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Molecular Detection and Phylogenetic Analysis of Fowlpox virus in Turkeys from Tikrit, Iraq

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A B S T R A C T

Fowlpox is a viral disease that affects a wide range of domestic birds including chickens, turkeys, pigeons, and other avian species, and poses notable health and economic challenges, especially in turkeys. The present study investigated the clinical manifestations of the disease, carried out molecular detection, and assessed the genetic relatedness of fowlpox virus in turkeys from Tikrit, Iraq. A total of 36 turkeys showing typical cutaneous lesions were examined, and tissue samples were collected from non-feathered areas for DNA extraction. Conventional PCR targeting the *p4b* gene, which encodes a major structural protein of the virus, produced a specific 578-bp amplicon in 34 samples, corresponding to a detection rate of 94.4%. Five PCR-positive samples were subsequently selected for Sanger sequencing. BLAST analysis results indicated high nucleotide similarity level of 98–99% with global isolates, especially with the Egyptian isolate (OL703787.1), with slight variation that did not affect the amino acid sequence. The sequences were deposited in GenBank (NCBI) under accession numbers PX649979, PX649980, PX649981, and PX649982. phylogenetic analysis using the Maximum Likelihood method under the Tamura–Nei model, placed the Iraqi isolates within Clade A, showing minimal genetic divergence, indicating the stability of the locally circulating strain. This study provides the first molecular evidence of fowlpox virus infection in turkeys in Iraq. It further highlights the importance of the p4b gene as a sensitive target for diagnosis and surveillance, and underscores the need to reinforce prevention and biosecurity measures to limit the spread of the virus in turkeys

Keywords: fowlpox virus, turkey, *p4b* gene, phylogenetic analysis

INTRODUCTION

Fowlpox virus (FPV) is considered one of the most important viruses of the genus Avipoxvirus within the family Poxviridae. It carries a remarkably large genome, estimated at about 288–300 kilobases, which places it among the largest viral genomes known to infect birds (**1**). To date, FPV has been reported in more than 200 species of wild and domesticated birds, underscoring its broad host range and their ability to spread across diverse geographical regions (**2**). Clinically, FPV infection is present in two distinct forms. The cutaneous (dry) form is present as proliferative, nodular lesions that typically develop on non-feathered regions such as the eyelids, face, and legs. In contrast, the diphtheritic (wet) form affects the mucous membranes of the mouth, pharynx, and upper respiratory tract and is frequently associated with higher mortality due to respiratory obstruction and reduced ability to feed due to difficulty in feeding (**3,4**). The severity of the disease infection is influenced by multiple factors, including the specific viral strain involved, the immune status of the birds, and the environmental conditions under which the flock is managed (**5**). Even though vaccination is commonly practiced in many countries in the region the outbreaks are

still observed in both commercial farms and household flocks. The ongoing presence of the virus indicates that local FPV strain may show genetic variation (**6**). From a diagnostic standpoint, polymerase chain reaction (PCR) is a key technique for accurate detection of FPV because of its high sensitivity and its ability to distinguish between different viral strains. The *p4b* gene (also known as FPV167) is among the most targeted markers in molecular diagnostics, as it is highly conserved across most FPV isolates and encodes proteins essential to the structural integrity of the virus (**7**). Sequencing of this gene is also commonly applied in evolutionary and phylogenetic research to differentiate the major genetic clusters of FPV, which are frequently associated to specific hosts or geographic origins (**8**). Recent molecular analyses have identified difference within genomic regions that were previously considered relatively stable, emphasizing the importance of continuous monitoring of genetic changes in locally circulating isolates (**9**).

In Iraq, although clinical cases of FPV in turkeys have been reported, molecular investigations focusing on viral detection and the characterization of its evolutionary relationships remain scarce. Accordingly, the present study aims to detect FPV in turkeys from Tikrit using PCR, sequence the p4b gene, and construct a phylogenetic tree to elucidate the evolutionary relationships between the local isolates and those documented worldwide. This work wase designed as a cross-sectional molecular diagnostic study.

