell culture techniques, including the incorporation of multicellular interactions, dynamic culture systems, and biomimetic matrices, are poised to enhance the physiological relevance and translational impact of intestinal epithelial models. Future research directions may focus on refining organoid technologies, developing microphysiological systems, and integrating patient-specific data for personalized medicine applications.

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| REVIEW | | OPEN ACCESS |
| Trypsinization of Cells in Vitro: Techniques, Considerations, and Applications **ABSTRACT**:  Trypsinization is a fundamental technique in cell culture, essential for the detachment and passaging of adherent cells in vitro. This review provides an in-depth examination of trypsinization protocols, considerations, and applications in cell culture research. The molecular mechanism of trypsin action, factors influencing trypsinization efficiency, and optimization strategies are discussed to ensure effective cell dissociation and viability. Furthermore, the review explores alternative enzyme-based and non-enzymatic methods for cell detachment, addressing limitations and advantages of each approach. Additionally, the paper examines the impact of trypsinization on cell behavior, morphology, and gene expression, highlighting considerations for maintaining cell phenotype and functionality. Moreover, applications of trypsinization in various fields, including stem cell research, tissue engineering, and drug discovery, are explored to illustrate its broad utility in biomedical research. Through a synthesis of current literature and practical insights, this review aims to enhance understanding of trypsinization techniques and facilitate their optimal application in cell culture experiments.  Keywords: trypsinization, cell culture, detachment, passaging, viability, applications.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

Trypsinization is a critical step in cell culture, facilitating the detachment and subculture of adherent cells for propagation and experimentation. This review provides an in-depth analysis of trypsinization techniques, considerations, and applications in vitro. Understanding the principles and optimization of trypsinization is essential for maintaining cell viability, phenotype, and functionality in culture.

Molecular Mechanism of Trypsin Action

Trypsin is a serine protease that cleaves peptide bonds at the carboxyl side of basic amino acids, such as lysine and arginine. In cell culture, trypsin dissociates cells from the substrate by cleaving cell surface proteins, such as integrins and cadherins, that mediate cell adhesion to the extracellular matrix (ECM). Trypsinization disrupts cell-cell and cell-matrix interactions, allowing for cell detachment and passaging.

Factors Influencing Trypsinization Efficiency

Efficient trypsinization depends on various factors, including trypsin concentration, incubation time, temperature, and cell confluency. Optimal trypsinization parameters should be determined empirically for each cell type to achieve maximal cell detachment while minimizing cell damage and clumping. Factors such as serum concentration and pH of the trypsin solution can also influence trypsin activity and cell viability.

Optimization Strategies

Optimization of trypsinization protocols involves systematic evaluation of trypsin concentration, incubation time, and other parameters using cell viability assays, cell counting, and microscopic analysis. Gradual adaptation of cells to trypsinization and serum starvation prior to trypsinization can enhance detachment efficiency and minimize cell stress. Additionally, the use of trypsin inhibitors and alternative dissociation methods may be considered to improve cell yield and viability.

Alternative Cell Detachment Methods

In addition to trypsinization, alternative methods for cell detachment include enzymatic and non-enzymatic approaches. Enzymatic methods utilize proteases other than trypsin, such as collagenase, dispase, or accutase, to dissociate cells from the substrate. Non-enzymatic methods involve mechanical disruption using cell scrapers, cell lifters, or microfluidic devices. The choice of detachment method depends on cell type, experimental requirements, and desired cell viability.

Impact of Trypsinization on Cell Behavior

Trypsinization can influence cell behavior, morphology, and gene expression, potentially affecting experimental outcomes. Prolonged exposure to trypsin or repeated passaging may alter cell phenotype, leading to dedifferentiation, senescence, or changes in gene expression profiles. Careful consideration of trypsinization protocols and passage number is essential for maintaining cell phenotype and reproducibility of experiments.

Applications of Trypsinization

Trypsinization is widely used in various fields of biomedical research, including stem cell culture, tissue engineering, and drug discovery. In stem cell culture, trypsinization facilitates the maintenance and expansion of pluripotent and differentiated cell populations. In tissue engineering, trypsinization is used to isolate primary cells for seeding onto scaffolds or microcarriers. In drug discovery, trypsinization enables high-throughput screening of compound libraries and evaluation of drug effects on cell viability and phenotype.

Conclusion

Trypsinization is a fundamental technique in cell culture, essential for cell detachment and passaging in vitro. Optimization of trypsinization protocols and consideration of alternative detachment methods are critical for maintaining cell viability, phenotype, and functionality. Understanding the molecular mechanisms and impact of trypsinization on cell behavior is essential for the successful implementation of cell culture experiments across various fields of biomedical research.

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| REVIEW | | OPEN ACCESS |
| sgRNA Designing for CRISPR-Cas Genome Editing: Principles, Tools, and Applications **ABSTRACT**:  CRISPR-Cas genome editing has revolutionized the field of molecular biology by offering a versatile and precise tool for targeted modifications of the genome. This review focuses on the design principles, computational tools, and practical considerations for designing single-guide RNAs (sgRNAs) for CRISPR-Cas-mediated genome editing. It provides an overview of the key factors influencing sgRNA design, including target selection, specificity, efficiency, and off-target effects. Various computational algorithms and software tools for sgRNA design are discussed, highlighting their features, strengths, and limitations. Furthermore, the review explores advanced strategies for optimizing sgRNA performance, such as sequence modifications, secondary structure prediction, and off-target prediction algorithms. Additionally, the applications of sgRNA design in gene knockout, gene activation, and gene editing in various organisms are examined to illustrate the broad utility and versatility of CRISPR-Cas technology. Through a synthesis of current literature and practical insights, this review aims to provide guidance and recommendations for effective sgRNA design in CRISPR-Cas genome editing experiments.  Keywords: sgRNA design, CRISPR-Cas, genome editing, target selection, specificity, efficiency.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

CRISPR-Cas genome editing has emerged as a powerful tool for precise and targeted modifications of the genome, offering unprecedented opportunities for basic research, biotechnology, and therapeutic applications. Central to CRISPR-Cas-mediated genome editing is the design of single-guide RNAs (sgRNAs), which guide the Cas nuclease to specific target sites within the genome. This review provides an overview of the principles, tools, and applications of sgRNA design in CRISPR-Cas genome editing.

Principles of sgRNA Design

2.1. Target Selection: The selection of target sites for sgRNA design is crucial for achieving specific and efficient genome editing. Factors such as sequence composition, GC content, and proximity to functional elements (e.g., exons, regulatory regions) influence target site selection and sgRNA performance.

2.2. Specificity: Ensuring high specificity of sgRNA binding is essential for minimizing off-target effects and unintended mutations. Computational algorithms and bioinformatics tools are employed to predict potential off-target sites and evaluate sgRNA specificity.

2.3. Efficiency: Maximizing sgRNA efficiency is essential for achieving robust genome editing outcomes. Optimization of sgRNA sequence, secondary structure, and delivery method can enhance editing efficiency and minimize variability between experiments.

Computational Tools for sgRNA Design

3.1. CRISPR Design Tools: Various online platforms and software tools are available for designing sgRNAs, including CRISPR design algorithms, such as CRISPRscan, CRISPOR, and Benchling, which facilitate target site selection and evaluation of sgRNA efficiency and specificity.

3.2. Off-Target Prediction Tools: Computational algorithms, such as CRISPRoff, CCTop, and COSMID, are used to predict potential off-target sites based on sequence homology and mismatches between sgRNA and genomic DNA.

3.3. Secondary Structure Prediction: Prediction of sgRNA secondary structure and stability using tools like RNAfold and Mfold can aid in optimizing sgRNA design and enhancing editing efficiency.

Optimization Strategies for sgRNA Design

4.1. Sequence Modifications: Rational design strategies, such as truncation, modification of the protospacer adjacent motif (PAM), and incorporation of chemical modifications (e.g., locked nucleic acids, 2'-O-methyl groups), can improve sgRNA stability, specificity, and editing efficiency.

4.2. Secondary Structure Prediction: Prediction of sgRNA secondary structure and avoidance of stable RNA secondary structures can enhance Cas nuclease accessibility and editing efficiency at target sites.

4.3. Off-Target Minimization: Utilization of high-fidelity Cas nucleases (e.g., Cas9 variants, such as SpCas9-HF and eSpCas9) and optimization of sgRNA sequence and target site selection can minimize off-target effects and increase editing specificity.

Applications of sgRNA Design

5.1. Gene Knockout: sgRNAs are widely used for inducing targeted gene knockout by introducing frameshift mutations or premature stop codons, resulting in loss-of-function phenotypes.

5.2. Gene Activation: CRISPR activation (CRISPRa) techniques utilize engineered sgRNAs to recruit transcriptional activators to target gene promoters, enabling robust and specific gene activation.

5.3. Gene Editing: sgRNAs combined with Cas nucleases, such as Cas9, Cas12a, and Cas13, enable precise and targeted gene editing, including base editing, prime editing, and homology-directed repair (HDR).

Conclusion

Effective sgRNA design is essential for successful CRISPR-Cas genome editing experiments, with considerations for target selection, specificity, and efficiency. Computational tools and optimization strategies aid in sgRNA design and enhance editing outcomes. The versatility and applications of sgRNA design in gene knockout, gene activation, and gene editing illustrate the transformative potential of CRISPR-Cas technology in diverse fields of research and biotechnology.

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| REVIEW | | OPEN ACCESS |
| Superovulation in Goats: Techniques, Mechanisms, and Applications **ABSTRACT**:  Superovulation, the induction of multiple ovulations in a single estrous cycle, is a valuable reproductive technique utilized in goat breeding programs to enhance genetic selection and accelerate genetic progress. This review provides an in-depth analysis of superovulation techniques, underlying mechanisms, and applications in goat reproduction. Various protocols for superovulation induction, including hormone-based and gonadotropin-releasing hormone (GnRH) agonist protocols, are discussed, highlighting their efficacy, limitations, and practical considerations in goat management. Furthermore, the review explores the physiological mechanisms governing superovulation response, including follicular development, ovulation induction, and corpus luteum function, to provide insights into optimizing superovulatory outcomes. Additionally, the applications of superovulation in goat breeding programs, such as embryo transfer, multiple ovulation and embryo transfer (MOET), and in vitro embryo production, are examined, emphasizing their contributions to genetic improvement and reproductive efficiency. Through a synthesis of current literature and practical insights, this review aims to enhance understanding of superovulation techniques in goats and their potential to advance breeding strategies and genetic selection programs.  Keywords: superovulation, goats, hormone protocols, gonadotropins, embryo transfer, genetic selection.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

Superovulation, the induction of multiple ovulations in a single estrous cycle, offers a powerful tool for enhancing reproductive efficiency and genetic selection in goat breeding programs. This review provides an overview of superovulation techniques, mechanisms, and applications in goat reproduction, with a focus on optimizing outcomes and genetic progress.

Superovulation Techniques

2.1. Hormone-Based Protocols: Hormone-based superovulation protocols involve the administration of exogenous gonadotropins, such as follicle-stimulating hormone (FSH) and luteinizing hormone (LH), to stimulate follicular development and ovulation. Various hormone regimens, including FSH alone, FSH/LH combinations, and FSH priming followed by LH administration, have been employed to induce superovulation in goats.

2.2. Gonadotropin-Releasing Hormone (GnRH) Agonist Protocols: GnRH agonist protocols utilize synthetic analogs of GnRH to induce endogenous gonadotropin release and follicular development. By mimicking the natural pulsatile secretion of GnRH, these protocols offer an alternative approach to hormone-based superovulation, potentially reducing the risk of ovarian hyperstimulation syndrome (OHSS) and improving embryo quality.

Mechanisms of Superovulation Response

3.1. Follicular Development: Superovulation is characterized by the recruitment and development of multiple ovarian follicles in response to exogenous gonadotropin stimulation. FSH plays a key role in promoting follicular growth and granulosa cell proliferation, leading to the development of multiple preovulatory follicles capable of ovulation.

3.2. Ovulation Induction: The administration of LH or its analogs triggers the final maturation and ovulation of preovulatory follicles, leading to the release of multiple oocytes into the oviducts. Ovulation induction is essential for synchronizing ovulation and maximizing the yield of recoverable embryos for subsequent transfer or in vitro production.

3.3. Corpus Luteum Function: Following ovulation, the corpus luteum forms from the remnants of the ovulated follicles and secretes progesterone, which is essential for maintaining pregnancy and supporting embryo development. The functionality of the corpus luteum is critical for embryo survival and successful establishment of pregnancy after superovulation.

Applications of Superovulation

4.1. Embryo Transfer: Superovulation combined with embryo transfer enables the production of multiple embryos from genetically superior donors for transfer into recipient does, thereby accelerating genetic progress and dissemination of desirable traits within the goat population.

4.2. Multiple Ovulation and Embryo Transfer (MOET): MOET involves the superovulation of multiple donors followed by embryo collection and transfer, allowing for the rapid multiplication of elite genetics and the generation of large numbers of offspring for performance testing and selection.

4.3. In Vitro Embryo Production: Superovulation can also be combined with in vitro embryo production techniques, such as in vitro fertilization (IVF) or intracytoplasmic sperm injection (ICSI), to generate embryos outside the female reproductive tract. This approach offers advantages in terms of embryo production efficiency and genetic preservation.

Conclusion

Superovulation is a valuable reproductive technique in goat breeding programs, offering opportunities for genetic improvement, accelerated multiplication of elite genetics, and enhanced reproductive efficiency. Optimization of superovulation protocols and understanding of underlying mechanisms are essential for maximizing superovulatory response and embryo yield. Through integration with assisted reproductive technologies, such as embryo transfer and in vitro embryo production, superovulation contributes to advancing breeding strategies and genetic selection programs in goats.

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| REVIEW | | OPEN ACCESS |
| Cold Tolerance in Goats: Physiological Adaptations, Management Practices, and Genetic Considerations **ABSTRACT**:  Cold tolerance is a critical aspect of goat husbandry, particularly in regions characterized by cold climates and harsh environmental conditions. This review examines the physiological adaptations, management practices, and genetic considerations associated with cold tolerance in goats. It explores the mechanisms by which goats acclimatize to cold stress, including changes in metabolic rate, thermogenesis, insulation, and behavioral adaptations. Additionally, the review discusses management strategies for optimizing cold tolerance in goats, such as shelter provision, dietary supplementation, and breed selection. Furthermore, the genetic basis of cold tolerance traits in goats is explored, highlighting potential candidate genes and genomic regions associated with adaptation to cold environments. Through a synthesis of current literature and practical insights, this review aims to enhance understanding of cold tolerance mechanisms in goats and provide guidance for goat farmers and breeders to improve cold resilience and welfare in their herds.  Keywords: cold tolerance, goats, physiological adaptations, management practices, genetic considerations.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

Cold tolerance is essential for the health, welfare, and productivity of goats, especially in regions where cold weather conditions prevail for extended periods. This review explores the mechanisms underlying cold tolerance in goats and discusses strategies for enhancing their resilience to cold stress.

Physiological Adaptations to Cold Stress

2.1. Metabolic Rate Regulation: In response to cold exposure, goats undergo metabolic adjustments to maintain body temperature, including increased metabolic rate and energy expenditure to generate heat through shivering thermogenesis and non-shivering thermogenesis.

2.2. Thermogenesis: Cold-tolerant goats exhibit efficient thermogenic mechanisms, such as activation of brown adipose tissue (BAT) and uncoupling protein 1 (UCP1)-mediated heat production, which contribute to maintaining body temperature during cold exposure.

2.3. Insulation: The thick coat of goats serves as insulation against cold temperatures by trapping air close to the body surface, reducing heat loss, and preserving body heat.

2.4. Behavioral Adaptations: Goats exhibit behavioral adaptations to cold stress, including seeking shelter, huddling, and altering grazing patterns to minimize heat loss and conserve energy.

Management Practices for Enhancing Cold Tolerance

3.1. Shelter Provision: Adequate shelter, such as barns, sheds, or windbreaks, is essential for protecting goats from extreme cold temperatures, precipitation, and wind chill effects.

3.2. Dietary Supplementation: Providing energy-dense feeds, such as high-quality forages, grains, and supplemental fats, can support increased metabolic demands and thermogenesis in cold-stressed goats.

3.3. Water Provision: Access to clean and unfrozen water is crucial for maintaining hydration and thermoregulation in cold conditions, as water intake supports metabolic processes and heat production.

3.4. Breed Selection: Breeding for cold tolerance traits, such as thick coats, compact body conformation, and efficient thermogenic capacity, can improve the resilience of goat herds to cold stress and adverse weather conditions.

Genetic Considerations for Cold Tolerance

4.1. Candidate Genes: Several candidate genes associated with cold tolerance have been identified in goats, including genes involved in thermogenesis (e.g., UCP1), hair growth and insulation (e.g., PRLH, BMP12), and metabolic regulation (e.g., PPARs).

4.2. Genomic Regions: Genome-wide association studies (GWAS) and genomic selection approaches have identified genomic regions associated with cold tolerance traits in goats, providing insights into the genetic architecture of cold adaptation.

4.3. Marker-Assisted Selection: Marker-assisted selection (MAS) based on genetic markers linked to cold tolerance traits offers potential for accelerating genetic improvement in cold-adapted goat populations by selecting for desired traits more efficiently.

Conclusion

Cold tolerance is a multifaceted trait influenced by physiological adaptations, management practices, and genetic factors in goats. Understanding the mechanisms of cold tolerance and implementing appropriate management strategies are essential for promoting the welfare and productivity of goats in cold climates. Furthermore, leveraging genetic tools and selection strategies can enhance cold resilience and adaptation in goat populations, contributing to sustainable livestock production in challenging environments.

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| REVIEW | | OPEN ACCESS |
| Myostatin Gene in Goats: Physiology, Genetic Variants, and Potential Applications **ABSTRACT**:  Myostatin, also known as growth differentiation factor 8 (GDF-8), is a negative regulator of muscle growth and development in mammals. In goats, variations in the myostatin gene (MSTN) have been associated with alterations in muscle phenotype, including increased muscle mass and reduced fat deposition. This review provides an overview of the physiology of myostatin, genetic variants identified in goats, and potential applications of myostatin modulation in goat production systems. It explores the molecular mechanisms by which myostatin regulates muscle growth and differentiation, highlighting the significance of MSTN mutations in modulating muscle phenotypes. Additionally, the review discusses genetic polymorphisms identified in the MSTN gene of goats, their effects on muscle traits, and their potential for selective breeding and genetic improvement programs. Furthermore, it examines the applications of myostatin modulation in goat production, including enhanced meat production, improved carcass quality, and increased muscle yield. Through a synthesis of current literature and practical insights, this review aims to provide a comprehensive understanding of myostatin genetics in goats and its implications for goat breeding and production.  Keywords: myostatin, goats, muscle growth, genetic variants, selective breeding, meat production.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

Myostatin is a key regulator of muscle growth and development, playing a crucial role in determining muscle phenotype and body composition in mammals. In goats, genetic variations in the myostatin gene (MSTN) have been associated with alterations in muscle mass, growth rates, and carcass traits. This review explores the physiology of myostatin, genetic variants in the MSTN gene of goats, and their implications for goat production systems.

Physiology of Myostatin

2.1. Molecular Function: Myostatin is a member of the transforming growth factor-beta (TGF-β) superfamily and acts as a negative regulator of skeletal muscle growth by inhibiting myoblast proliferation and differentiation, as well as promoting muscle atrophy and adipogenesis.

2.2. Regulation of Muscle Growth: Myostatin signaling pathway involves binding to its receptor (activin receptor type IIB, ActRIIB) and activation of downstream signaling cascades, leading to inhibition of muscle cell proliferation and differentiation, and activation of muscle protein degradation pathways.

2.3. Genetic Regulation: MSTN expression is tightly regulated at the transcriptional and post-transcriptional levels, with genetic mutations in the MSTN gene affecting its expression and function, thereby influencing muscle phenotype and growth characteristics.

Genetic Variants in MSTN Gene of Goats

3.1. Structural Variants: Several genetic polymorphisms, including single nucleotide polymorphisms (SNPs), insertions, and deletions, have been identified in the MSTN gene of goats, with some variants associated with altered muscle traits and carcass characteristics.

3.2. Functional Effects: Functional studies have demonstrated the effects of MSTN mutations on muscle mass, growth rates, and meat quality traits in goats, with certain variants associated with increased muscle hypertrophy and reduced fat deposition.

3.3. Breed Differences: Variations in MSTN gene frequencies and allele distributions have been observed among different goat breeds, reflecting genetic diversity and selective pressures for muscle phenotypes in specific production systems.

Applications in Goat Production

4.1. Selective Breeding: Knowledge of MSTN genetic variants provides opportunities for selective breeding programs aimed at improving meat production efficiency, carcass quality, and muscle yield in goat populations.

4.2. Marker-Assisted Selection: Marker-assisted selection (MAS) using MSTN genetic markers enables targeted breeding strategies for enhancing muscle traits and selecting animals with desirable growth characteristics and meat quality attributes.

4.3. Biotechnological Interventions: Manipulation of MSTN expression through gene editing technologies, such as CRISPR-Cas9, offers potential for enhancing muscle growth and improving meat production efficiency in goats.

Conclusion

Genetic variations in the myostatin gene play a significant role in modulating muscle phenotypes and growth characteristics in goats. Understanding the physiology of myostatin and its genetic regulation provides insights into the mechanisms underlying muscle development and offers opportunities for genetic improvement in goat production systems. Integration of genetic information on myostatin variants into selective breeding programs and biotechnological interventions holds promise for enhancing meat production efficiency and carcass quality in goats.

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| REVIEW | | OPEN ACCESS |
| Ceftiofur as an Intervention for Hemorrhagic Septicemia in Livestock: Mechanisms, Efficacy, and Considerations **ABSTRACT**:  Hemorrhagic septicemia (HS) is a severe bacterial disease affecting various livestock species, particularly cattle and buffalo, caused by Pasteurella multocida. The emergence of antibiotic resistance poses challenges for the treatment and control of HS, highlighting the need for effective antimicrobial interventions. Ceftiofur, a third-generation cephalosporin antibiotic, has shown promise as a treatment option for HS due to its broad-spectrum activity and pharmacokinetic properties. This review explores the mechanisms of action of ceftiofur against Pasteurella multocida, its efficacy in the management of HS, and considerations for its use in livestock. It discusses the bactericidal activity of ceftiofur against Pasteurella multocida, including its mode of action, spectrum of activity, and resistance mechanisms. Additionally, the review examines the clinical efficacy of ceftiofur in field trials and experimental studies for the treatment and prevention of HS, highlighting its role in reducing mortality, morbidity, and economic losses associated with the disease. Furthermore, it addresses considerations for the prudent use of ceftiofur in livestock production, including dosing regimens, withdrawal periods, antimicrobial stewardship, and strategies to mitigate antimicrobial resistance. Through a synthesis of current literature and practical insights, this review aims to provide a comprehensive understanding of ceftiofur as an intervention for hemorrhagic septicemia in livestock and guide its rational use in disease management programs.  Keywords: ceftiofur, hemorrhagic septicemia, Pasteurella multocida, antibiotic resistance, livestock, antimicrobial stewardship.  Citation: Calle-González, N.; Lo Feudo, C.M.; Ferrucci, F.; Requena, F.; Stucchi, L.; Muñoz, A. Objective Assessment of Equine Locomotor Symmetry Using an Inertial Sensor System and Artificial Intelligence: A Comparative Study. Animals 2024, 14, 921. https://doi.org/10.3390/ ani14060921 | | |
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Introduction

Hemorrhagic septicemia (HS) is a significant bacterial disease of livestock caused by Pasteurella multocida, leading to severe economic losses and welfare concerns in affected populations. The emergence of antimicrobial resistance underscores the importance of identifying effective treatment options for HS, with ceftiofur emerging as a potential intervention due to its broad-spectrum activity and pharmacokinetic properties.

Mechanisms of Action of Ceftiofur

2.1. Mode of Action: Ceftiofur exerts its bactericidal activity by inhibiting bacterial cell wall synthesis through binding to penicillin-binding proteins (PBPs), disrupting peptidoglycan cross-linking, and inducing cell lysis in susceptible pathogens such as Pasteurella multocida.

2.2. Spectrum of Activity: Ceftiofur demonstrates broad-spectrum activity against Gram-negative bacteria, including Pasteurella spp., Escherichia coli, Salmonella spp., and Haemophilus spp., making it a valuable therapeutic agent for the treatment of HS and other bacterial infections in livestock.

2.3. Resistance Mechanisms: Despite its efficacy, the emergence of ceftiofur resistance in Pasteurella multocida and other bacterial pathogens poses a concern, with mechanisms including β-lactamase production, alterations in PBPs, efflux pump overexpression, and plasmid-mediated resistance genes contributing to reduced susceptibility.

Efficacy of Ceftiofur in Hemorrhagic Septicemia

3.1. Clinical Trials: Field trials and experimental studies have demonstrated the clinical efficacy of ceftiofur in the treatment and prevention of HS in cattle and buffalo, with significant reductions in mortality rates, fever, clinical signs, and bacterial shedding observed following ceftiofur administration.

3.2. Pharmacokinetic Considerations: Ceftiofur exhibits favorable pharmacokinetic properties, including rapid absorption, distribution to target tissues, and prolonged systemic exposure, enabling convenient dosing regimens and extended duration of therapeutic effect in livestock.

3.3. Combination Therapy: Combinations of ceftiofur with other antimicrobial agents, supportive therapies, and immunomodulators may enhance treatment outcomes and reduce the risk of treatment failure or relapse in severe cases of HS.

Considerations for Prudent Use of Ceftiofur

4.1. Dosing Regimens: Optimal dosing regimens should be based on pharmacokinetic parameters, disease severity, animal species, and susceptibility testing results to ensure adequate antimicrobial concentrations at the site of infection and minimize the risk of resistance development.

4.2. Withdrawal Periods: Adherence to appropriate withdrawal periods is essential to prevent drug residues in animal products, comply with regulatory requirements, and safeguard food safety and consumer health.

4.3. Antimicrobial Stewardship: Prudent use of ceftiofur involves adherence to antimicrobial stewardship principles, including judicious selection, appropriate dosing, and responsible use practices to preserve antimicrobial efficacy, minimize selection pressure, and mitigate the spread of resistance. Ceftiofur as an Intervention for Hemorrhagic Septicemia in Livestock is presented in Table 1.

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| **Table 1: Ceftiofur as an Intervention for Hemorrhagic Septicemia in Livestock** | |
| **Aspect** | **Details** |
| Disease | Hemorrhagic septicemia (HS) is caused by Pasteurella multocida and affects various livestock species, including cattle, buffalo, and goats. |
| Antibiotic | Ceftiofur, a third-generation cephalosporin antibiotic, is commonly used for the treatment of bacterial infections in livestock, including HS. |
| Mechanism of Action | Ceftiofur inhibits bacterial cell wall synthesis by binding to penicillin-binding proteins, leading to cell lysis and death. |
| Spectrum of Activity | Ceftiofur exhibits broad-spectrum activity against Gram-negative and some Gram-positive bacteria, including P. multocida. |
| Pharmacokinetics | - Absorption: Ceftiofur is rapidly absorbed after intramuscular or subcutaneous administration. |
|  | - Distribution: It achieves therapeutic concentrations in various tissues and body fluids, including lung, liver, and serum. |
|  | - Metabolism: Ceftiofur is metabolized to desfuroylceftiofur, an active metabolite, in the liver. |
|  | - Excretion: It is primarily excreted via urine, with a small proportion eliminated in feces. |
| Clinical Efficacy | - Field Trials: Ceftiofur has demonstrated clinical efficacy in field trials for the treatment of HS, with rapid resolution of clinical signs and improvement in survival rates. |
|  | - Experimental Studies: Experimental studies have shown that ceftiofur effectively reduces bacterial loads and promotes recovery in animals challenged with P. multocida. |
| Dosage and Administration | - Dosage: Ceftiofur is typically administered at a dosage of 1-2 mg/kg body weight, once or twice daily, depending on the severity of the infection. |
|  | - Route: It can be administered via intramuscular or subcutaneous injection for systemic delivery. |
| Practical Considerations | - Withdrawal Period: Ceftiofur has established withdrawal periods to ensure residue avoidance in food products derived from treated animals. |
|  | - Antimicrobial Resistance: Prudent use of ceftiofur is essential to minimize the development of antimicrobial resistance in bacterial populations. |
|  | - Veterinary Oversight: Ceftiofur should be used judiciously under veterinary supervision, following appropriate diagnostic and treatment protocols. |

This table provides an organized summary of key aspects related to the use of ceftiofur in the treatment of hemorrhagic septicemia in livestock, including its mechanism of action, pharmacokinetics, clinical efficacy, dosage and administration, and practical considerations for veterinary practitioners and livestock producers.

Conclusion

Ceftiofur represents a valuable therapeutic option for the management of hemorrhagic septicemia in livestock, offering broad-spectrum activity, favorable pharmacokinetics, and demonstrated clinical efficacy. However, its prudent use is essential to optimize treatment outcomes, preserve antimicrobial efficacy, and mitigate the risk of resistance emergence in veterinary medicine.

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