RESEARCH ARTICLE

SABRAO Journal of Breeding and Genetics
58 (5) 2119-2126, 2026
http://doi.org/10.54910/sabrao2026.58.5.12
http://sabraojournal.org/
pISSN 1029-7073; eISSN 2224-8978

MONITORING AND MOLECULAR GENETIC CHARACTERIZATION OF PHYTOVIRUSES INFECTING CHICKPEA

B. ABDIKARIMOV[1*], Z. KADIROVA[2], A. SHERIMBETOV[2], B. AKHMADALIEV[2], and B. GULOMOV[2]

[1]Institute of Basic and Applied Research, National Research University, Tashkent, Uzbekistan
[2]Institute of Genetics and Plants Experimental Biology, Academy of Sciences, Tashkent, Uzbekistan
*Corresponding author's email: Sezr014@gmail.com
Email addresses of co-authors: zarifakodirova@yahoo.com, sher.anvar1981@gmail.com, boburmirzoaxmadaliyev4042@gmail.com, gulomovboburbek595@gmail.com

SUMMARY

Chickpea (*Cicer arietinum* L.) is an economically important legume crop cultivated in Uzbekistan, and viral infections negatively affect plant growth, development, and grain yield. This study aimed to monitor virus-associated symptoms in chickpea fields and molecularly characterize the *Polerovirus* species infecting this crop. Field surveys carried out in the Tashkent Region revealed typical virus symptoms, including leaf curling, chlorosis, reddening of leaf margins, thickened lamina, and delayed flowering. A total of 103 symptomatic plant samples incurred analysis using the tissue blot immunoassay (TBIA) and reverse transcription polymerase chain reaction (RT-PCR). Immunological analysis identified luteoviruses in 47.5% of the samples. Molecular assay confirmed the presence of beet western yellows virus (BWYV) and cucurbit aphid-borne yellows virus (CABYV) in chickpea plants. The coat protein (*CP*) gene of the BWYV-TS1 isolate underwent sequencing before being deposited in the GenBank (PQ671646). Phylogenetic analysis disclosed the highest similarity between the Uzbek isolate and Eurasian isolates, forming a regional cluster. The results provide the first molecular evidence of BWYV infecting chickpea in Uzbekistan and highlight the need for future virus management strategies and resistance breeding.

Keywords: Chickpea (*Cicer arietinum* L.), luteoviruses, *Polerovirus* RT-PCR, phylogenetic analysis, BWYV, growth, grain yield

Key findings: Beet western yellows virus (BWYV) identification succeeded in naturally infected chickpea (*C. arietinum* L.) plants for the first time in Uzbekistan. According to a phylogenetic relationship, the mutations within the coat protein (CP) polypeptide revealed regional evolutionary patterns affecting chickpea health.

Communicating Editor: Dr. Hida Arliani Nur Anisa

Manuscript received: January 30, 2026; Accepted: June 28, 2026.
© Society for the Advancement of Breeding Research in Asia and Oceania (SABRAO) 2026

Citation: Abdikarimov B, Kadirova Z, Sherimbetov A, Akhmadaliev B, Gulomov B (2026). Monitoring and molecular genetic characterization of phytoviruses infecting chickpea. *SABRAO J. Breed. Genet. 58 (5) 2119-2126. http://doi.org/10.54910/sabrao2026.58.5.12*.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is an annual leguminous crop belonging to the family *Leguminosae*, distinguished by the highest content of proteins, vitamins, and minerals. Based on nutritional properties, it is one of the staple food sources in hot and arid regions (Sandhu *et al*., 2023). According to Food and Agriculture Organization (FAO) data, chickpea ranks third among the most widely cultivated legume crops worldwide, with India and China being the leading producers, contributing substantially to global production. The increasing global population has resulted in a growing demand for protein-rich foods with high contents of essential amino acids, minerals, and vitamins. Furthermore, climate change, coupled with the widespread distribution of insect pests and pathogenic microorganisms, considerably reduces the productivity of major crops and leads to significant economic losses.

