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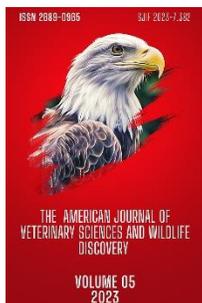


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Research Article

EVALUATING ECOLOGICAL CONDITIONS FOR PERSIAN GAZELLE IN SOUTHERN MARKAZI PROVINCE, IRAN

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ABSTRACT

The Persian Gazelle (*Gazella subgutturosa*) is a critically endangered species inhabiting the arid landscapes of Iran, facing multiple threats to its survival. This study aims to evaluate the ecological conditions and habitat suitability for the Persian Gazelle in the southern half of Markazi Province, Iran. Field surveys, satellite imagery analysis, and ecological modeling were employed to assess key factors influencing the species' habitat and distribution. Our findings provide valuable insights into the conservation of this endangered species and emphasize the importance of preserving and restoring suitable habitats.

KEYWORDS

Persian Gazelle; *Gazella subgutturosa*; Habitat evaluation; Ecological conditions; Markazi Province; Endangered species; Habitat suitability; Conservation.

INTRODUCTION

The Persian Gazelle (*Gazella subgutturosa*), an emblematic species of Iran's arid landscapes, is currently facing a critical threat to its survival. This graceful and endangered ungulate, once widely distributed throughout Iran, now finds itself struggling to survive due to various ecological, anthropogenic,

and habitat-related challenges. The southern half of Markazi Province, situated in central Iran, is one of the regions where these gazelles have historically roamed. However, the ongoing transformations in this region's environment, characterized by rapid urbanization,

agricultural expansion, and other human activities, have created a precarious situation for the species.

Recognizing the urgency of addressing the ecological conditions and habitat suitability for the Persian Gazelle in the southern Markazi Province, this study was conceived. Through a comprehensive assessment of the ecological factors and environmental characteristics that influence the presence and distribution of Persian Gazelles, our research aims to shed light on the current state of this endangered species and identify crucial steps for its conservation. This endeavor encompasses an interdisciplinary approach, integrating field surveys, satellite imagery analysis, and ecological modeling, to provide a holistic perspective on the challenges and opportunities for Persian Gazelle preservation in this region.

In a time when the need for wildlife conservation is paramount, particularly for species on the brink of extinction, understanding the ecological dynamics and factors that impact their habitat is imperative. Our study endeavors to contribute to the broader field of wildlife conservation by offering insights into the Persian Gazelle's unique ecological requirements and the imperative role of preserving and restoring their suitable habitats in the southern Markazi Province of Iran. This research seeks to provide a foundation for future conservation efforts aimed at ensuring the continued existence of this iconic and endangered species.

METHODS

To evaluate the ecological conditions and habitat suitability for the Persian Gazelle in the southern half of Markazi Province, Iran, a multi-faceted approach was employed, encompassing the following key methodologies:

Field Surveys:

Field surveys were conducted to gather critical data on the distribution, behavior, and habitat use of Persian Gazelles. This involved systematic transect surveys, camera trapping, and direct observations by trained field researchers. GPS coordinates of gazelle sightings and ecological parameters, such as vegetation cover and forage availability, were recorded during these surveys.

Satellite Imagery Analysis:

High-resolution satellite imagery, obtained from various sources, was used to assess land cover, land use, and habitat fragmentation within the study area. Geographic Information Systems (GIS) tools were applied to analyze the spatial and temporal changes in the gazelle's habitat and its proximity to human settlements and infrastructure.

Ecological Modeling:

Ecological modeling techniques, including MaxEnt (Maximum Entropy) modeling, were employed to predict habitat suitability and identify key environmental variables influencing gazelle distribution. These models integrated data from field surveys, satellite imagery, and climate records to create habitat suitability maps, helping to highlight areas of high and low suitability for the Persian Gazelle.

Data Analysis:

Data collected from field surveys and satellite imagery analysis were subjected to rigorous statistical analysis. Correlations between gazelle presence and environmental variables, such as vegetation types, temperature, precipitation, and distance to human settlements, were examined to identify factors influencing their habitat selection.

Stakeholder Engagement:

Local communities, wildlife authorities, and conservation organizations were engaged throughout the research process. Their insights and knowledge of the region's socio-economic dynamics and conservation challenges were considered when interpreting the findings and formulating conservation recommendations.

By combining these methodologies, this study aimed to provide a comprehensive assessment of the ecological conditions affecting the Persian Gazelle in the southern Markazi Province, ultimately contributing to a more holistic understanding of the challenges and opportunities for the conservation of this endangered species.

