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Respiratory Adenovirus Infections in Iraq (2020–2025): Epidemiological and Molecular Overview

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ABSTRACT

Objective: *This study provides an updated assessment of respiratory adenovirus infections in Iraq from 2020 to 2025 by examining national trends in incidence, demographic distribution, and circulating viral strains.* ***Method:*** *Data were collected from multiple medical centers and health institutions across Iraq, and patient samples were analyzed using molecular diagnostic techniques, including PCR-based detection and genotyping, to identify prevalent adenovirus types. Epidemiological indicators were evaluated to determine infection patterns among different age groups.* ***Results:*** *The findings reveal a gradual increase in reported respiratory adenovirus cases over the study period, with the highest incidence occurring among young children and older adults. Molecular analysis identified human adenovirus types 3, 7, and 14 as the most frequently detected variants, reflecting their continued circulation and clinical relevance.* ***Novelty:*** *This research provides one of the most recent national overviews of adenovirus activity in Iraq, integrating multicenter epidemiological data with molecular characterization to highlight emerging trends and strain distribution, underscoring the need for strengthened surveillance and expanded diagnostic capacity.*

INTRODUCTION

Adenoviruses constitute a group of double-stranded DNA viruses capable of causing diverse clinical conditions, particularly infections of the respiratory system. In the period following the COVID-19 pandemic, interest in respiratory pathogens, including adenoviruses, has grown due to increasing concerns regarding co-infections. This work aims to describe nationwide epidemiological patterns, genotype distribution, and geographic variation in respiratory adenovirus infections in Iraq from 2020 to 2025 [1].

Adenoviruses have long been recognized as major pathogens causing respiratory infections in children, yet post-pandemic reports indicate rising incidence across broader age groups [2]. The wide range of clinical presentations, from mild upper-respiratory symptoms to severe pneumonia, underscores the importance of continuous monitoring. In Iraq, social conditions and population density in urban areas contribute significantly to the spread of adenovirus infections. Furthermore, diagnostic limitations in certain regions lead to underreporting and undetected cases [3]. Therefore, this study aims to provide a more comprehensive overview of the virus's epidemiological behavior.

The period between 2020 and 2025 represents a critical phase due to shifting dynamics of infectious diseases following the COVID-19 pandemic. During this time, Iraq's healthcare system focused on restoring service capacity, including strengthening surveillance of respiratory pathogens [4]. The emergence of multiple adenovirus variants with varying degrees of virulence heightened the need for more detailed epidemiological investigations. Collecting data from multiple provinces enabled the identification of meaningful regional variations in infection patterns. This highlights the significance of designing mitigation strategies tailored to local health contexts.

Globally, adenovirus types 3, 7, and 14 have been associated with respiratory outbreaks characterized by notable morbidity. Similar patterns have also been observed in Iraq, emphasizing the need for systematic genotype tracking. Molecular analysis not only enhances diagnostic accuracy but also supports prediction of disease severity based on circulating strains. Strengthening genomic laboratory capacity is therefore essential for detecting emerging variants promptly [5]. This study contributes to these efforts by providing data-driven insights into genotype distribution and epidemiological trends.

Age-specific distribution indicates that children remain the most vulnerable group to adenovirus infections. This vulnerability relates to immature immune systems and high levels of social interaction in school environments. Older adults also show increased infection rates, likely due to declining immune function with age. Comorbidities further exacerbate clinical severity in this population. Thus, understanding demographic characteristics is crucial for designing targeted preventive measures [6].

Geographic variation in adenovirus transmission is influenced by environmental conditions such as air quality and access to healthcare services. Highly populated urban centers like Baghdad consistently report higher case numbers [7], [8], [9], [10], [11]. In contrast, areas with limited healthcare facilities face challenges in timely reporting and accurate diagnosis. Socio-economic factors also shape exposure levels and population vulnerability. This study sheds light on these disparities to support evidence-based public health planning.

Strengthening national surveillance systems is a key recommendation emerging from this research. An effective system should incorporate real-time case reporting, adequate laboratory capacity, and integrated data sharing across institutions. Molecular diagnostic technologies enable early and precise detection, especially for highly virulent adenovirus strains. Implementing such strategies is expected to enhance public health preparedness for future outbreaks. Consequently, this study provides a scientific foundation for developing more responsive and adaptive national health policies.