MATERIALS AND METHODS

Ethical Approval

Ethical approval No. (Tu. Vet.156) was obtained from the Committee for the Care and Use of Animals in Scientific Research at the College of Veterinary Medicine, Tikrit University, on March 3, 2025).

Sample Collection and Clinical Signs

Samples were collected between April and July 2025 from several locations in and around Tikrit. A total of thirty-six samples were collected, and this sample size was selected to provide molecular confirmation of infection. The study was designed as a molecular diagnostic investigation based on sample collection during a single defined period, with the aim of confirming FPV in Turkeys showing clinical signs suspected to be caused by this viral infection. Clinical examination was performed to assess the presence of dry scabs and wart-like nodules in featherless regions, especially around the eyes, the base of the beak, the face, and the wattles, as well as localized swelling, redness, and difficulty in opening the eyes in some cases (**10**). This examination was used to support the suspicion of infection prior to laboratory examination. Skin lesions were collected using sterile, serrated tissue forceps, then placed directly into sterile Eppendorf tubes, accurately labelled, and immediately preserved in liquid nitrogen (-196°C) to ensure the preservation of viral DNA integrity, in line with current recommendations for the preservation of sensitive viral samples (**11,12**).

DNA Extraction

DNA was extracted from turkey skin lesions using Presto™ Mini gDNA Kit (Geneaid Biotech Ltd., Taiwan), according to the manufacturer's instructions. After thawing the samples, approximately 0.2–0.5 g of the skin was placed in an Eppendorf tube with the analytical solution, and the sample was hybridized using a Vortex device to break down the tissue. This was followed by chloroform treatment and centrifugation to isolate the DNA-containing top layer. Proteinase K and the second analytical solution were then added before incubation at 60°C. After the addition of ethanol, the samples were run through an extraction column and washed. The DNA was then dissolved in 100 µL of the solute and stored at −20°C until PCR analysis.

PCR Amplification and Agarose Gel Electrophoresis

A specific PCR assay was performed to amplify a 578-bp fragment of the *p4b* gene of FPV using primers previously described by Lee and Lee (**7**). The primers were commercially synthesized by Macrogen Inc. (Seoul, South Korea): forward 5′-CAG-CAG-GTG-CTA-AAC-AAC-AA-3′ and reverse 5′-CGG-TAG-CTT-AAC-GCC-GAA-TA-3′. In the conventional PCR procedure, the reaction mixture consisted of the components shown in **Table 1**, with the final reaction volume being 20 µL. After preparing the mixture and performing a rapid centrifuge for 7 seconds, the tubes were inserted into a thermal cycler (Applied Biosystems, USA) to perform the *p4b* gene amplification program (**13**), as shown in **Table 2.** PCR amplicons were subjected to electrophoresis on 1.5% agarose gel stained with ethidium bromide for 40 min at 100 V/mA and photographed under UV light.

Table 1. Components of the PCR mixture

PCR mixture	Volume
DNA template	2.0 µL
Forward primer (10 pmol/µL)	0.5 µL
Reverse primer (10 pmol/µL)	0.5 µL
Master mix (2×)	10 µL
Free nucleus water	7 µL
Total	20 µL

Table 2. Thermocycler program used in PCR

PCR mixture	Temperature (°C)	Time	Cycle
Pre-denaturation	94	5 min	1
Denaturation	94	30 sec	
Annealing	52	45 sec	35
Extension	72	1 min	
Final extension	72	5 min	1

Sequence Analysis

Five positive samples from the PCR products were selected for genetic sequencing of the *p4b* core gene. The amplification products were sent to Macrogen (Seoul, South Korea) for Sanger sequencing. Sequence alignment and phylogenetic analyses were performed using MEGA 11 software with the Maximum Likelihood method and the Tamura–Nei model , and the sequences were compared with reference sequences using the BLAST tool.

RESULTS

Clinical Findings

Affected birds showed skin lesions on unfeathered areas like the face, eyelids, and beak (**Figure 1**). The lesions began as small yellowish bumps that gradually developed into firm nodules covered with thick brown crusts. In advanced cases, swelling around the eyes caused partial or complete closure, and lesions near the nostrils occasionally led to breathing difficulty.

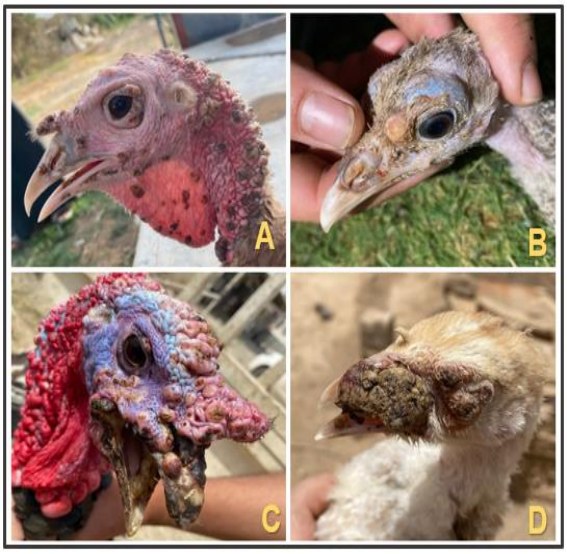

Figure 1. shows distinct cutaneous lesions on the unfeathered areas (A), (B) the early stage of lesion development near the eye, (C) the progression of lesions into firm nodules and thick crusts and (D) the coalescence of these crusts into a rough, thickened layer forming a wart-like lesion, accompanied by swelling of the eyelids and surrounding tissues of the beak

PCR Results

PCR analysis revealed a clear amplification band of 578 bp for the *p4b* core protein gene in suspected turkey samples, of the 36 examined samples, 34 were positive (94.4%). The remaining two samples did not yield any visible band during electrophoresis and were therefore considered negative, which may reflect either low amount of viral DNA. These findings indicate that the *p4b*-based PCR assay provides high sensitivity and accuracy (**Figure 2**).

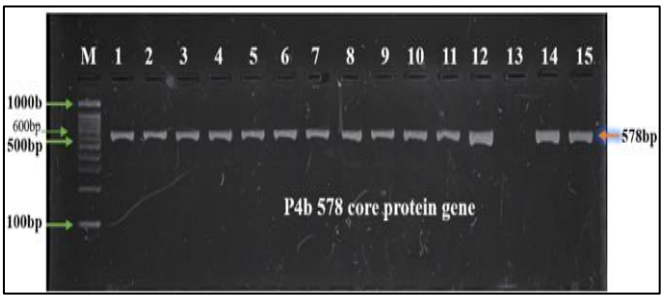

Figure 2. Amplification of the *p4b* core protein gene (578 bp) from infected turkey tissue samples using PCR. Lane M represents the molecular weight marker, while lanes 1–15 show a distinct band at 578 bp confirming the presence of the fowlpox virus, except for lane 13 which tested negative

Sequence Analyses

Sequence analysis of the *p4b* gene from five field isolates of fowlpox virus in turkeys showed a high genetic identity, confirming the virus identity and its close relationship to global strains. BLAST results revealed 98–99% similarity with the Egyptian reference strain (OL703787.1) (**Table 3**), with only minor nucleotide variations (transition, transversion, and small gaps) and no changes affecting amino acid composition or protein function (**Figure 3**). The results of study indicate that the *p4b* gene has a high genetic stability it a gene that can be trusted and referred to molecular and virological studies to track fowlpox virus and study its phylogenetic relationships.

Following completion of molecular analysis, the *p4b* core gene sequencing extracted from fowlpox virus was registered in the GenBank database of the NCBI with accession numbers PX649979, PX649980, PX649981, and PX649982.

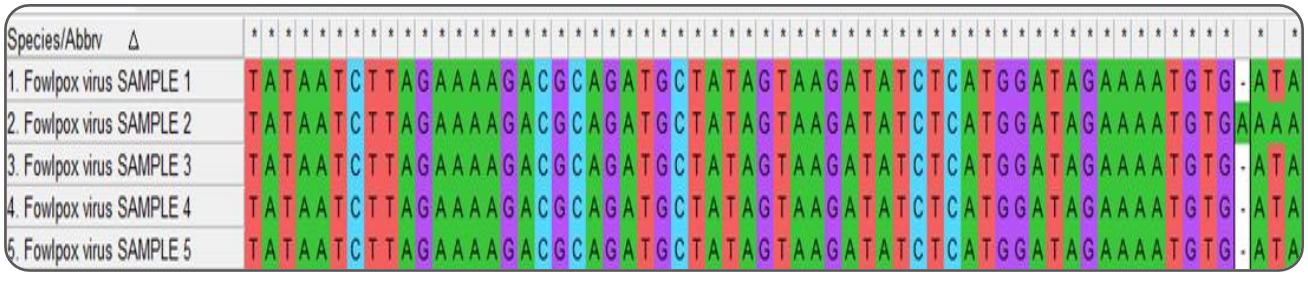

Figure 3. Multiple sequence alignment of the *p4b* gene among five Iraqi fowlpox virus isolates showing a high degree of nucleotide similarity with only a few substitutions among the analysed sequences

Table 3. Genetic mutations in the *p4b* gene of fowlpox virus isolates compared with the reference sequence (OL703787.1). Samples 1–5 represent the field isolates

No.	Type of substitution	Location	Nucleotide	Sequence ID with compare	Source	Identities
S1	GAP	10	G/-	OL703787.1	Fowlpox virus isolate Cx A2324 core protein 4b gene, partial cds	99%
	GAP	16	-/G			
	TRANSITION	497	G/A			
	GAP	500	C/-			
	TRANSITION	520	G/A			
S2	GAP	10	G/-	OL703787.1	fowlpox virus isolate Cx A2324 core protein 4b gene, partial cds	98%
	GAP	379	A/-			
	TRANSVERSION	381	A/T			
	GAP	494	*/A			
	TRANSITION	497	G/A			
	TRANSVERSION	498	C/A			
	GAP	517	-/A			
	TRANSVERSION	530	G/C			
	TRANSVERSION	532	C/A			
	TRANSITION	533	G/A			
	GAP	539	-/A			
	TRANSVERSION	543	C/G			
S3	GAP	16	-/G	OL703787.1	fowlpox virus isolate Cx A2324 core protein 4b gene, partial cds	99%
	TRANSITION	464	G/A			
	TRANSVERSION	513	T/G			
	TRANSVERSION	515	T/A			
S4	GAP	16	-/G	OL703787.1	fowlpox virus isolate Cx A2324 core protein 4b gene, partial cds	99%
	TRANSITION	464	G/A			
	TRANSVERSION	513	T/G			
	TRANSVERSION	515	T/A			
S5	TRANSITION	517	G/A	OL703787.1	Fowlpox virus isolate Cx A2324 core protein 4b gene, partial cds	99%
	TRANSVERSION	515	T/A			
	TRANSITION	513	A/G			
	GAP	512	T/-			

Table 4. Genetic distances among fowlpox virus isolates (S1–S5) using MEGA11

	FPV_S_1	FPV_S_2	FPV_S_3	FPV_S_4	FPV_S_5
FPV_S_1					
FPV_S_2	0.0168				
FPV_S_3	0.02431	0.02045			
FPV_S_4	0.03385	0.02065	0.0282		
FPV_S_5	0.01913	0.01725	0.0211	0.0076	

Phylogenetic Analysis

Phylogenetic analysis showed that the five FPV field isolates (S1–S5) collected from turkeys in Salahuddin province clustered together within Clade A, indicating a shared evolutionary origin. The genetic distance among these isolates ranged from 0.0076 to 0.0338 (**Table 4**), indicating limited genetic variation. The bootstrap values supporting this clustering ranged from 94% to 98% (**Figure 4**), indicating strong statistical support for the inferred evolutionary relationships, these high values reflect a high level of confidence that the field samples (S1–S5) share a common origin and exhibit notable genetic stability in the p4b gene. When the Iraqi FPV isolates were compared with global reference strains in the external phylogenetic analysis, they showed approximately 97% nucleotide identity. The level of similarity was observed with strains from France (MF766432.1), India (PQ202261.1), the Republic of Korea (MW558073.1), the USA (MH719203.1), and Australia (MW142017.1) (**Figure 4).**

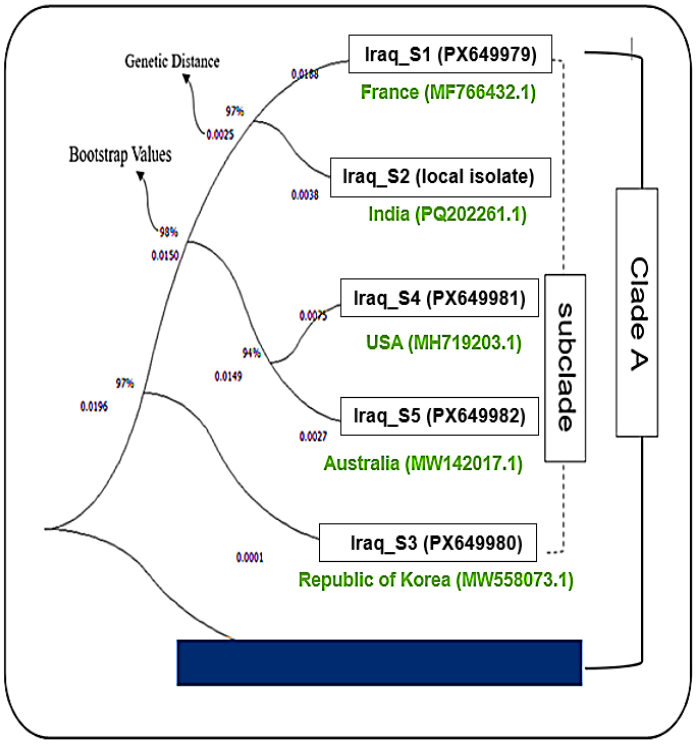

Figure 4. Maximum likelihood phylogenetic tree based on partial *p4b* gene sequences showing the relationship between Iraqi FPV isolates (Iraq_S1–Iraq_S5) and global reference strains from GenBank. Accession numbers are indicated; Iraq_S2 has no accession number

DISCUSSION

The results of the current study showed that turkeys infected with the cutaneous form of FPV exhibited distinct and characteristic skin changes. The lesions began as small, pale white or yellow granules in the featherless areas, then gradually progressed to thick, wart-like nodules and scabs, particularly on the face, eyelids, beak, comb, wattles, and legs. As the disease progressed, the scabs became thicker and more pronounced, leading in some birds to swollen eyelids and difficulty opening the eyes. These clinical signs are consistent with previous scientific reports of FPV infections, as described by Mohan and Fernandez (**14**) and Hibl et al. (**15**), thus reinforcing the reliability of the current study's findings and confirming the prevalence of the cutaneous form of the virus among turkeys in the region.

From a molecular perspective, the current study confirmed that the p4b gene is a highly stable and reliable target for detecting FPV, as the positive samples produced clear amplification bands. These findings are consistent with previous studies demonstrating the high sensitivity and diagnostic accuracy of the p4b gene for the molecular detection of FPV infections (**16-18**). Two samples did not produce any visible bands in the agarose gel. The absence of amplification may be attributed to poor DNA quality, the presence of PCR inhibitors in the tissue samples, the absence of detectable FPV DNA in the examined lesions, or insufficient viral infection in the collected tissue. In addition, substances present in a damaged skin, such as blood residues or inflammatory materials, may interfere with the PCR reaction and reduce amplification efficiency. However, the negative PCR results may also indicate that FPV was not present in some samples, or that the observed lesions were caused by other pathogens producing similar clinical signs. Similar findings have been reported in previous studies, where negative results were mainly attributed to poor sample quality, DNA degradation, or the presence of PCR inhibitors (**19**).

The p4b gene is widely recognized as a reliable molecular marker for the detection and phylogenetic analysis of FPV due to its high conservation among FPV isolates and the successful amplification of a 578-bp diagnostic fragment by PCR (**20**). In the present study, FPV infection was further confirmed by Sanger sequencing of selected PCR-positive samples followed by BLAST analysis. The obtained sequences showed 98–99% nucleotide identity with the regional reference FPV isolate OL703787.1, while slightly lower identity approximately 97% was observed when compared with global FPV reference strains. The high sequence similarity confirms the reliability of p4b-based PCR for the FPV detection and indicates that the Iraqi isolates belong to a conserved lineage, supporting its use for routine molecular diagnosis.

A comparison between the result of this study with previously published local studies within Iraq show noticeable variation in the reported infection rates. For

instance, Hassan et al. (**21**) reported comparatively lower detection rates of FPV in chicken in Tikrit, whereas Faisal and Al-Azzawi (**10**) documented complete detection rates in chicken and pigeon samples using the same target gene. Similarly, Khalifa et al. (**22**) recorded a moderate infection rate among pigeons in Basra. Such difference between governorates may reflect variations in environmental conditions, poultry management practices, vaccination coverage, and the intensity of viral circulation within each region.

At the regional level, the results of the present study are in agreement with findings reported from neighboring countries. In Egypt, Elgharbawy et al. (**23**) reported clear amplification of the *p4b* gene at 578 bp in cases of turkey pox, highlighting its diagnostic relevance. Likewise, studies conducted in Iran between 2019 and 2022 showed more than 99% genetic similarity among local isolates using the same genetic target (**24**). In India, Pawade et al. (**13**) demonstrated that the p4b gene is a sensitive and consistently amplifiable marker for the detection of natural FPV infections in turkeys. Collectively, these regional observations support the genetic conservation of the p4b gene and its suitability for detecting a broad range of FPV isolates.

In this study, phylogenetic analysis showed that FPV isolates obtained from turkeys in Iraq clustered within Clade A and exhibited a high degree of genetic similarity, indicating limited genetic variation among them. This pattern is consistent with previous studies on FPV isolates from chickens and pigeons, which reported clustering within evolutionarily stable clades (**8,18**). These finding further confirm the importance of the p4b gene in tracing evolutionary relationships and supporting comparative molecular studies.

The high detection rate recorded in this study, which is accompanied by close genetic similarity among the isolates, indicate the presence of FPV among turkey in Iraq. In light of the absence of previous studies investigation FPV infection in turkey, this study provides the first in Iraq to extensive molecular and phylogenetic evidence confirming the presence and genetic characteristics of the virus in this host. These findings, from a molecular perspective, show that the virus infects a host that has not been adequately studied before and indicate the need for continued molecular monitoring, strengthened biosecurity measures, and improved diagnostic monitoring in the country.

This study provides the first molecular confirmation of FPV infection in turkeys in Iraq. A high detection rate was obtained using the p4b gene, and the observed skin lesions were compatible with the cutaneous form of the disease. Phylogenetic analysis showed that the Iraqi isolates clustered within Clade A and shared a high degree of genetic similarity, suggesting circulation of a genetically conserved strain in the region. Together, these results support the use of molecular approaches for accurate detection and highlight the need for improved monitoring and biosecurity practices in turkey production systems.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

AUTHOR CONTRIBUTIONS

Both authors contributed equally to this work.

ARTIFICIAL INTELLIGENT DECLARATION

The authors declare that they are responsible for the accuracy and integrity of all content of the manuscript, including part generated by AI, and it is not used as a co-author.