In Uzbekistan, past studies stated ecological circulation and certain biological and physical characteristics of several phytopathogenic viruses, including tomato mosaic virus (ToMV) (Akhmadaliev *et al*., 2024); tomato brown rugose fruit virus (ToBRFV) (Akhmadaliev *et al*., 2025); soybean mosaic virus (SMV) (Rustam *et al*., 2024; Abduvaliev *et al*., 2025); barley yellow dwarf virus (BYDV) in wheat (Makhmudov *et al*., 2023, 2026); potato leaf roll virus (Kholmatova *et al*., 2024).

Chickpea is one of the major crops cultivated in the arable lands of Southern Uzbekistan, particularly in the provinces of Kashkadarya, Jizzakh, and Tashkent. The grains produced are mainly for export to neighboring Asian countries, as well as to Australia and Austria. Cultivars' selection is dependent on the climatic and cultivation conditions and the locally adapted cultivars, such as Lazzat, Yulduz, Jahongir, and Iroda, widely grown throughout the country. During nationwide surveys, chickpea samples exhibiting phytopathological symptoms reached collection and subjection to immunological and molecular genetic analyses to identify *Luteovirus* species infecting the chickpea crop in Uzbekistan. Chickpeas receive infections from 40 viruses belonging to 11 families and 19 genera globally (Kumari *et al*., 2010; Salam *et al*., 2011; Hema *et al*., 2014; Makkouk, 2020; Sharman *et al*., 2021; Kumar *et al*., 2025).

In hot climates, manifestations of virus infection in chickpeas are by leaf curling, yellowing or reddening of leaf tips, thickened and brittle leaf tissues, delayed flowering, and stunted plant growth. However, these symptoms have shown an association with viruses, such as chickpea chlorotic stunt virus (CpCSV), soybean dwarf virus (SbDV), and bean leaf roll virus (BLRV). Others are chickpea chlorotic dwarf virus (CpCDV), faba bean necrotic yellows virus (FBNYV), beet western yellows virus (BWYV), and cucurbit aphid-borne yellows virus (CABYV), as reported by European and Asian phytopathologists (Hema *et al*., 2014; Rashed *et al*., 2018). The aforementioned viruses belong to the small subfamily *Regressovirinae* within the family *Tombusviridae* and the genus *Luteovirus*. Among economically significant pathogens affecting chickpea are barley yellow dwarf virus (BYDV) in wheat, bean leaf roll virus (BLRV, *Luteovirus phaseoli*), and soybean dwarf virus (SbDV) in legumes. Luteoviruses encode a read-through protein (RTD) rich in arginine, which facilitates virus accumulation in the hemolymph cells of insect vectors and allows prolonged persistence (Makkouk *et al*., 2003; Ali *et al.,* 2014, 2018). This virus characteristic enables its long-distance transmission via vector insects. Considering these factors, determining the distribution and prevalence of *Luteovirus* species in Uzbekistan represents a primary research objective.

Initial isolation of the BWYV was by Duffus from sugar beets in the Western United States (Byrne *et al*., 2019). The disease symptoms induced by BWYV closely resemble those caused by the beet mild yellowing virus (BMYV) (Beuve *et al.,* 2008). However, the molecular studies demonstrated that leaf yellowing in sugar beet can result from co-infection with BMYV and BWYV. Further surveys documented the widespread occurrence of BWYV in sugar beet fields in the western U.S. (Beuve *et al*., 2008). BWYV has had reports of infecting a wide range of host plants, primarily the family *Chenopodiaceae*, including *Beta*

vulgaris, as well as other species, such as *Spinacia oleracea*, *Lactuca sativa*, and *Brassica oleracea* var. *Italica*. The infected plants typically exhibited the chlorosis, stunted growth, and delayed development, which are ascribable to BWYV infection. BWYV was considerably highly polyphagous, capable of infecting over 150 plant species across the 23 families (Beuve *et al*., 2008; Byrne *et al*., 2019). Reports of BWYV also detailed with extensive distribution in sugar beet and cabbage fields in the United Kingdom (Russell and Duffus*,* 1970). Serological differentiation between BWYV and BMYV reached validation using both immunological and molecular genetic methods (Beuve *et al*., 2008).