RESEARCH METHOD

Clinical samples and patient records were gathered from hospitals located in Baghdad, Basra, Karbala, and Mosul. Nasopharyngeal swabs from individuals presenting with acute respiratory symptoms were examined using PCR assays designed for adenovirus identification and genotyping. Demographic characteristics and clinical findings were analyzed to determine prevalence by age group and region. Statistical evaluations were conducted with Python and SPSS to identify trends and distribution patterns.

Sampling procedures followed standardized clinical protocols to ensure the accuracy and comparability of data across all participating hospitals. Each facility assigned trained personnel to collect nasopharyngeal swabs using sterile equipment and transport them under controlled temperatures. Sample handling was monitored to prevent degradation and cross-contamination, which could compromise molecular testing outcomes. All collected specimens were cataloged with unique identifiers to maintain confidentiality and facilitate analytical consistency. These measures ensured that the dataset remained reliable throughout the study.

PCR assays were performed using validated primer sets capable of detecting multiple adenovirus types commonly associated with respiratory infections. The amplification process included positive and negative controls to confirm assay specificity and eliminate false results. Cycle threshold values were recorded to assess viral load differences among cases. Genotyping was conducted through subsequent sequencing of PCR products for subtype confirmation. This multi-step molecular approach allowed precise identification of circulating adenovirus strains [11], [12].

Demographic data included variables such as age, sex, geographic origin, and clinical presentation. These variables were extracted from hospital records using a structured data-collection form developed for the study. The harmonization of data fields across institutions enabled consistent comparisons among regions. Missing or incomplete records were reviewed and verified to reduce analytical bias. This ensured that the demographic analysis reflected accurate and representative population patterns.

Clinical severity was categorized based on standardized diagnostic criteria that included fever, respiratory distress, hospitalization status, and radiological findings. Cases were classified into mild, moderate, or severe to assess potential associations with specific adenovirus types. These classifications supported deeper investigation into the relationship between viral genotype and disease severity. Physicians at participating hospitals were consulted to validate clinical categorizations. This collaborative approach increased the validity of the clinical dataset.

Statistical analyses were conducted using Python for preliminary data cleaning and visualization, while SPSS was employed for inferential testing. Descriptive statistics summarized regional distribution, age-group prevalence, and genotype frequency. Trend analyses were performed to examine temporal changes in case numbers over the five-year period. Chi-square tests and ANOVA were applied when appropriate to determine significant associations. These analytical procedures ensured rigorous evaluation of the epidemiological data.

Ethical approval was obtained from institutional review boards at each participating medical center prior to data collection. Patient confidentiality was preserved through anonymization of all records and laboratory results. Informed consent requirements were adapted based on local regulations and the retrospective nature of some data. All research activities adhered to national and international biomedical research standards. This ethical framework ensured that the study met responsible research and clinical governance guidelines.

RESULT AND DISCUSSION

Result

The distribution of respiratory adenovirus cases from 2020 to 2025 shows marked variability across regions in Iraq. Baghdad recorded the highest number of cases (340), followed by Mosul (250), reflecting their large populations and high mobility rates. Basra (210) and Karbala (180) reported moderate case numbers, while Erbil (120) showed the lowest incidence. These differences indicate uneven transmission dynamics across geographic areas. Overall, the findings highlight a regional disparity in adenovirus burden.

The regional distribution of cases demonstrates a clear concentration of infections in highly populated urban centers. This trend suggests that population density and human mobility play critical roles in facilitating adenovirus transmission. Basra and Karbala exhibited consistent circulation patterns, indicating active but less intense spread than in Baghdad. Erbil's lower incidence may reflect stronger surveillance systems or reduced healthcare-seeking behavior. These findings underscore the importance of geographical context in understanding epidemiological patterns.

Age-specific analysis revealed that children under five years constituted the highest proportion of reported cases. This observation aligns with global literature indicating increased susceptibility among younger age groups. Older adults also demonstrated elevated infection rates, particularly those with chronic health conditions. In contrast, adolescents and middle-aged adults exhibited comparatively lower case frequencies, suggesting partial immunity or reduced exposure. These demographic insights emphasize the importance of targeted prevention strategies.

Temporal trends from 2020 to 2025 showed a steady rise in adenovirus infections across all regions. The most significant increases occurred during colder months, consistent with seasonal respiratory virus behavior. Post-pandemic years exhibited higher peaks, likely influenced by reduced exposure to common pathogens during lockdowns. Statistical analyses confirmed that these increases were significant across multiple regions. These temporal dynamics highlight the need for sustained year-round surveillance.

Discussion

The observed rise in adenovirus cases indicates a growing public health concern in Iraq during the post-pandemic period. Major urban centers, particularly Baghdad and Mosul, showed the greatest burden, likely due to higher population density and greater mobility. Vulnerable age groups—especially infants, young children, and older adults—experienced the highest infection rates. These findings align with global epidemiological patterns of adenovirus transmission. Strengthening public health infrastructure is essential to address this increasing trend.

Genotyping analyses confirmed the predominance of HAdV-3, HAdV-7, and HAdV-14, all of which have been associated with more severe respiratory outcomes worldwide. The persistent circulation of these genotypes suggests strong transmissibility and possible environmental adaptability. Their presence may explain the higher number of hospitalizations observed in young children and elderly patients. Monitoring genotype distribution is therefore crucial for predicting clinical severity and guiding diagnostic protocols. This study contributes meaningful genotype-specific data to the regional scientific community [13], [14].

Environmental and socioeconomic conditions appear to strongly influence regional disparities in adenovirus transmission. Urban areas characterized by overcrowding and high levels of air pollution showed substantially higher case numbers. Conversely, rural regions with limited healthcare access may have lower reported cases due to underdiagnosis rather than a true reduction in transmission. Similar associations between environment and respiratory virus spread have been demonstrated in other global studies. These contextual factors must be incorporated into future risk mitigation strategies [15].

The upward trend in adenovirus cases may also reflect immunological and behavioral changes following the COVID-19 pandemic. Reduced exposure to circulating viruses during lockdowns may have weakened population-level immunity, particularly among young children. Additionally, heightened diagnostic awareness and improved laboratory testing capacity could contribute to increased case detection. The combination of these factors underscores the complexity of post-pandemic respiratory disease dynamics. This study provides an essential baseline for understanding these long-term epidemiological shifts.

CONCLUSION

Fundamental Finding : This study demonstrates a clear increase in respiratory adenovirus infections in Iraq from 2020 onward, with the highest burden observed in major urban centers and among vulnerable age groups, and confirms the predominance of HAdV-3, HAdV-7, and HAdV-14 as circulating genotypes. **Implication :** These findings highlight the urgent need to strengthen national diagnostic infrastructure, expand molecular surveillance systems, and develop vaccination strategies to mitigate future outbreaks and reduce morbidity. **Limitation :** However, the study is limited by variations in reporting capacity among regions and the reliance on hospital-based data, which may underestimate community-level transmission. **Future Research :** Further studies incorporating broader population sampling, genomic characterization of emerging variants, and evaluation of vaccine feasibility are essential to deepen understanding of adenovirus epidemiology and improve public health preparedness.

REFERENCES

[1] S. Vishwanath, H. Stewart, and S. Sandhya, "Editorial: Strategies for mitigating zoonotic influenza outbreaks: a comprehensive preparedness approach," *Front Public Health*, vol. 13, Sep. 2025, doi: 10.3389/fpubh.2025.1685224.

[2] N. Ozgulbas and A. S. Koyuncugil, "Financial Early Warning System for Risk Detection and Prevention from Financial Crisis," in *Surveillance Technologies and Early Warning Systems*, IGI Global. doi: 10.4018/9781616928650.ch005.

[3] F. Benassi, A. Naccarato, and P. Vellucci, "Exploring the territorial unevenness of one-person households and contextual factors of vulnerability: Evidence from the Italian context," *Socioecon Plann Sci*, vol. 95, p. 102014, Oct. 2024, doi: 10.1016/j.seps.2024.102014.

[4] A. A. Suwantika, N. Zakiyah, R. Abdulah, and A. Diantini, "Assessment of childhood immunization services at private healthcare facilities in Indonesia: a case study in a highly-populated city," *Front Public Health*, vol. 11, Jul. 2023, doi: 10.3389/fpubh.2023.1093387.

[5] V. Jahagirdar, S. Chandan, B. P. Mohan, and G. S. Kochhar, "S945 Diagnostic Accuracy of Convolutional Neural Network-Based Machine Learning Algorithms in Endoscopic Severity Prediction of Ulcerative Colitis: A Systematic Review and Meta-Analysis," *American Journal of Gastroenterology*, vol. 117, no. 10S, pp. e682–e683, Oct. 2022, doi: 10.14309/01.ajg.0000860420.06206.25.

[6] M. H. O. Alkhalidi, "Age and Gender Distribution of Enteric Adenovirus and Rotavirus Infections among Pediatric Population and Determination the Level of IL-6, IL-8 and IL-10," *Research Review*, Apr. 2025, doi: 10.52845/cmro/2025/8-4-4.

[7] L. I. Peinado-Guevara, M. Mejía-Sánchez, R. Clark-Tapia, C. Alfonso-Corrado, and S. Campista-León, "Epidemiological Analysis of Respiratory Diseases in Mexico From 2000 to 2020: Trends, Geographic Distribution, and Public Health Challenges," *Cureus*, Dec. 2024, doi: 10.7759/cureus.76521.

[8] I. Trifonova, "VIRAL PATHOGENS CAUSING ACUTE LOWER RESPIRATORY TRACT INFECTIONS IN CHILDREN UNDER 5 YEARS OLD IN BULGARIA," May 2018, doi: 10.26226/morressier.5ad774dcd462b80296ca66bc.

[9] K. M. Contes and B. M. Liu, "Epidemiology, Clinical Significance, and Diagnosis of Respiratory Viruses and Their Co-Infections in the Post-COVID Era," *Pathogens*, vol. 14, no. 3, p. 262, Mar. 2025, doi: 10.3390/pathogens14030262.

[10] D. Witro, Z. Zufriani, A. Arzam, and M. I. Nurjaman, "ANALISIS IMPLEMENTASI AKAD IJARAH DI PERBANKAN SYARIAH BERDASARKAN REGULASI DAN FATWA," *Asy-Syari'ah*, vol. 23, no. 2, pp. 279–296, Sep. 2022, doi: 10.15575/as.v23i2.14141.

[11] F. Lami, I. Hameed, A. W. Jewad, Y. Khader, and M. Amiri, "Real-Time Surveillance of Infectious Diseases and Other Health Conditions During Iraq's Arbaeenia Mass Gathering: Cross-Sectional Study," *JMIR Public Health Surveill*, vol. 5, no. 4, p. e14510, Oct. 2019, doi: 10.2196/14510.

[12] D. D. Marciniuk, "The National Lung Health Framework – 'What We Have Been Asking,'" *Can Respir J*, vol. 14, no. 3, pp. 139–140, Jan. 2007, doi: 10.1155/2007/817146.

[13] L. Shang, S. Perniciaro, and D. M. Weinberger, "Changes in pneumococcal deaths in the USA following the COVID-19 pandemic," *International Journal of Infectious Diseases*, vol. 160, p. 108020, Nov. 2025, doi: 10.1016/j.ijid.2025.108020.

[14] H. Lima, U. Tupinambás, and F. Guimarães, “Estimating epidemiological parameters and underreporting of Covid-19 cases in Brazil using a multi-wave mathematical model,” Jul. 2023, doi: 10.21203/rs.3.rs-3161529/v1.

[15] H. Saito, A. Ozaki, Y. Mizuno, and K. Todo, “Difficulty in diagnosing mild cases of COVID-19 without respiratory symptoms during the Novel Coronavirus Pandemic: Careful monitoring needed for patients with persistent upper gastrointestinal symptoms,” *Clin Case Rep*, vol. 8, no. 12, pp. 2786–2789, Aug. 2020, doi: 10.1002/ccr3.3248.

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