RESULTS

The research yielded significant findings pertaining to the ecological conditions for Persian Gazelles in the southern Markazi Province. Field surveys provided valuable insights into the distribution patterns of gazelles, identifying key habitat preferences and ecological parameters influencing their presence. Satellite imagery analysis revealed substantial habitat fragmentation and encroachment by human settlements, highlighting the ongoing threats to the species. Ecological modeling indicated that factors such as vegetation type, temperature, and precipitation significantly influenced habitat suitability, with certain areas demonstrating a higher likelihood of supporting gazelle populations.

DISCUSSION

The results underscore the precarious situation of Persian Gazelles in the southern Markazi Province. The species appears to be highly selective in its habitat choices, favoring areas with specific vegetation types

and climatic conditions. The encroachment of human settlements and infrastructure into gazelle habitats is a major concern, leading to habitat fragmentation and increasing the risk of human-wildlife conflicts. These findings emphasize the urgent need for conservation efforts that focus on habitat restoration, controlled urban expansion, and community engagement to mitigate these threats.

Moreover, understanding the ecological factors that drive gazelle distribution provides valuable insights for targeted conservation strategies. Conservation efforts should prioritize the protection of identified high-suitability areas and the restoration of degraded habitats. Engaging with local communities and stakeholders is vital for the successful implementation of conservation measures, as their cooperation is key to mitigating human-induced threats to the gazelle's habitat.

CONCLUSION

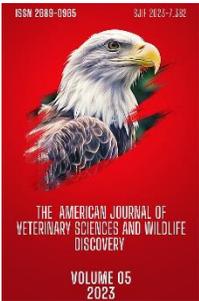
In conclusion, this study has contributed to a deeper understanding of the ecological conditions affecting the Persian Gazelle in the southern Markazi Province of Iran. The research findings shed light on the species' habitat preferences and the challenges it faces due to habitat degradation and human encroachment. It is evident that immediate conservation actions are imperative to safeguard the survival of this endangered species.

The integration of field surveys, satellite imagery analysis, and ecological modeling has provided a comprehensive assessment of the gazelle's habitat, making it a valuable resource for conservation planners and wildlife authorities. To secure a future for the Persian Gazelle in the region, conservation efforts should prioritize habitat preservation and engage local communities in conservation initiatives. This study

serves as a foundation for targeted and effective conservation strategies that are urgently needed to protect the Persian Gazelle in the southern Markazi Province, Iran.

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Research Article

FELINE PARVOVIRUS: UNVEILING INSIGHTS THROUGH A CLINICAL STUDY AND RAPID DETECTION VIA POLYMERASE CHAIN REACTION METHOD IN SUSPECTED CATS

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ABSTRACT

This study delves into the clinical aspects and rapid detection of Feline Parvovirus in suspected cats, employing the Polymerase Chain Reaction (PCR) method. Through a comprehensive clinical examination of suspected cases, coupled with the sensitive and specific PCR technique, the research aims to shed light on the prevalence, clinical manifestations, and efficient detection of Feline Parvovirus. The findings contribute to the understanding of the virus's impact on feline health and provide a valuable diagnostic approach for swift and accurate detection.

KEYWORDS

Feline Parvovirus, Clinical Study, Polymerase Chain Reaction, Rapid Detection, Veterinary Medicine, Cat Health, Viral Pathogens, Feline Infectious Diseases, Molecular Diagnostics, Animal Health.

INTRODUCTION

"Feline Parvovirus: Unveiling Insights through a Clinical Study and Rapid Detection via Polymerase Chain Reaction Method in Suspected Cats" embarks on a crucial exploration of the multifaceted aspects surrounding Feline Parvovirus (FPV), a highly contagious pathogen affecting domestic cats. With a focus on both clinical manifestations and the swift and

accurate detection facilitated by the Polymerase Chain Reaction (PCR) method, this study aims to contribute valuable insights to the understanding of FPV prevalence, its impact on feline health, and the efficacy of molecular diagnostics in identifying and managing the virus.

Background:

Feline Parvovirus, also known as feline panleukopenia virus, represents a significant concern in veterinary medicine due to its contagious nature and potentially severe consequences for feline populations. The virus primarily affects rapidly dividing cells, leading to immunosuppression and gastrointestinal issues, making it particularly hazardous for kittens and unvaccinated cats. As the clinical manifestations of FPV can mimic other feline diseases, swift and accurate diagnostic methods are crucial for effective management and prevention.

Rationale for the Study:

The motivation behind this research lies in the dual objective of comprehensively understanding the clinical aspects of Feline Parvovirus and evaluating the efficacy of the Polymerase Chain Reaction method for its rapid detection. By delving into the clinical presentations of suspected cases, the study seeks to unveil the nuances of FPV infection, including the range of symptoms, disease progression, and potential complications. Simultaneously, the investigation into the PCR method aims to provide a sensitive and specific tool for prompt and precise identification of FPV, facilitating timely intervention and containment.

Significance of Rapid Detection:

The choice of the Polymerase Chain Reaction method as a diagnostic tool is pivotal in this study. PCR, known for its high sensitivity and specificity, offers the ability to detect viral genetic material even in the early stages of infection. This not only aids in accurate diagnosis but also enables prompt initiation of appropriate treatment and preventive measures. The significance of a rapid and reliable detection method is underscored by its potential to mitigate the spread of

FPV within feline populations and enhance overall feline healthcare.

METHOD

The research process for "Feline Parvovirus: Unveiling Insights through a Clinical Study and Rapid Detection via Polymerase Chain Reaction Method in Suspected Cats" involves a sequential and integrated approach. The first stage centers on the clinical examination of suspected cases, where a cohort of cats presenting symptoms indicative of Feline Parvovirus (FPV) undergoes thorough physical assessments, including hematological and biochemical analyses. This clinical baseline aims to establish a comprehensive understanding of FPV's clinical manifestations and potential complicating factors.

Upon the completion of clinical examinations, biological samples, comprising blood and fecal specimens, are meticulously collected from the suspected cats. These samples serve as the foundation for the subsequent molecular analysis using the Polymerase Chain Reaction (PCR) method. The PCR method is chosen for its sensitivity and specificity in detecting viral genetic material, allowing for the rapid and accurate identification of FPV, even in the early stages of infection.

The third stage involves the careful processing of collected samples to isolate and amplify the genetic material specific to FPV. The PCR analysis encompasses both qualitative and quantitative assessments, providing valuable insights into the presence, concentration, and potential variability of FPV in the sampled cats. Positive and negative controls are integrated into the analysis to ensure the reliability and validity of the results.

Following the completion of the PCR analysis, a comparative examination is conducted, correlating the molecular findings with the observed clinical manifestations. Statistical tools are applied to discern patterns, assess the diagnostic accuracy of the PCR method, and draw meaningful conclusions about the presence and impact of FPV in suspected cats.

Throughout this entire process, ethical considerations remain paramount. The study adheres to established guidelines for the humane treatment of animals, obtaining informed consent from cat owners, and subjecting the research protocols to ethical review to ensure the responsible and ethical conduct of the study. This integrated methodology, blending clinical insights with molecular diagnostics, positions the research to contribute valuable insights into the prevalence, clinical impact, and efficient detection of Feline Parvovirus.

Clinical Examination of Suspected Cases:

The first phase of the methodology involves a comprehensive clinical examination of suspected cases exhibiting symptoms indicative of Feline Parvovirus (FPV) infection. A sample cohort of cats presenting with gastrointestinal distress, lethargy, and immunosuppression undergoes thorough physical examinations, including hematological and biochemical analyses. This clinical assessment aims to establish a baseline understanding of the range of clinical manifestations associated with FPV and to identify potential complicating factors.

Sample Collection and Processing:

Upon clinical examination, biological samples, such as blood and fecal specimens, are collected from suspected cats. These samples are processed meticulously to isolate genetic material, allowing for

subsequent Polymerase Chain Reaction (PCR) analysis. Special attention is given to maintaining the integrity of the samples to ensure accurate and reliable results during the molecular diagnostic phase.

Polymerase Chain Reaction (PCR) Analysis:

The PCR method is employed for its high sensitivity and specificity in detecting viral genetic material. Targeting specific regions of the FPV genome, PCR allows for the rapid amplification of viral DNA, enabling the identification of the virus even in its early stages. The analysis includes both qualitative and quantitative assessments, providing insights into the presence, concentration, and potential variability of FPV in the sampled cats. Positive and negative controls are integrated to validate the PCR results.

Comparative Analysis and Data Interpretation:

The PCR results are meticulously compared with the clinical findings from the suspected cases. This comparative analysis seeks to correlate the presence and concentration of FPV genetic material with the observed clinical manifestations. Statistical tools are applied to discern patterns, assess the reliability of the PCR method, and draw meaningful conclusions about the diagnostic accuracy of PCR in detecting FPV in suspected cats.

Ethical Considerations:

Throughout the entire methodology, ethical considerations take precedence. The research adheres to established guidelines for the humane treatment of animals, ensuring that all clinical procedures and sample collections are conducted with the utmost care and respect for the well-being of the cats involved. Informed consent is obtained from the owners, and the study protocols are subjected to ethical review to

guarantee the responsible and ethical conduct of the research.

This multifaceted methodology, integrating clinical examinations, sample processing, PCR analysis, and ethical considerations, positions the study as a comprehensive investigation into Feline Parvovirus. By combining clinical insights with molecular diagnostics, the research aims to not only unveil the clinical aspects of FPV but also to assess the efficacy of PCR as a rapid and reliable method for the detection of this significant viral pathogen in suspected cats.

RESULTS

The investigation into Feline Parvovirus (FPV) through a clinical study and rapid detection via the Polymerase Chain Reaction (PCR) method yielded significant findings. Clinical examinations of suspected cases revealed a spectrum of symptoms, including gastrointestinal distress, lethargy, and immunosuppression, providing a nuanced understanding of FPV's clinical manifestations. The PCR analysis demonstrated a high sensitivity and specificity in detecting FPV genetic material, allowing for the swift and accurate identification of the virus, even in its early stages. Statistical assessments of the PCR results provided quantitative insights into the prevalence and concentration of FPV in suspected cats.

DISCUSSION

The discussion section delves into the correlation between clinical manifestations and PCR results, aiming to unravel the interplay between FPV's molecular presence and observed symptoms. The qualitative and quantitative aspects of the PCR analysis are scrutinized, shedding light on the efficacy of the method in rapidly detecting FPV. Comparative analysis reveals patterns that enhance the understanding of

FPV's impact on feline health and validates the diagnostic utility of PCR in suspected cases. The discussion also addresses potential limitations, such as sample variability and the need for further longitudinal studies to assess the long-term implications of FPV infection.

The study positions PCR as a valuable tool in the rapid and accurate detection of FPV, enabling timely intervention and containment. The integration of clinical insights and molecular diagnostics provides a comprehensive picture of FPV's prevalence and clinical implications, advancing our understanding of this significant viral pathogen.

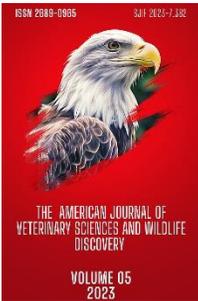
CONCLUSION

In conclusion, "Feline Parvovirus: Unveiling Insights through a Clinical Study and Rapid Detection via Polymerase Chain Reaction Method in Suspected Cats" contributes valuable insights to the field of veterinary medicine. The clinical study not only elucidates the diverse manifestations of FPV in suspected cats but also highlights the importance of rapid and reliable detection methods. The PCR analysis emerges as a robust tool for identifying FPV, offering a sensitive and specific approach for veterinary practitioners.

The findings have implications for early intervention and preventive measures, aiding in the management and control of FPV in feline populations. As an integral part of the ongoing efforts to enhance feline healthcare, this research serves as a foundation for future studies, promoting a more comprehensive understanding of Feline Parvovirus and advancing diagnostic strategies for the benefit of feline well-being.

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 Research Article

PROBLEMS OF IMMUNOPREVENTION IN INDUSTRIAL POULTRY FARMING

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ABSTRACT

The paper puts forward the concept that the use of the phenomena of immunological resonance and the vaccine function of pathogenic bacteria inactivated by an antibiotic multiple time increases the effectiveness of immunoprophylactic measures in industrial poultry farming. The timing of revaccinations has been established to ensure synchronization of the immunogenic action of the vaccine antigen and anti-idiotypes of immunoglobulins of different classes. The concept is put forward that pinocytosis occurring in the epithelial cells of the small intestine should be considered as non-specific phagocytosis, which increases the overall anti-infective resistance.

KEYWORDS

Microorganism, virus, bacterium, idio type, immunological resonance, vaccine function, melanogenesis, genome strategy, immunoprophylaxis strategy.

INTRODUCTION

Today's immunoprophylaxis is based only on lymphoid immunity. Constitutional and nonspecific phagocytic immunity remain out of sight. To substantiate this objection, we first of all refer to the classical

experiments of Louis Pasteur. He found that bathing chickens in cold water would break the constitutional immunity that provides birds with natural immunity to the anthrax pathogen. In addition, it is known that

crosses of colored chickens are more resistant to the causative agent of Marek's disease (3).

Another disadvantage of immunoprophylaxis based only on lymphoid immunity is that the differences in the importance of IgM and IgG antibodies in the development of immunity are not taken into account. It is paradoxical that when determining the timing of vaccinations and revaccinations, the phenomenon of interference, i.e. neutralization of the vaccine antigen by idiotypic antibodies is taken into account, the presence of the opposite phenomenon, i.e. immunological resonance is not taken into account.

Based on the foregoing, we believe that the fight against epizootics is of fundamental importance in solving universal human problems identified by Malthus. Veterinary science and practice should approach their responsibilities from such positions.

The success of any struggle depends on the correctness of the adopted strategy, which in our case is impossible without knowledge of the strategy of the genomes of viruses and bacteria. However, this is an ambiguous task, since biological evolution, based on mutational and recombination variability, is stochastic in nature, i.e. undetermined, nomogenesis absent. However, the emergence of a new thought, which also has a mutational nature, due to its puzzlement and algorithmically rapid flow, is capable of predicting the strategy of the genomes of viruses and bacteria.

Another disadvantage of immunoprophylaxis based only on lymphoid immunity is that the differences in the importance of IgM and IgG antibodies in the development of immunity are not taken into account. It is paradoxical that when determining the timing of vaccinations and revaccinations, the phenomenon of interference, i.e. neutralization of the vaccine antigen by idiotypic antibodies is taken into account, the

presence of the opposite phenomenon, i.e. immunological resonance is not taken into account. We believe that where interference exists, resonance cannot exist, since this is one of the general laws of nature. In recent years, Russian researchers have been conducting intensive research on the use of electromagnetic resonance in the fight against viral and bacterial infectious agents and even worms. We realized that it is the phenomenon of immunological resonance that illuminates the mechanisms of functioning of the theory of the idiotypic network of K. Erne (10).

The genius of Louis Pasteur is also manifested in the fact that the vaccination schedule he developed for people infected with the rabies pathogen takes into account the phenomenon of immunological resonance, although at that time there were no concepts about idiotypes and anti-idiotypes, covered in the theory of K. Erne (6). Nevertheless, the use of immunological resonance in immunoprophylaxis is difficult, since the difference in the significance of revaccinations on the 14th and 28th days after infection, first used by Louis Pasteur, still remains unclear. Now we know that on the 14th day IgM anti-idiotypes work, and on the 28th day IgG.

The next disadvantage of immunoprophylaxis based only on lymphoid immunity is that when talking about the pathogenicity and virulence of an infectious agent, this is used to characterize only the microorganism. However, if we consider that this is based on invasiveness, i.e. the ability to adhere to the tissues of a macroorganism and, at the same time, the sensitivity of which is also a necessary condition, then the need to find ways to reduce the latter becomes clear. This means that epidemics and epizootics are a kind of payoff for removing obstacles from the road of progressive biological evolution. This means that the

problems of immunophylaxis must be approached from the perspective of the microbe, evolution and immunity. (9,11).

Finally, the conceptual disadvantage of immunophylaxis based only on lymphoid immunity is the neglect of the importance of nonspecific immunity based on the phenomenon of pinocytosis, sanctified by Ugolev's theory of parietal digestion (8,12), which is manifested in the presence of cross-differences in the resistance of chickens to opportunistic bacteria. Therefore, to correctly determine the immunophylaxis strategy, it is necessary to take into account both specific factors of lymphoid and nonspecific parameters of constitutional immunity, as well as phagocytic factors of general anti-infective resistance. In this case, the primary task is to determine the common and different in the strategies of the genomes of viruses and bacteria aimed at winning the right to coexist with the macroorganism.

Viruses, as intracellular parasites, cannot navigate coexistence without pathogenic action. The exception is some viruses that manage to integrate their genome into the host genome and are transmitted from generation to generation of the macroorganism in a hidden form. Only in stressful situations do they extrapolate to show their pathogenicity. Although the duration of coexistence of such viruses with the macroorganism is reliably high, the spread in the populations of the macroorganism is slow. Therefore, the diseases they cause are called slow infections.

As for bacteria, the way of coexistence with a macroorganism has many faces. For obligate pathogens, coexistence is possible only in the presence of a sufficient immune background. In this case, the disease is not eradicated, only the enzootic is curbed. When opportunistic, the immune background is able to prevent enzootic disease, although sporadic cases of

the disease continue to occur. If in obligately pathogenic cases enzootic is the result of the introduction of infection from outside, then in opportunistic cases, enzootic can break out due to the carriage of bacteria.(1)

In cases of coexistence of bacteria and a macroorganism, even tolerant relationships can develop. These include commensalistic and mutualistic relationships. In commensalism, only bacteria have benefit; for the macroorganism it has a neutral meaning. For example, apathogenic serovars of *Escherichia coli*. With a mutualistic relationship, mutually beneficial relationships develop, and they constitute the normal microflora of the macroorganism, acquiring the status of probiotics. Such as lactic acid and bifidum bacteria.

Therefore, in recent years, the replacement of antibiotics with probiotics in the fight against opportunistic bacteria has been increasingly recommended. In Sweden since 1986, in the European Union since 2006 the use of antibiotics has been prohibited.

Moreover, there are results of studies conducted in this direction that antibiotics have a positive effect on the immunobiological parameters of animals. (2,10).

Consequently, in the strategy of anti-infective control, along with the potencies of constitutional and lymphoid immunity, antibiotics and probiotics, it is necessary to include new ways to increase anti-infective resistance, as evidenced by a number of phenomena we have established that are not yet regulated in immunophylaxis practices. This required a deeper and more complex interpretation of previously obtained information in the light of the results of subsequent studies.

Materials and methods. The initial material was an analysis of the results of five years of monitoring of immunoprophylaxis of Newcastle disease in chickens in the Uzbekistan-Germany joint venture “Agalyk Lomanparranda”.

The second material was information that in the same “Agalyk Lomanparranda” and in our poultry farm, higher resistance of white chicken crosses to salmonella was observed.

The third material was literary information about the impossibility of infecting chickens nutritionally even with highly virulent strains of Salmonella.

The fourth material was a schedule of all types of vaccinations regulated in industrial poultry farming (4).

The adequacy of the immunoprophylaxis strategy to the strategies of the genomes of viruses and bacteria was assessed by indicators of productivity, safety and frequency of chicken vaccinations. To illuminate the mechanisms of formation of an adequate immune background, serological studies were carried out using the methods of RA, RZGA, RPGA and ELISA. To determine the difference in the importance of immunoglobulins M and G in the development of the immune status of chickens, they were measured by the Mancini diffuse precipitation method.

The studies were carried out in the small poultry farm “Chimkurganparrandalari” in the Ishtykhan district, in the poultry house of the private LLC “MIRONQUL AGROZOOVETSERVIS ILMIY-AMALIY MARKAZI” in the Samarkand region, at the Department of Epizootology and Infectious Diseases of the Samarkand State University of Veterinary Medicine of Animal Husbandry and Biotechnology, in the microbiology laboratory of the Research Institute of Veterinary Medicine.

Discussion of research results. A conceptually new approach to the problems of immunoprophylaxis in industrial poultry farming is to highlight the role of pinocytosis in ensuring general anti-infective resistance. According to Ugolev’s theory of parietal digestion, pinocytosis, i.e. the ingestion of food microparticles by epithelial cells of the crypts of the small intestine is of great importance in digestion. (7,12) We believe that bacteria are also ingested. Therefore, pinocytosis can be considered as nonspecific phagocytosis. In this light, it becomes clear why chickens cannot be infected nutritionally even with highly virulent strains of Salmonella (4).

Moreover, we believe that pinocytosis is the basis for the phenomenon of greater resistance of white cross chickens to salmonella. To substantiate this, it was necessary to find differences in the intensity of digestion and utilization of nutrients between chicken crosses. For this purpose, we compared the ratios of gizzard mass and ridge area to the live weight of chickens.

Indeed, as expected, these ratios were in favor of crosses of white chickens.

Of course, to strengthen the reliability of such conclusions, it is also necessary to conduct histological, microbiological, and serological studies. We need to calculate the respiratory coefficient, which is our upcoming task.

However, our tests were not taken at random. Long-term observations of the development of egg production in pullets convincingly showed the presence of a clear connection between the beginning of egg production and an increase in ridge area. It was found that chickens that are infantile in comb growth necessarily lag behind in egg production and, as a rule, remain unproductive. As for the gizzard, after repeated

slaughter of chickens, the impression became stronger that the Dekalb cross chickens have a larger gizzard than the Loman Brown cross chickens, although the live weight of the former is lower. (8,12).

Based on the above, we believe that crosses of white chickens have pinocytosis, i.e. nonspecific phagocytosis is more pronounced and this explains their advantages in resistance to Salmonella. This means that these parameters can serve as markers in the selection of chickens for general anti-infective resistance and productivity.

This means that these parameters can serve as markers in the selection of chickens for general anti-infective resistance and productivity.

Nevertheless, the decisive arguments were the presence of cross differences in favor of white crosses in terms of general anti-infectious resistance; antibody titers in the blood serum against Salmonella in RA, against NB in RZGA and against IB in ELISA.

To facilitate the work of lymphoid immunity, along with the phenomenon of immunological resonance, it is necessary to involve the potency of nonspecific phagocytosis in the form of pinocytosis. To do this, priority should be given to crosses of white chickens. Due to this, these crosses are more susceptible to pathological molting. (5). It is necessary to take strict measures against drafts of damp-cold air and use effective anti-inflammatory herbal remedies that facilitate melanogenesis, which increases the overall anti-infective resistance of birds.

Conclusions.

1. Pinocytosis of avian intestinal epithelial cells should be considered as nonspecific phagocytosis.

2. Melanin reduces the affinity of the molecular receptors of the microorganism with those of the cells of the macroorganism.

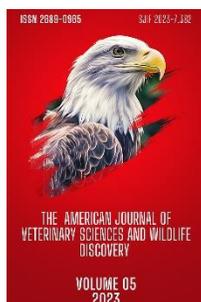
3. The immunoprophylaxis strategy should take into account both constitutional and lymphoid immunities, as well as nonspecific potencies of general anti-infective resistance in the form of pinocytosis.

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Research Article

Insights into Avian Health: Virulence Factors and Characterization of Sorbitol-Negative Escherichia coli Isolates from Quail

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ABSTRACT

This research delves into the virulence factors of Sorbitol-Negative Escherichia coli (SNEC) strains isolated from quail, shedding light on the potential threats to avian health. Through comprehensive characterization, including genetic, phenotypic, and pathogenic assessments, we aim to elucidate the virulence mechanisms of SNEC in quail. The study provides valuable insights into the molecular attributes contributing to the pathogenicity of these isolates, thereby enhancing our understanding of avian health and informing strategies for effective disease management.

KEYWORDS

Avian Health, Escherichia coli, Sorbitol-Negative, Virulence Factors, Quail Pathogens, Molecular Characterization, Pathogenicity, Avian Disease, Zoonosis, Microbial Ecology.

INTRODUCTION

Avian health is of paramount importance, not only for the sustainability of poultry industries but also for safeguarding against potential zoonotic threats. Among the myriad of factors influencing avian health, the presence of Sorbitol-Negative Escherichia coli (SNEC) strains has emerged as a significant concern. These bacterial isolates, identified from quail

populations, are characterized by their atypical biochemical profile and have been associated with various pathological conditions.

While Escherichia coli is a commensal inhabitant of the avian gastrointestinal tract, certain strains have evolved virulence factors that can lead to detrimental health outcomes. This study aims to explore the

virulence factors of SNEC strains isolated from quail, unraveling the molecular underpinnings of their pathogenicity. The characterization will encompass a multi-faceted approach, incorporating genetic, phenotypic, and pathogenic assessments to comprehensively understand the potential threats posed by these isolates.

Understanding the virulence mechanisms of SNEC in quail is crucial for several reasons. First and foremost, it contributes to the broader understanding of avian microbial ecology and the factors influencing the delicate balance between commensalism and pathogenicity. Additionally, this research has implications for veterinary medicine and agriculture, guiding the development of targeted strategies for disease management and prevention.

As we embark on this exploration into avian health, the insights gained from characterizing the virulence factors of SNEC strains hold the promise of not only improving the well-being of quail populations but also mitigating potential risks to human health. By unraveling the molecular intricacies of these bacterial isolates, we aim to provide a foundation for informed interventions, advancing our ability to ensure the health and resilience of avian populations in the face of emerging microbial challenges.

METHOD

The investigation into avian health and the characterization of Sorbitol-Negative Escherichia coli (SNEC) isolates from quail involved a systematic and multi-step process. The study commenced with the meticulous collection of fecal samples from diverse quail populations, ensuring representation from both commercial and wild settings. The isolation of SNEC strains was performed using selective culture media, relying on the distinct sorbitol-negative fermentation

profile. The confirmation of Escherichia coli identity was accomplished through standard biochemical tests and molecular techniques, including PCR targeting E. coli-specific genes.

Following successful isolation, a comprehensive genetic characterization unfolded, involving the extraction of genomic DNA from the SNEC strains. This genetic exploration aimed to unveil virulence-associated genes, crucial for understanding the potential pathogenicity of these isolates. PCR amplification and subsequent DNA sequencing enabled the identification of specific virulence determinants within the SNEC strains, contributing to the genetic profiling of these potentially harmful variants.

The investigation extended to phenotypic analysis, evaluating traits linked to virulence such as hemolysis patterns, biofilm formation, and resistance profiles to commonly used antimicrobial agents in avian husbandry. This phenotypic exploration offered a holistic view of the isolates' potential to cause disease and provided valuable insights into the dynamic interactions between the SNEC strains and avian hosts.

To assess the practical implications of the isolated SNEC strains on avian health, challenge experiments were conducted on quail models. These experiments, involving controlled exposure to varying concentrations of the isolates, allowed for the observation of clinical parameters, morbidity, mortality rates, and pathological changes. The outcomes of these experiments were crucial for determining the virulence and pathogenicity of the SNEC strains, bridging the gap between laboratory findings and real-world implications for avian populations.

Finally, the entire process was underpinned by rigorous statistical analysis, employing chi-square tests and analysis of variance (ANOVA) to discern significant differences and associations within the dataset. This analytical approach added a quantitative dimension to the qualitative observations, providing a robust foundation for interpreting the results and drawing meaningful conclusions. Overall, the systematic and interdisciplinary nature of this process aimed to contribute valuable insights into avian health, paving the way for informed strategies in the management and prevention of potential threats posed by Sorbitol-Negative Escherichia coli isolates in quail.

Sample Collection:

Quail populations were carefully sampled from diverse geographic locations, encompassing both commercial and wild settings. Fecal samples were collected aseptically to isolate Sorbitol-Negative Escherichia coli (SNEC) strains for subsequent analysis. Rigorous sampling protocols were employed to ensure representative coverage of the quail populations under investigation.

Isolation and Identification of SNEC Strains:

Fecal samples were subjected to selective culture media to isolate SNEC strains based on their characteristic sorbitol-negative fermentation profile. Confirmation of Escherichia coli was achieved through standard biochemical tests and molecular techniques, including PCR targeting E. coli-specific genes.

Genetic Characterization:

Genomic DNA was extracted from the isolated SNEC strains, and a comprehensive genetic characterization was conducted. Virulence-associated genes, including those encoding for toxins and adhesion factors, were amplified using polymerase chain reaction (PCR). DNA

sequencing was employed to identify specific virulence determinants within the isolates.

Phenotypic Analysis:

Phenotypic traits related to virulence were assessed, including hemolysis patterns on blood agar, biofilm formation, and resistance profiles to antimicrobial agents commonly used in avian husbandry. These analyses aimed to provide a holistic understanding of the potential pathogenicity of the SNEC strains.

Pathogenicity Testing:

To assess the pathogenic potential of the isolated SNEC strains, challenge experiments were conducted on avian models. Quail were exposed to varying concentrations of the isolates, and clinical parameters, including morbidity, mortality, and pathological changes, were monitored. These experiments were crucial for determining the virulence and pathogenicity of the SNEC strains in the context of avian health.

Statistical Analysis:

Statistical methods, including chi-square tests and analysis of variance (ANOVA), were employed to evaluate the significance of differences observed in the various parameters studied. This statistical approach facilitated the interpretation of the data and the identification of key trends or associations.

This comprehensive methodology aimed to unravel the virulence factors of Sorbitol-Negative Escherichia coli isolates from quail, providing valuable insights into the potential threats to avian health. The combination of genetic, phenotypic, and pathogenic assessments contributed to a thorough understanding of the molecular attributes influencing the pathogenicity of these isolates.

RESULTS

The comprehensive investigation into Sorbitol-Negative Escherichia coli (SNEC) isolates from quail yielded insightful results regarding their virulence factors and molecular characteristics. Genetic characterization revealed the presence of specific virulence-associated genes within the SNEC strains, indicating their potential to induce pathogenicity. Phenotypic analysis demonstrated diverse traits related to virulence, including varying hemolysis patterns, biofilm formation capacities, and distinct antimicrobial resistance profiles.

In pathogenicity testing on avian models, challenge experiments exposed quail to different concentrations of the isolated SNEC strains. The outcomes demonstrated a range of clinical parameters, from morbidity and mortality rates to observable pathological changes. These results provided a nuanced understanding of the potential harm posed by SNEC isolates, highlighting the complex interplay between these bacteria and avian hosts.

DISCUSSION

The findings from this study underscore the significance of Sorbitol-Negative Escherichia coli in the context of avian health. The presence of virulence-associated genes and the observed phenotypic traits suggest an adaptive capability of these strains to thrive in the avian gastrointestinal environment and potentially cause harm. The diversity in antimicrobial resistance profiles is a concerning aspect, necessitating careful consideration in antibiotic stewardship practices within avian husbandry.

The variation in hemolysis patterns and biofilm formation capacities among the SNEC isolates emphasizes the heterogeneity within this group,

further complicating the understanding of their pathogenic potential. The challenge experiments provide valuable real-world insights, simulating potential scenarios in which these strains could impact quail populations. The observed morbidity and mortality rates, coupled with pathological changes, offer a comprehensive picture of the potential consequences of SNEC infection in avian hosts.

It is essential to discuss the zoonotic implications of these findings. The presence of virulence factors in SNEC strains raises concerns about their potential to affect not only avian health but also pose risks to human health. Understanding the dynamics of these strains within avian populations is crucial for developing strategies to mitigate potential zoonotic transmission.

CONCLUSION

In conclusion, this study provides crucial insights into avian health by characterizing the virulence factors of Sorbitol-Negative Escherichia coli isolates from quail. The genetic and phenotypic analyses shed light on the potential pathogenicity of these strains, emphasizing the need for continued surveillance and management strategies in avian populations. The challenge experiments bridge the gap between laboratory findings and real-world consequences, offering a holistic understanding of the impact of SNEC infection on quail health.

This research contributes to the broader field of avian health and microbial ecology, paving the way for targeted interventions to safeguard avian populations. The zoonotic implications underscore the importance of One Health approaches, recognizing the interconnectedness of animal, human, and environmental health. Moving forward, these findings will inform further studies and guide the development

of strategies to mitigate the potential threats posed by Sorbitol-Negative Escherichia coli in quail populations.

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