BWYV, a member of the genus *Polerovirus*, primarily infects sugar beet as its main host, and the virion comprises a protein capsid encapsulating a positive-sense RNA (+RNA) genome (Beuve *et al*., 2008). The genome spans 5.6–5.9 kb, with the viral protein genome-linked (VPg) attached to the 5′ end, which is essential for ribosome binding and viral genome assembly within host cells (Byrne *et al*., 2019). The virus shows considerable transmission from phloem-feeding insects, and it enters the insect gut during feeding, crosses the gut epithelium, and accumulates in hemolymph cells (Byrne *et al*., 2019). BWYV does not replicate within the insect vector but can persist throughout the vector's lifespan. Key viral proteins, including the capsid protein, movement protein, and read-through domain (RTD), are critical for viral evolution and efficient vector-mediated transmission. The ORF1, ORF2, ORF3, and ORF4 gene fragments exhibited the highest sequence conservation (Beuve *et al*., 2008; Byrne *et al*., 2019), while the RTD protein is particularly crucial for efficient virus transmission by aphid vectors (Beuve *et al*., 2008). The phylogenetic relationships of BWYV isolates detected in chickpea fields in Uzbekistan sustained analysis and comparison with isolates from other regions. Bioinformatic analyses focused on the coat protein (*CP*) gene, which encodes the structural capsid protein. The initial identification of BWYV relied on *CP* gene sequences.

MATERIALS AND METHODS

Sample collection

Field surveys conducted in chickpea (*C. arietinum* L.) fields occurred in the districts of Kibray, Akkurgan, Yukari Chirchik, and Urta Chirchik, Tashkent Region, Uzbekistan. Chickpea plants showing typical virus-like symptoms were specimens selected for laboratory analysis. The upper 10–15 cm stem portions required excision using sterile scissors before transporting them to the laboratory for analysis.

Tissue blot immunoassay (TBIA)

TBIA, as performed in the study, followed ICARDA (International Center for Agricultural Research in the Dry Areas) protocols. Fresh stem sections, as pressed onto nitrocellulose membranes, underwent washing three times with PBS (pH 7.4). Membranes received incubation in PBST (PBS + 0.5% Tween-20) for 1 h at room temperature, followed by incubation with primary antibodies diluted in PBS for another hour. After washing, membranes entailed treatment with conjugate buffer (2% polyvinylpyrrolidone and 0.2% egg albumin). Achieving color development used the NBT/BCIP substrate solution. The stopping of reactions used PBS, with signals examined under a stereomicroscope (Hsu and Lawson*,* 1991).

RNA extraction, cDNA synthesis, and PCR amplification

Total RNA extraction occurred from symptomatic chickpea leaf tissues using the RNeasy Plant Mini Kit according to the manufacturer's instructions (Qiagen, Germany). First-strand cDNA synthesis used the M-MLV reverse transcriptase. Briefly, 3 µl of total RNA preceded mixing with the reverse primer and dNTPs, incubation at 65 °C for 5 min, and immediate chilling on ice. Reverse transcription, as performed, proceeded at 37 °C for 50 min, followed by enzyme inactivation at 70 °C for 15 min. The synthesized cDNA necessitated storage at -20 °C for subsequent PCR analysis.

For molecular identification of the beet western yellows virus (BWYV), PCR amplification continued using specific primers designed in this study: BWYV_F (5′-CTAGCAGGATTTGCATCAG-3′) and BWYV_R (5′-GCCATTATACGGGTCGCT-3′), targeting the coat protein (*CP*) gene. The expected amplicon size was 828 bp.

RESULTS AND DISCUSSION

The investigation of phytopathogenic viruses infecting chickpea (*Cicer arietinum* L.) in Uzbekistan enabled the conduct of comprehensive phenological observations in chickpea fields across the Tashkent Region. During field surveys, disease symptoms typical of *Luteovirus* infection required consistent observations. These symptoms included curling of leaves in the upper canopy, yellowing and reddening along the leaf margins, leaf lamina thickening and brittleness, generalized chlorosis in severely affected plants, and delayed flowering. Similar symptomatology has reached wide reports for viruses belonging to the genus *Polerovirus* (family *Solemoviridae*) infecting leguminous crops (Domier and D'Arcy, 2008; Abraham *et al*., 2008).

Field-based identification of *Luteovirus* infections is inherently challenging because viruses belonging to the genus *Polerovirus* frequently induce symptoms that closely resemble those caused by mineral deficiencies, particularly magnesium (Mg) and iron (Fe) (Domier and D'Arcy, 2008). During the surveys conducted in the presented study, symptoms, such as leaf curling and yellowing in the upper-stem region, along with systemic chlorosis in severely infected plants, were the most prevalent and widely distributed compared with other disease manifestations (Figure 1).

Figure 1. Disease symptoms of *Luteovirus* infection in chickpea plants: a) Yellowing at leaf roll b) Leaf curling and reddening, and c, d) Chickpea fields exhibiting symptoms characteristic of *Luteovirus* infection.

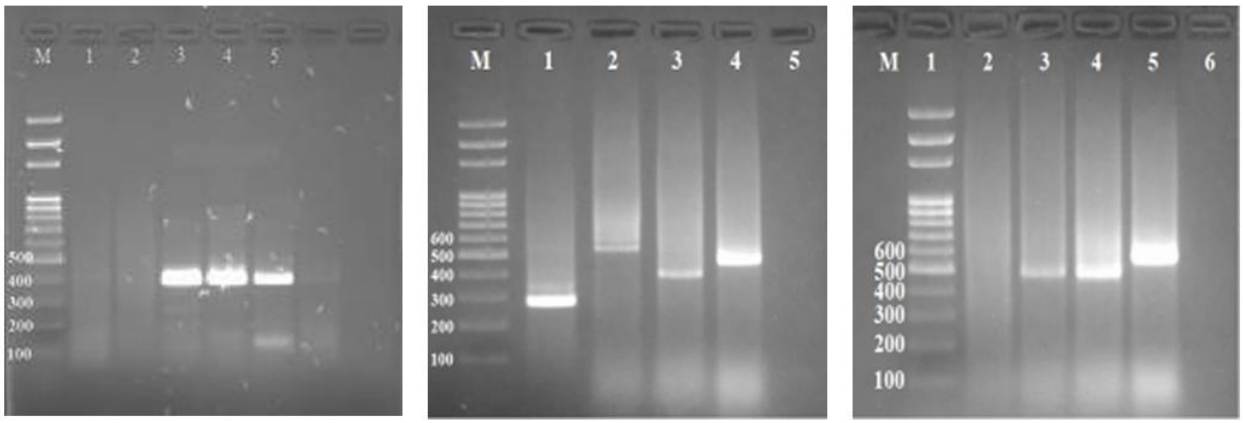

Figure 2. Electrophoretic profiles of Luteoviruses infecting chickpea: a) Luteoviruses identified in biological samples, b) Beet western yellows virus (BWYV), and c) Cucurbit aphid-borne yellows virus (CABYV).

For laboratory investigations, a total of 103 plant samples collected came from the upper 10–15 cm of stems of symptomatic chickpea plants using sterile scissors. The collected samples obtained subjection to immunological analysis using membrane-based assays. The membranes carrying the printed samples entailed assessment at the Virology Laboratory of the ICARDA (Beirut, Lebanon). The use of a universal broad-spectrum polyclonal antibody (5G4), specific for luteoviruses infecting chickpea plants, served for detection (Abraham *et al*., 2008). Immunological analysis revealed that 47.5% of the tested samples showed infection with luteoviruses, indicating the widespread occurrence of these viruses in chickpea fields of the Tashkent Region. The 5G4 antibody has gained wide application for detecting *Luteovirus* in leguminous crops and has demonstrated high reliability in serological diagnostics (Abraham *et al*., 2008; Sharman *et al*., 2015). The results suggested the presence of mixed infections involving *Polerovirus* in the surveyed chickpea populations (Figure 2).

In validating the immunological findings and enabling precise viral identification, molecular genetic analyses took place. Total RNA extraction ensued from the collected samples using the Mackenzie RNA extraction protocol (QIAGEN RNeasy Plant Mini Kit, Cat. No. 74104) before storage at -20 °C. Complementary DNA (cDNA) attained subsequent synthesis from the extracted RNA for PCR amplification. Universal primers Pol3870 (forward) and AS3 (reverse), which target conserved regions of luteoviruses, produced an amplicon of approximately 370 bp (Abraham *et al.,* 2008; Sharman *et al.,* 2015). Both immunological and molecular analyses confirmed the presence of *Luteovirus* infections in chickpea plants collected from the study area (Figure 2).

In a subsequent stage, employment of virus-specific primers sought to accurately identify the species of *Luteovirus* infecting chickpea crops in Uzbekistan. Molecular diagnostic results revealed the presence of beet western yellows virus (BWYV) (276 bp) and cucurbit aphid-borne yellows virus (CABYV) (474 bp) in chickpea samples collected from the Kybray District. Both viruses belong to the genus *Polerovirus* within the family *Solemoviridae*.

BWYV is a widely distributed plant virus whose primary host is sugar beet; however, it has many reports of infecting plant species belonging to more than 10 dicotyledonous families (Beuve *et al.,* 2008). The virion consists of a positive-sense single-stranded RNA genome approximately 5.6–5.9 kb in length. The viral genome has links to the viral protein genome-linked (VPg) at the 5′ end, which plays an essential role in viral replication and interaction

with host ribosomes (Mayo, 2008). Under natural conditions, the transmission of the virus efficiently occurs via aphid vectors in a persistent, circulative manner. When aphids feed on infected plants, the virus enters the insect gut, passes into the hemolymph, and accumulates within insect tissues. Although the virus does not replicate within the insect vector, it remains transmissible throughout the insect's lifespan (Mayo*,* 2008).

The coat protein (*CP*) gene of the BWYV isolate circulating in Uzbekistan underwent amplification and sequencing using the Sanger sequencing method. The obtained sequence, designated BWYV-TS-1, proceeded to be deposited in the NCBI GenBank database under accession number PQ671646. The viral genome contains several conserved open reading frames (ORF1–ORF4) that are essential for viral replication, movement, and virion assembly (Hauser *et al.,* 2000). In particular, the *CP* gene encoded by ORF3 plays a crucial role in virion formation and vector-mediated transmission.

In the assessment of the evolutionary relationships of the identified virus, phylogenetic analyses conducted depended on nucleotide sequences of the *CP* gene. A BLAST search identified isolates with the highest sequence similarity to the Uzbek isolate. Comparative analysis of pairwise nucleotide distances using the MEGA11 software revealed that the *CP* gene sequence of the Uzbek BWYV isolate differed by approximately 0.01% from isolates reported in China and Japan. Meanwhile, its greater divergence (up to 0.05%) was evidently relative to isolates reported from Iran and the United Kingdom. Additionally, nucleotide sequences of the ORF3 gene from isolates IPP and Gals2, previously identified in Germany and Switzerland, differed by approximately 0.13%, indicating relatively low genetic variability among global isolates.

The further clarification of evolutionary relationships among BWYV isolates had the study construct a phylogenetic tree using the neighbor-joining (NJ) method based on *CP* gene sequences (Figure 3). The phylogenetic analysis revealed clear geographical clustering of BWYV isolates. