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Ornithobacteriosis in Poultry: Etiology, Epidemiology, Pathogenesis, Diagnosis, and Integrated Prevention Strategies

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Abstract

Purpose: This review was conducted to synthesize current national and international scientific literature on the etiology, epizootiology, pathogenesis, clinical manifestations, pathological changes, diagnostic approaches, and integrated prevention strategies for ornithobacteriosis, a bacterial respiratory disease of poultry caused by *Ornithobacterium rhinotracheale*, and to identify practical implications for commercial poultry production in transitional economies such as Uzbekistan.

Research methodology: A narrative literature review approach was applied, systematically searching peer reviewed veterinary and agricultural journals, institutional repositories, and conference proceedings published mainly between 2021 and 2026, supplemented by earlier foundational taxonomic sources where necessary for historical context.

Results: The disease predominantly affects the respiratory tract of chickens and turkeys, frequently occurs as part of a multifactorial respiratory complex, is associated with airsacculitis, pneumonia, and pleuritis, and causes substantial reductions in growth performance, feed efficiency, and egg production, with increasing reports of antimicrobial resistance among circulating isolates.

Conclusions: Effective control requires integration of biosecurity, rational antimicrobial use, and serotype informed vaccination rather than reliance on any single intervention.

Limitations: The review relies on secondary published sources and regional prevalence data that may not generalize across all production systems.

Contributions: The article consolidates dispersed evidence into a regionally relevant framework that can guide veterinary practitioners and policymakers in Central Asian poultry industries.

Keywords: *Biosecurity, Ornithobacteriosis, Ornithobacterium Rhinotracheale, Poultry Respiratory Disease, Vaccination*

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1. Introduction

Poultry production occupies a central place in global agriculture because it supplies affordable animal protein to a rapidly growing human population while requiring comparatively modest land and water

resources. The steady rise in demand for chicken meat, turkey meat, and table eggs has pushed producers toward increasingly intensive rearing systems, where thousands of birds are housed within a single shed under controlled but often crowded conditions. This intensification has undoubtedly improved productivity per unit area, yet it has also created an environment in which infectious respiratory diseases can spread with remarkable speed and severity (Yehia et al., 2023). Among the many pathogens that challenge the respiratory tract of commercial poultry, *Ornithobacterium rhinotracheale*, the causative agent of ornithobacteriosis, has emerged over the last three decades as one of the most economically damaging bacterial agents affecting chickens and turkeys worldwide.

Ornithobacteriosis is characterized by rhinotracheitis, tracheitis, airsacculitis, fibrinous pneumonia, and pleuritis, lesions that closely resemble those produced by several other avian respiratory pathogens, which makes the disease notoriously difficult to diagnose in the field without laboratory confirmation (Abd El-Ghany, 2021). The infection rarely occurs in isolation. It is instead commonly detected together with Newcastle disease virus, infectious bronchitis virus, avian metapneumovirus, Escherichia coli, and Mycoplasma gallisepticum, a pattern of co-infection that intensifies clinical severity and complicates both diagnosis and treatment (Liu et al., 2025; Salles et al., 2023). Flocks affected by ornithobacteriosis typically show depressed growth rates, poorer feed conversion, reduced hatchability, and a noticeable drop in egg production, all of which translate directly into financial losses for producers (Kursa et al., 2022). A regional review from Belarus similarly described ornithobacteriosis as a relatively new but rapidly consolidating respiratory disease within post-Soviet industrial poultry farming, recommending a coordinated package of veterinary and sanitary measures, immunity monitoring, and rational antibiotic use as the foundation for effective control (Gisko, 2022).

The geographic spread of *Ornithobacterium rhinotracheale* has been documented across Europe, Asia, Africa, and the Americas, and the organism has been recovered not only from commercial chickens and turkeys but also from ducks, geese, guinea fowl, pheasants, quails, ostriches, pigeons, gulls, and several other free living and captive avian species (Abd El-Ghany, 2021; Barbosa et al., 2020). This wide host range, combined with the ability of wild birds to act as silent reservoirs, means that even farms with reasonably good internal hygiene remain vulnerable to introduction of the pathogen from outside sources. The expansion of intensive poultry systems, elevated stocking densities, suboptimal ventilation, accumulation of ammonia within poultry houses, and various physiological stressors associated with modern production have all been identified as conditions that favor the establishment and spread of ornithobacteriosis within a flock (Zikibayeva et al., 2025).

Interest in ornithobacteriosis has grown substantially in recent years, in part because the organism has repeatedly demonstrated an ability to acquire resistance to commonly used antimicrobial agents, a trend that has been documented in turkey producing regions of Poland, Iran, and elsewhere (Blanda et al., 2026; Karim, 2022). Rising antimicrobial resistance narrows the therapeutic options available to veterinarians and increases reliance on preventive strategies such as biosecurity and vaccination. At the same time, serological surveys continue to reveal a high seroprevalence of *Ornithobacterium rhinotracheale* antibodies in both commercial and backyard flocks in several countries, indicating that exposure to the organism is widespread even where clinical disease is not always recognized (Rasheed et al., 2023).

The broader post-Soviet veterinary literature has long recognized that infectious disease prevention in intensive animal husbandry depends on a coordinated system of anti-epizootic measures rather than on curative treatment alone (Bakulin, 2006; Gulyukin, 2009). This principle applies with particular force to poultry respiratory disease, where the immune response of the flock, the intensity of vaccination programs, and the rational use of therapeutic agents together determine the practical success of any control strategy (Gulyukin & Stepanova, 2017; Krokhin et al., 2018).

In the Republic of Uzbekistan, as in several other countries of Central Asia, the poultry sector has expanded considerably over the past decade, driven by government programs supporting domestic meat and egg production and by growing consumer demand. Field veterinarians working in commercial poultry enterprises in this region have anecdotally reported respiratory disease patterns

consistent with ornithobacteriosis, yet systematic epidemiological data describing the true prevalence, serotype distribution, and economic burden of the disease within the country remain scarce. This gap in locally generated evidence limits the ability of veterinary authorities to design targeted vaccination programs or evidence based biosecurity guidelines suited to regional farming conditions.

Against this background, the present article undertakes a comprehensive review of the scientific literature on avian ornithobacteriosis, drawing on both classical foundational studies and more recent national and international research published mainly within the last five years. The review addresses the etiological agent and its taxonomy, the epizootiology and transmission routes of the disease, its clinical manifestations and pathological and anatomical changes, the diagnostic techniques currently available, and the therapeutic and preventive measures, including biosecurity practices and vaccination strategies, that have proven effective in reducing the impact of the disease. By consolidating this dispersed body of knowledge into a single, structured account, the article aims to provide veterinary practitioners, poultry producers, and policymakers, particularly those working in Central Asian production systems, with a practical foundation for improving the diagnosis, prevention, and control of ornithobacteriosis.

2. Literature Review

2.1 Etiology and Taxonomic Characteristics

Ornithobacterium rhinotracheale is a Gram-negative, pleomorphic, non-motile rod-shaped bacterium belonging to the phylum Bacteroidota, within the Cytophaga-Flavobacterium-Bacteroides group. The organism was first isolated from turkeys with respiratory disease in Germany in 1981, at which point it was tentatively classified as a Pasteurella-like bacterium because of superficial phenotypic similarities to members of that genus (Vandamme et al., 1994). A more detailed morphological and biochemical description followed in 1991, and in 1994 the organism was formally established as a new genus and species, *Ornithobacterium rhinotracheale*, based on comprehensive polyphasic taxonomic analysis (Vandamme et al., 1994). An earlier North American case series had already characterized a similar pleomorphic Gram-negative rod associated with avian respiratory disease before the formal taxonomic description was published, illustrating that the organism was independently recognized in more than one region prior to full resolution of its identity (Charlton et al., 1993). Genetic studies have since confirmed that all known strains of the organism are closely related to one another and that the genus is phylogenetically situated near Riemerella, Flavobacterium, Cytophaga, and related genera within the same bacterial lineage, a classification now summarized in standard veterinary reference texts (Chin et al., 2013).

Biochemically, *Ornithobacterium rhinotracheale* is oxidase positive, catalase negative, and indole negative, and the majority of isolates are urease positive and beta-galactosidase positive. The bacterium does not produce hemolysis on sheep blood agar and does not grow on MacConkey agar, features that assist in distinguishing it from several other Gram-negative respiratory pathogens of poultry. Cultivation is technically demanding because the organism grows slowly and has fastidious nutritional requirements. Optimal growth is achieved on blood agar enriched to approximately 0.5 percent and incubated at 37 degrees Celsius under aerobic, microaerophilic, or anaerobic conditions for 48 to 72 hours. Because contaminating flora can easily overgrow the slow-growing target organism, selective media supplemented with gentamicin and polymyxin are frequently used in diagnostic laboratories. Under these conditions, small non-pigmented pinpoint colonies typically become visible after approximately 24 hours, developing after 48 hours into small, round, smooth, grayish-white to white colonies, occasionally surrounded by a faint reddish halo and emitting a characteristic odor reminiscent of volatile fatty acids. Under prolonged or suboptimal culture conditions, small-colony variants of the organism have also been described, displaying atypical morphology and reduced growth rate that can further complicate laboratory identification (Zahra et al., 2013).

Serological classification of *Ornithobacterium rhinotracheale* has identified twelve recognized serotypes, designated A through L, based on differences in surface antigen composition. Large scale serotyping surveys involving isolates collected from chickens and turkeys in multiple countries have consistently found that serotype A predominates among chicken derived isolates, accounting for

roughly ninety five percent of strains recovered from that host species, whereas turkey derived isolates display considerably greater serotype diversity and are distributed more evenly across several serotypes, most commonly A, B, D, and E, which together account for the great majority of turkey isolates (Blanda et al., 2026). A recent Polish study examining more than seven hundred isolates collected from turkeys between 2016 and 2022 similarly found that serotype diversity remained an important epidemiological feature, with one particular serotype accounting for close to thirty percent of the tested strains, underscoring that serotype distribution can vary meaningfully by country and by host species (Blanda et al., 2026).

Considerable phenotypic and genotypic differences in virulence have been documented among *Ornithobacterium rhinotracheale* isolates. Interestingly, neither the geographic origin of an isolate nor its assigned serotype appears to correlate reliably with pathogenicity, meaning that virulence must ultimately be assessed empirically for individual strains rather than inferred from serotype alone. This variability has direct practical implications for vaccine development, because a vaccine formulated against one serotype or strain may provide incomplete cross protection against a genetically divergent field strain circulating in a different region, a consideration that has motivated calls for locally adapted vaccine antigens in countries such as Uzbekistan where the circulating strain profile has not yet been comprehensively characterized.

2.2 Epizootiology, Host Range, and Transmission

Ornithobacteriosis has now been reported from commercial poultry operations on every inhabited continent, and the organism has been isolated not only from domesticated chickens and turkeys but also from a remarkably broad range of other avian species, including ducks, geese, guinea fowl, ostriches, partridges, pheasants, pigeons, quails, gulls, and corvids (Abd El-Ghany, 2021). Many of these non-gallinaceous species can harbor the bacterium in the respiratory tract without displaying overt clinical signs, effectively acting as asymptomatic carriers, a pattern first described in detail in one of the earliest comprehensive reviews of the organism. Despite its broad host range and clear economic importance, ornithobacteriosis is not classified as a zoonotic disease, and international trade risk assessments of poultry meat have not identified *Ornithobacterium rhinotracheale* as posing a direct hazard to human health, in contrast with several other non-OIE-listed avian pathogens that receive comparable trade scrutiny (Cobb & Smith, 2015). This characteristic is epidemiologically significant because it means that wild bird populations surrounding a commercial farm can function as a persistent environmental reservoir from which the pathogen may periodically spill over into domestic flocks, particularly where free range or semi-intensive husbandry systems allow direct or indirect contact between wild and farmed birds (Zikibayeva et al., 2025).

Transmission of *Ornithobacterium rhinotracheale* occurs principally through direct contact between infected and susceptible birds and through aerosolized respiratory secretions, a route consistent with the organism's predilection for the upper and lower respiratory tract. Experimental studies have additionally demonstrated that intratracheal and intravenous inoculation can reliably reproduce infection under laboratory conditions, confirming the respiratory and systemic tropism of the organism. Vertical transmission through the egg has also been suggested by several investigators, although the precise mechanism, whether through infection of the ovary and oviduct or through bacterial penetration of eggshell pores during or after lay, remains incompletely resolved. Supporting evidence for vertical transmission comes from experimental work in breeder turkey hens, in which *Ornithobacterium rhinotracheale* was shown to persist within the ovaries and oviduct without producing overt clinical disease, raising the possibility that subclinically infected breeders could seed infection in their progeny (Abd El-Ghany, 2021).

Maternally derived antibodies against *Ornithobacterium rhinotracheale* have been detected in hatching eggs and in day old chicks originating from seropositive breeder flocks, indicating that passive immunity is transferred from hen to offspring in a manner broadly analogous to other avian pathogens. While such maternal antibodies may afford some early protection, their titers decline over the first weeks of life, potentially leaving young birds susceptible during a critical developmental window that often coincides with peak exposure risk in commercial rearing houses.

Environmental and managerial factors play a substantial role in determining whether exposure to *Ornithobacterium rhinotracheale* progresses to clinical disease. High stocking density, inadequate ventilation, elevated ammonia concentrations within poultry houses, abrupt changes in temperature, and various nutritional or transport related stressors have each been implicated as predisposing conditions that compromise mucosal defenses and increase susceptibility to infection (Azhmuldinov et al., 2018; Zikibayeva et al., 2025). A space-time analysis of turkey pathogen distribution in the United States likewise found that *Ornithobacterium rhinotracheale* detections clustered geographically alongside Pasteurella multocida detections, suggesting that shared environmental and management risk factors operate across production regions rather than being confined to any single farm (Campler et al., 2023). A cross-sectional epidemiological investigation of poultry infectious diseases conducted in Kazakhstan between 2021 and 2024 similarly identified dense farm populations and gaps in vaccination coverage as recurring risk factors associated with outbreaks of major respiratory pathogens in the region, a pattern that likely applies with equal force to neighboring Central Asian countries including Uzbekistan (Zikibayeva et al., 2025).

Clinically, ornithobacteriosis in laying hens is most frequently observed during the peak production period, typically between approximately twenty four and fifty two weeks of age, when metabolic demand is highest and the reproductive tract is under the greatest physiological strain. Outbreaks during this window are commonly accompanied by a measurable decline in egg production, a reduction in egg size, and deterioration in eggshell quality, although the magnitude of these effects varies considerably between flocks, and some field outbreaks have produced only minimal measurable impact on overall productivity and hatchability, underscoring the influence of concurrent infections, management quality, and host immune status on clinical outcome.

2.3 Clinical Signs and Pathological Findings

The clinical presentation of ornithobacteriosis varies according to host age, concurrent infections, and management conditions, but several features recur consistently across published case reports and field investigations. Affected birds commonly show depression, reduced appetite, decreased weight gain, nasal discharge, sneezing, and facial or infraorbital sinus swelling. In young growing poultry, the disease manifests primarily as an inflammatory condition of the respiratory tract, with pneumonia frequently accompanied by coughing, rhinitis, conjunctivitis, sinusitis, and, in more advanced cases, blood tinged respiratory exudate. As the infection progresses, birds typically develop ruffled feathers, dyspnea, lethargy, and reduced feed and water intake. In severe or advanced cases, the infection can extend beyond the respiratory tract to involve the central nervous system, producing encephalitic signs and, occasionally, sudden death (Rozhdestvenskaya et al., 2020).

At necropsy, the hallmark lesions of ornithobacteriosis include unilateral or bilateral airsacculitis, characterized by thickened, opaque air sac membranes containing a foamy, caseous, or yoghurt-like exudate, together with fibrinous pneumonia and pleuritis (Abd El-Ghany, 2021). These lesions are frequently most pronounced in the caudal thoracic and abdominal air sacs, though the precise distribution can vary between outbreaks. In layer flocks, additional pathological changes may include salpingitis and, in severe systemic cases, involvement of the joints, presenting as a purulent or fibrinous arthritis with associated lameness. The severity and distribution of gross lesions generally correlate with the presence of concurrent viral or bacterial pathogens, since ornithobacteriosis rarely behaves as a purely primary pathogen under commercial field conditions and instead most often develops as part of a multifactorial respiratory disease complex.

Histopathological examination of affected respiratory tissues typically reveals heterophilic and lymphocytic infiltration of the tracheal and bronchial mucosa, epithelial hyperplasia, and, in the lungs, areas of fibrinopurulent bronchopneumonia with necrotic foci. Microscopic lesions in the air sacs often demonstrate a thickened, fibrinocellular exudate covering a hyperplastic mesothelial lining, consistent with the gross appearance of airsacculitis described above. Because these microscopic and macroscopic changes overlap considerably with those produced by Escherichia coli, Mycoplasma gallisepticum, avian metapneumovirus, and other respiratory pathogens, pathological examination alone cannot provide a definitive etiological diagnosis and must be interpreted alongside epizootiological data, clinical history, and laboratory confirmation. A regional serosurvey examining antibodies against avian metapneumovirus, *Ornithobacterium rhinotracheale*, and Chlamydia psittaci

in commercial flocks similarly found a statistically meaningful association between exposure to more than one of these agents and the occurrence of airsacculitis, reinforcing that gross and microscopic air sac lesions are best interpreted as the product of combined rather than single pathogen exposure (Zuo et al., 2018).

2.4 Laboratory Diagnosis

Definitive diagnosis of ornithobacteriosis requires laboratory confirmation, typically involving bacterial isolation, biochemical characterization, and, increasingly, molecular or serological testing. For bacteriological examination, specimens should ideally be collected during the early stages of clinical disease, since the organism is more readily recovered before secondary bacterial overgrowth or antibiotic administration reduces its detectability. Appropriate diagnostic specimens include blood serum, pericardial exudate, air sac exudate, infraorbital sinus contents, nasal discharge, and tracheal swabs, with additional samples such as brain, ovary, oviduct, spleen, and joint fluid recommended in laying hens or in birds displaying systemic signs.

Cultivation on blood agar supplemented with gentamicin, typically at a concentration in the range of five to ten micrograms per cubic centimeter, allows selective recovery of *Ornithobacterium rhinotracheale* from mixed respiratory flora, yielding the small pleomorphic rod-shaped colonies described in the preceding section, generally measuring approximately one to three micrometers in length. Because cultivation is slow and requires specialized media, many diagnostic laboratories have adopted molecular methods, particularly polymerase chain reaction assays targeting the sixteen S ribosomal ribonucleic acid gene, as a faster and more sensitive alternative or complement to culture (Karim, 2022). Polymerase chain reaction based approaches have also been used successfully to characterize the genetic relatedness of field isolates through techniques such as enterobacterial repetitive intergenic consensus polymerase chain reaction and randomly amplified polymorphic deoxyribonucleic acid analysis, both of which have demonstrated the ability to differentiate isolate clusters within a given geographic region (Karim, 2022). Similar molecular confirmation approaches, amplifying a defined fragment of the sixteen S ribosomal ribonucleic acid gene directly from clinical tissue, have been applied successfully in turkey flocks in Iran, further supporting the reliability of this diagnostic target across different national contexts (Doosti et al., 2011).

Serological methods, most commonly the enzyme linked immunosorbent assay, are widely used for flock level surveillance because they allow rapid, relatively inexpensive screening of large numbers of birds and can detect prior exposure even when the organism itself is no longer culturable. A recent investigation conducted in broiler flocks in Mosul, Iraq, used indirect enzyme linked immunosorbent assay testing on serum samples collected from multiple small scale farms and confirmed that antibodies against *Ornithobacterium rhinotracheale* were present at meaningful prevalence, illustrating the practical value of serological surveillance for regional epidemiological assessment (Rasheed et al., 2023). Serological testing does, however, have important limitations, since maternally derived antibodies, prior vaccination, and cross reactivity with related organisms can all complicate the interpretation of results, meaning that a positive serological finding should generally be corroborated with clinical, pathological, or molecular evidence before a definitive flock diagnosis is made.

Table 1. Principal laboratory diagnostic methods used for Ornithobacterium rhinotracheale, their typical specimens, main advantages, and main limitations

Diagnostic method	Typical specimen	Main advantage	Main limitation
Bacterial culture on enriched blood agar	Tracheal swab, air sac exudate, sinus content	Confirms viable organism, enables susceptibility testing	Slow growth, 48 to 72 hours, requires selective antibiotics in media
Polymerase chain reaction targeting 16S rRNA	Tracheal or sinus swab, tissue homogenate	Rapid, highly sensitive and specific	Requires molecular laboratory infrastructure

Diagnostic method	Typical specimen	Main advantage	Main limitation
Enzyme linked immunosorbent assay	Serum	Suitable for large scale flock screening	Cannot distinguish active infection from past exposure or vaccination
Histopathology	Trachea, lung, air sac tissue	Documents lesion severity and distribution	Not organism specific, overlaps with other respiratory pathogens

Table 1 summarizes the principal laboratory methods currently used for the diagnosis of *Ornithobacterium rhinotracheale* infection, together with their main advantages and limitations. As shown in the table, no single diagnostic method is sufficient on its own. Bacterial culture remains the reference standard for definitive identification and for subsequent antimicrobial susceptibility testing, but its slow turnaround time and fastidious growth requirements limit its usefulness for rapid on farm decision making. Molecular methods offer speed and high sensitivity but require specialized equipment and reagents that may not be readily available in all veterinary diagnostic laboratories, particularly in resource limited settings. Serological testing is well suited to large scale flock screening and retrospective exposure assessment but cannot reliably distinguish active infection from past exposure or vaccination. In practice, an integrated diagnostic approach that combines epizootiological investigation, clinical examination, pathological assessment, and at least one confirmatory laboratory method is recommended for reliable diagnosis of ornithobacteriosis under field conditions.

2.5 Immunological Aspects and Host Response

The host immune response to *Ornithobacterium rhinotracheale* infection involves both innate and adaptive components, although the precise mechanisms by which the organism evades early clearance remain incompletely understood compared with better characterized avian pathogens such as Mycoplasma gallisepticum or Newcastle disease virus. Following mucosal colonization, local heterophil and macrophage recruitment produces the characteristic inflammatory exudate observed in air sacs and lung tissue, while systemic spread in more severe cases appears to depend on the ability of the organism to survive within phagocytic cells long enough to disseminate hematogenously to distant sites such as joints and the central nervous system. Humoral antibody responses, detectable by enzyme linked immunosorbent assay within one to two weeks of exposure, appear to correlate with reduced clinical severity upon re-exposure, which provides part of the rationale underlying current vaccination strategies, yet antibody titers alone do not fully explain observed differences in protection between vaccinated and naturally exposed birds, suggesting that cell mediated immune mechanisms also contribute meaningfully to protective immunity. A more complete understanding of these immunological pathways would likely support the rational design of next generation vaccines with improved cross-serotype protection.

3. Research Methodology

This article follows a narrative literature review design, an approach commonly used in veterinary and agricultural science when the objective is to synthesize a broad and heterogeneous body of evidence on a single disease entity rather than to answer a narrowly defined quantitative research question. The review does not attempt a formal systematic review with pre-registered inclusion criteria, since the epidemiological and diagnostic literature on *Ornithobacterium rhinotracheale* spans several decades, multiple languages, and a wide variety of study designs that would not be readily comparable within a strict meta-analytic framework.

The literature search was conducted across several bibliographic sources, including international indexing platforms and open access repositories, national veterinary science journals from the Russian Federation, Turkey, Iran, Iraq, Poland, Indonesia, and other countries, as well as institutional repositories maintained by research institutes and universities. Search terms combined the keywords *Ornithobacterium rhinotracheale*, ornithobacteriosis, avian respiratory disease, poultry airsacculitis, and poultry biosecurity, applied individually and in combination. Priority was given to peer reviewed journal articles carrying an active digital object identifier and published between 2021 and 2026, in keeping with the objective of reflecting the most current understanding of the disease. A smaller

proportion of earlier, historically important publications, including the original taxonomic description of the genus Ornithobacterium and early clinical case reports, were retained where they provided essential background that has not been superseded by more recent work.

Screening of retrieved records proceeded in two stages. During the first stage, titles and abstracts were examined to exclude publications that, despite matching the search terms, addressed unrelated topics or lacked sufficient methodological detail to be informative. During the second stage, the full text of the remaining articles was read in order to extract information relevant to six thematic categories: etiology and taxonomy, epizootiology and transmission, clinical signs, pathological and anatomical findings, diagnostic methods, and prevention and control, including treatment and vaccination. Data extracted under each theme were then organized narratively, with particular attention paid to areas of consensus across studies as well as to conflicting findings that merited further discussion.

In addition to the core veterinary and epizootiological literature, the review also drew selectively on the broader regional open access agricultural and animal science literature in order to contextualize the production conditions typical of developing and transitional economies, where biosecurity infrastructure and diagnostic capacity often differ substantially from those available in high income poultry producing countries. Examples of this supplementary literature include studies of reproductive performance in smallholder livestock systems (Getso et al., 2021), physiological and toxicological research methods applicable to animal husbandry (Tama et al., 2023), and analyses of agricultural production constraints in similarly structured developing economies (Indaryati et al., 2026), all of which helped frame the discussion of feasible, locally appropriate control measures presented later in this article.

Because the review synthesizes previously published data rather than generating new primary data, no laboratory procedures, animal experiments, or statistical hypothesis testing were performed by the author. All quantitative figures reported in the following sections, such as isolation rates, serotype proportions, and antimicrobial susceptibility percentages, are drawn directly from the cited primary studies and are presented here for descriptive and comparative purposes only. Readers seeking the original experimental protocols underlying these figures are encouraged to consult the primary sources cited throughout the text.

4. Results and Discussions

4.1 Differential Diagnosis and the Multifactorial Respiratory Disease Complex

One of the most consistent themes emerging from the reviewed literature is that ornithobacteriosis rarely presents as a clinically isolated infection under commercial field conditions. Instead, it typically forms part of what is often described as the avian respiratory disease complex, a syndrome in which multiple viral and bacterial agents interact to produce a clinical picture more severe than that caused by any single pathogen alone (Yehia et al., 2023). Newcastle disease virus, infectious bronchitis virus, avian metapneumovirus, Escherichia coli, and Mycoplasma gallisepticum are the agents most frequently implicated alongside *Ornithobacterium rhinotracheale*, and their combined effects on ciliary function, mucosal integrity, and local immune competence appear to create favorable conditions for secondary bacterial colonization (Salles et al., 2023). Avian metapneumovirus in particular damages the ciliated respiratory epithelium during the acute phase of infection, a mechanism that has been proposed as a key enabling step for subsequent bacterial invasion by *Ornithobacterium rhinotracheale* and other secondary invaders in turkeys (Kaboudi & Lachheb, 2021).

This overlapping etiology has direct practical consequences for differential diagnosis. Clinical signs such as nasal discharge, sneezing, conjunctivitis, and depressed production, along with gross lesions such as airsacculitis and fibrinous pneumonia, are shared across most of the pathogens mentioned above, meaning that clinical examination and necropsy alone cannot reliably distinguish ornithobacteriosis from infections caused by avian metapneumovirus, Escherichia coli, or Mycoplasma gallisepticum (Liu et al., 2025). A recent comprehensive review of poultry respiratory syndromes emphasized that accurate differentiation among these overlapping conditions increasingly depends on a combination of molecular detection technologies and careful epizootiological reasoning rather than on gross pathology alone (Liu et al., 2025). Similarly, a systematic examination of avian

metapneumovirus surveillance in non-vaccinated Brazilian broiler flocks documented substantial co-infection rates with avian pathogenic Escherichia coli, reinforcing the general principle that respiratory pathogens in commercial poultry rarely act in isolation and that diagnostic workups should routinely screen for multiple agents rather than assuming a single etiological explanation (Salles et al., 2023).

The practical implication of this multifactorial pattern is that veterinary practitioners investigating a respiratory disease outbreak in a poultry flock should adopt a panel based diagnostic strategy, testing simultaneously for the principal viral and bacterial candidates rather than pursuing a single suspected pathogen sequentially. Such an approach not only shortens the time to an accurate diagnosis but also better informs treatment and vaccination decisions, since the presence of concurrent infections may substantially alter both the choice of antimicrobial therapy and the expected response to a vaccination program targeting *Ornithobacterium rhinotracheale* alone.

4.2 Antimicrobial Therapy and the Growing Challenge of Resistance

Historically, antimicrobial therapy has served as a mainstay of ornithobacteriosis control in affected flocks, with tetracyclines, florfenicol, and certain beta-lactam agents generally reported as effective against susceptible strains. However, an increasing body of recent evidence indicates that antimicrobial resistance among *Ornithobacterium rhinotracheale* isolates is becoming a significant and growing problem. A study examining more than seven hundred isolates collected from turkeys in Poland between 2016 and 2022 found that, while amoxicillin combined with clavulanic acid, doxycycline, florfenicol, and lincomycin combined with spectinomycin remained the most effective agents overall, resistance patterns nonetheless varied by serotype and by year, underscoring the dynamic nature of antimicrobial susceptibility in this organism (Blanda et al., 2026). Comparable findings have been reported from broiler flocks in Khuzestan Province, Iran, where isolates displayed high resistance rates to several commonly used antimicrobials, with susceptibility largely confined to a narrower set of agents such as tetracycline, florfenicol, and cephalexin.

This trend toward reduced antimicrobial susceptibility mirrors a broader pattern documented across the poultry sector more generally. A recent review examining antibiotic resistance in poultry from a One Health perspective concluded that historical overuse of antimicrobials for both disease prevention and growth promotion has substantially accelerated the emergence of resistant bacterial populations, with implications that extend beyond animal health to encompass human and environmental health as well (Sana et al., 2025). The same review highlighted probiotics, prebiotics, enzymes, and essential oils as viable, evidence supported alternatives capable of reducing reliance on antimicrobial agents while maintaining flock productivity, a direction that appears equally relevant for the future management of ornithobacteriosis (Sana et al., 2025).

In light of these resistance trends, several authors have argued that antimicrobial therapy should be viewed as a supportive rather than a stand-alone control measure for ornithobacteriosis, to be guided wherever possible by laboratory determined susceptibility results rather than empirical selection, and to be combined systematically with non-antimicrobial preventive strategies such as biosecurity and vaccination (Ghodsian et al., 2024). This shift in emphasis reflects a broader recognition within veterinary medicine that sustainable long-term disease control cannot rely indefinitely on antimicrobial treatment alone, particularly for an organism that has already demonstrated a capacity to acquire multidrug resistance across geographically distinct populations.

4.3 Biosecurity and Environmental Management

Given the limitations of antimicrobial therapy and the wide host range of *Ornithobacterium rhinotracheale*, biosecurity has assumed an increasingly central role in disease prevention strategies. Biosecurity in poultry production encompasses a coordinated set of practices including cleaning and disinfection between production cycles, control of personnel and vehicle movement onto and off the farm, pest and rodent control, appropriate carcass disposal, and restriction of contact between commercial flocks and wild or free-roaming birds. A recent systematic review focused on colibacillosis prevention in broiler production concluded that consistently applied biosecurity measures meaningfully reduced the incidence of Escherichia coli associated respiratory disease, a

finding with clear relevance to ornithobacteriosis given the frequent co-occurrence of the two infections and their shared environmental risk factors (Tilli et al., 2024).

Environmental management within the poultry house itself is equally important. Maintaining adequate ventilation to control ammonia buildup, avoiding excessive stocking density, and ensuring appropriate litter management all help preserve the integrity of the respiratory mucosa, which serves as the primary physical barrier against colonization by *Ornithobacterium rhinotracheale* and other respiratory pathogens. Field observations from backyard and small-scale commercial operations, where biosecurity infrastructure is often minimal, have consistently documented substantially higher seroprevalence of *Ornithobacterium rhinotracheale* compared with well managed commercial operations, providing indirect but compelling evidence for the protective value of rigorous biosecurity practice.

Disinfection protocols have also received specific research attention. Laboratory testing has demonstrated that *Ornithobacterium rhinotracheale* is susceptible to a range of chemical disinfectants, including organic acids such as formic and glyoxylic acid, as well as aldehyde based products. Complete inactivation of the organism has been achieved following approximately fifteen minutes of exposure to a zero point five percent solution containing formic and glyoxylic acids, or to a twenty percent glutaraldehyde based disinfectant, providing practical guidance for terminal cleaning and disinfection procedures between successive flocks (Hafez & Schulze, 2003). Consistent application of such protocols during the down time between production cycles represents a relatively low cost, high value component of an integrated biosecurity program. Russian language veterinary literature addressing bacterial poultry diseases more broadly has similarly emphasized that a farm level system for ensuring epizootic safety, combining sanitation, monitoring, and coordinated vaccination, is more effective than any single disinfection or treatment measure applied in isolation (Pankratov et al., 2021; Ruzina & Pankratov, 2022).

4.4 Vaccination and Emerging Control Technologies

Vaccination remains one of the most promising long-term tools for reducing the impact of ornithobacteriosis, particularly in regions where antimicrobial resistance and biosecurity infrastructure limitations constrain other control options. Inactivated, oil adjuvanted bacterin vaccines have been the predominant vaccine type evaluated to date. A recent study conducted in Iran developed a formalin inactivated bacterin formulated with an oil adjuvant, based on a locally isolated strain of *Ornithobacterium rhinotracheale*, and reported a favorable immunogenic response in specific pathogen free chickens, supporting the feasibility of locally tailored vaccine development in regions with distinct circulating strains (Ghodsian et al., 2024). Earlier work using a similarly formulated inactivated vaccine and an experimental challenge system based on the LaSota strain likewise demonstrated measurable protective efficacy, reinforcing the general principle that inactivated whole cell vaccines can provide meaningful protection when matched appropriately to locally circulating serotypes.

Because serotype diversity, particularly among turkey isolates, can limit the cross protective efficacy of a single vaccine formulation, several authors have emphasized the importance of selecting vaccine antigens based on locally generated serotyping and molecular characterization data rather than relying exclusively on commercially available products developed against strains circulating elsewhere. This consideration is particularly relevant for Uzbekistan and neighboring Central Asian countries, where comprehensive serotype surveillance of circulating *Ornithobacterium rhinotracheale* strains has not yet been undertaken, and where locally adapted vaccine development, informed by regional isolate characterization, could substantially improve the practical effectiveness of vaccination programs.

Beyond traditional inactivated bacterin vaccines, broader technological developments in poultry vaccinology offer additional avenues that may eventually be applied to ornithobacteriosis control. Virus like particle platforms, for example, have been reviewed as a safer and more targeted alternative to traditional live attenuated vaccines for several avian viral pathogens, offering enhanced immunogenicity without the replication risks associated with live vaccines (Raji et al., 2024). Although virus like particle technology has so far been applied predominantly to viral rather than bacterial poultry pathogens, the broader principle of pursuing subunit or particle based antigen

delivery systems represents a potentially valuable direction for future *Ornithobacterium rhinotracheale* vaccine research, particularly given the practical and regulatory challenges associated with traditional whole cell bacterin production.

Whatever vaccine platform is ultimately selected, effective implementation requires attention to vaccination timing, dosing schedule, and route of administration, since these factors substantially influence the magnitude and duration of the resulting immune response. Breeder flock vaccination strategies designed to confer passive protection to offspring through maternally derived antibodies have shown particular promise, since young birds are often most vulnerable to ornithobacteriosis during the early weeks of life before their own active immune response has fully matured, a principle that parallels broader recommendations for bacterial vaccine deployment across the poultry sector as a whole (Rabie & Amin Girh, 2020).

4.5 Economic Impact and Regional Considerations for Uzbekistan

The cumulative economic burden of ornithobacteriosis arises from several interacting sources, including direct mortality, reduced weight gain and feed conversion efficiency in growing birds, decreased egg production and quality in layers, increased veterinary and antimicrobial treatment costs, and, in severe outbreaks, carcass condemnation at processing. Although comprehensive economic assessments specific to *Ornithobacterium rhinotracheale* remain relatively scarce in the published literature, broader analyses of respiratory disease losses in the poultry sector consistently identify these categories as the principal drivers of financial impact, and there is no reason to expect that ornithobacteriosis would differ substantially from this general pattern (Yehia et al., 2023).

For Uzbekistan specifically, the absence of systematically collected national prevalence and economic loss data represents an important gap that limits the ability of veterinary authorities and industry stakeholders to prioritize resources appropriately. Field level observations and practical experience reported by veterinary specialists working within the domestic poultry industry suggest that ornithobacteriosis is already recognized as an emerging challenge for commercial production, yet without dedicated epidemiological surveys it remains difficult to quantify the true scale of the problem or to track trends over time. Establishing a coordinated national surveillance program, potentially modeled on the cross-sectional epidemiological investigations recently conducted in neighboring Kazakhstan, would provide the evidence base needed to guide targeted interventions (Zikibayeva et al., 2025). Experience from public-private partnership models applied to veterinary disease control in the Ethiopian poultry sector suggests that combining government surveillance capacity with private sector diagnostic and distribution networks can accelerate the practical reach of disease control programs in resource constrained settings, an approach that may hold similar promise for strengthening ornithobacteriosis surveillance and vaccine distribution in Uzbekistan.

Given the interconnected regional poultry trade networks across Central Asia, and the demonstrated ability of *Ornithobacterium rhinotracheale* to spread across national borders through both commercial movement of birds and wild bird reservoirs, regional cooperation in surveillance and diagnostic capacity building would likely yield benefits beyond what any single country could achieve independently. Investment in local diagnostic laboratory capacity, including molecular detection methods, would additionally reduce reliance on sample transport to distant reference laboratories, shortening the time to diagnosis and enabling more timely implementation of control measures during active outbreaks.

5. Conclusions

5.1 Conclusion

Ornithobacteriosis, caused by *Ornithobacterium rhinotracheale*, remains one of the most economically important bacterial respiratory diseases affecting commercial poultry production worldwide. The organism possesses a broad host range spanning both domestic and wild avian species, spreads efficiently through direct contact and aerosolized secretions, and most often manifests clinically as part of a multifactorial respiratory disease complex in combination with viral and other bacterial pathogens rather than as an isolated infection. The resulting airsacculitis, pneumonia, and pleuritis translate into measurable reductions in growth performance, feed efficiency, and egg production, generating substantial financial losses for producers. Diagnosis requires an integrated

approach combining epizootiological assessment, clinical observation, pathological examination, and laboratory confirmation through bacterial culture, molecular detection, or serological testing, since no single method is sufficient in isolation. Rising antimicrobial resistance among circulating strains has progressively narrowed therapeutic options, elevating the relative importance of preventive strategies. Effective long-term control depends on the coordinated application of rigorous biosecurity practices, judicious and susceptibility guided antimicrobial use, and vaccination programs informed by locally relevant serotype and strain data, rather than reliance on any single intervention applied in isolation.

5.2 Research Limitations

This review is subject to several limitations that should be acknowledged. First, as a narrative rather than a systematic review, the selection and synthesis of source material, while conducted carefully and transparently, inevitably carries a degree of interpretive judgment that a fully systematic protocol with independent dual screening would reduce. Second, much of the quantitative evidence cited throughout the review, including prevalence estimates, serotype distributions, and antimicrobial susceptibility figures, originates from studies conducted in specific countries and production systems, and these findings may not generalize reliably to other regions with different climatic conditions, husbandry practices, or genetic backgrounds of both host birds and circulating bacterial strains. Third, the review was unable to draw upon dedicated primary epidemiological data from Uzbekistan itself, since no comprehensive national surveillance study of *Ornithobacterium rhinotracheale* has yet been published, meaning that the regional discussion presented here is necessarily inferential rather than empirically confirmed for the local context. Finally, because the field continues to evolve rapidly, particularly with respect to molecular diagnostics and emerging vaccine technologies, some of the information synthesized here may require updating as new primary research becomes available in the near future.

5.3 Suggestions and Directions for Future Study

Building on the limitations identified above, several directions for future research appear particularly promising. There is a clear need for dedicated epidemiological surveys within Uzbekistan and neighboring Central Asian countries to establish baseline prevalence, serotype distribution, and antimicrobial susceptibility profiles of *Ornithobacterium rhinotracheale* under regional production conditions, using standardized sampling and laboratory protocols that would allow meaningful comparison with data from other countries. Such surveillance should ideally be paired with economic impact assessment, allowing policymakers to quantify the true cost of the disease and to allocate control resources accordingly. Further research is also warranted into the development of locally adapted vaccine candidates formulated against regionally circulating strains, building on the promising methodology demonstrated in recent inactivated bacterin studies. Future work should additionally explore alternative and complementary control strategies, including probiotics, prebiotics, and other antimicrobial sparing interventions, as tools for reducing reliance on conventional antibiotics in the face of rising resistance. Finally, continued investment in accessible molecular diagnostic capacity within regional veterinary laboratories would support more rapid and accurate differentiation of *Ornithobacterium rhinotracheale* from the other pathogens that commonly co-circulate within the avian respiratory disease complex, ultimately supporting more timely and effective disease control decisions at the farm level.

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