REFERENCES

1. Afonso CL, Tulman ER, Lu Z, Zsak L, Kutish GF, Rock DL. The genome of fowlpox virus. J Virol. 2000;74(8):3815–31. 10.1128/jvi.74.8.3815-3831.2000
2. Giotis ES, Skinner MA. Spotlight on avian pathology: fowlpox virus. Avian Pathol. 2019;48(2):87–90. 10.1080/03079457.2018.1554893
3. Gilhare VR, Hirpurkar SD, Kumar A, Naik SK, Sahu T. Pock forming ability of fowl pox virus isolated from layer chicken. Vet World. 2015;8(3):245–250. 10.14202/vetworld.2015.245-250
4. Ferreira BC, Ecco R, Couto RM, Coelho HE, Rossi DA, Beletti ME, et al. Outbreak of cutaneous avian pox in vaccinated turkeys. Pesq Vet Bras. 2018;38(3):417–424. 10.1590/1678-5150-PVB-4463
5. Lebdah M, Ali AM, Ali AA, Hassanin O. Pathological and molecular characterization of avipoxviruses in Egypt. Br Poult Sci. 2019;60(6):666–674. 10.1080/00071668.2019.163914
6. Soud A, Ibrahim I, El-Moaty A. Antigenic and genomic characterization of local fowlpox virus isolate. J Appl Anim Res. 2020;5(3):31–9. 10.21608/javs.2020.98319
7. Lee LH, Lee KH. PCR diagnosis of fowlpox virus infection. J Virol Methods. 1997;63:113–119. 10.1016/S0166-0934(96)02119-2
8. Gyuranecz M, Foster JT, Dán Á, Ujvari D, Farkas SL, Kecskeméti S, et al. Worldwide phylogenetic relationship of avian poxviruses. J Virol. 2013;87(9):4938–4951. 10.1128/jvi.03183-12
9. Carulei O, Douglass N, Williamson AL. Comparative analysis of avian poxvirus genomes. BMC Genomics. 2017;18:1–13. 10.1186/s12864-017-4260-y
10. Faisal A, Al-Azzawi A. Molecular detection of avian poxvirus in chickens and pigeons of Diyala Province in Iraq. J World Poult Res. 2024;14(1):62–74. https://dx.doi.org/10.36380/jwpr.2024.7
11. Senaratne WMTN, Jayaweera JAAS. Comparison of microbial preservation methods: a narrative review. Germs. 2024;14(4):375–386. 10.18683/germs.2024.1447
12. Santos R, Duarte M, Alves L. Stability of avian viral pathogens under ultra-low temperature storage. Vet Microbiol. 2024;295:109–118. 123456789/263523
13. Pawade MM, Mhase PP, Muglikar DM, Lonkar VD, Mehere PV, Shelke PR, et al. Isolation and molecular characterization of Turkey pox virus from Maharashtra, India. Indian J Anim Res. 2024;58(2):347–349. 10.18805/IJAR.B-4468
14. Hibl BM, Blackwood RS, Simons BW, Collins DE. Poxvirus infection in a colony of laboratory pigeons (*Columba livia*). Comp Med. 2019;69(3):179–183. 10.30802/aalas-cm-18-000074
15. Alaarajy KHS, Almremdhy HAAE. Molecular diagnosis of natural pox virus infection in pigeons in Babylon Province, central Iraq. J Anim Health Prod. 2025;13(2):488–495. 10.17582/journal.jahp/2025/13.7.488.495
16. Fallavena LC, Canal CW, Salle CT. Presence of avipoxvirus DNA in avian dermal squamous cell carcinoma. Avian Pathol. 2002;31(3):241–246. 10.1080/03079450220136558

17. Akanbi OB, Obishakin ET, Gambo RA, Asala OO, Adedeji AJ. Pathology and characterization of fowlpox virus infection in a turkey-chicken backyard flock, Nigeria. Med Kedokt Hewan. 2022;33(3):177–187. 10.20473/mkh. v33i3.2022.177-187.
18. Jarmin S, Manvell R, Gough RE, Laidlaw SM, Skinner MA. Avipoxvirus phylogenetics: Identification of a PCR length polymorphism that discriminates between the two major clades. J Gen Virol. 2006; 87:2191–2201. 10.1099/vir.0.81738-0
19. Mohamed RI, Elsamadony HA, Alghamdi RA, El-Shemy A, Amer SAM, Bahshwan SM, et al. Molecular and pathological screening of the current circulation of fowlpox and pigeon pox virus in backyard birds. Poult Sci. 2024;103(12):104249. 10.1016/j.psj.2024.104249
20. Lüschow D, Hoffmann T, Hafez HM. Differentiation of avian poxvirus strains on the basis of nucleotide sequences of 4b gene fragment. Avian Dis. 2004;48(3):453-462. 10.1637/7111
21. Hasan II, Rasheed ST, Shakor MK. Pathological, molecular and phylogenic study of fowlpox virus in domesticated chickens of Tikrit City, Iraq. Braz J Vet Res Anim Sci. 2021;58: e176255. 10.11606/issn.1678-4456.bjvras.2021.176255
22. Khaleefah IA, Al-Tameemi HM, Kraidi QA, Najem HA, Ahmed JA, Alrafas HR. Clinical and molecular detection of fowl pox in domestic pigeons in Basrah, Southern Iraq. Korean J Vet Res. 2024;64(1):7–12. 10.14405/kjvr.20230048
23. Elgharbawy YA, Ali SS, El-Nahas EM, Ali MM. Turkey pox virus characterization from recurring infection in Egypt. J Adv Vet Res. 2024;14(5):895-898.
24. Eram N, Peighambari SM, Madani SA, Barin A. Molecular identification and isolation of avian poxviruses from different bird species in Iran. Arch Razi Inst. 2025;80(2):1–10. 10.32592/ARI.2025.80.2.417

العلامات السريرية والكشف الجزيئي والتحليل الوراثي لفيروس جدري الطيور في الديوك الرومي بمدينة تكريت، العراق

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فرع الاحياء المجهرية، كلية الطب البيطري، جامعة تكريت، تكريت، العراق

الخلاصة

يُعدّ مرض جدري الطيور من الأمراض الفيروسية واسعة الانتشار بين الطيور الداجنة، ويمثل مصدر قلق صحي واقتصادي واضح، خصوصًا في دجاج الرومي. هدفت هذه الدراسة إلى وصف العلامات السريرية، وإجراء الكشف الجزيئي، وتحليل العلاقات الوراثية لفيروس جدري الطيور في عينات من طيور رومي مصابة جُمعت من مدينة تكريت في العراق. شملت الدراسة فحص ستة وثلاثين طائرًا ظهرت عليها آفات جلدية مميزة، وتم جمع عينات من المناطق الخالية من الريش لاستخلاص الحمض النووي، أظهر فحص PCR التقليدي، الموجه نحو جين *P4b* المعروف بثباته الجيني ودوره في ترميز أحد البروتينات البنيوية الأساسية، وجود شريط واضح بطول 578 زوج قاعدة في 34 عينة، مما أدى إلى نسبة كشف بلغت 94.4%. وخضعت خمس عينات موجبة لعملية التسلسل بتقنية سانجر. وقد أظهر تحليل BLAST مستوى تطابق نوكليوتيدي مرتفعًا تراوح بين 98–99% مع عزلات عالمية، وخصوصًا العزلة المصرية (OL703787.1)، مع وجود اختلافات طفيفة لم تؤثر في تسلسل الأحماض الأمينية، أما التحليل الوراثي باستخدام طريقة Maximum Likelihood وفق نموذج Tamura–Nei فقد وضع العزلات العراقية ضمن Clade A مع درجة تباعد جيني منخفضة، مما يعكس استقرار السلالة المنتشرة محليًا. وتُعدّ هذه الدراسة أول دليل جزيئي موثّق يؤكد إصابة دجاج الرومي في العراق بفيروس جدري الطيور، كما تبرز أهمية جين *P4b* كأداة حساسة في التشخيص والتتبع الوبائي، وتؤكد الحاجة إلى تعزيز إجراءات الوقاية والأمن الحيوي للحد من انتشار الفيروس في دجاج الرومي.

الكلمات المفاحية: جدري الطيور، الديك الرومي، جين (*P4b* core)، تحليل نشوء التطوري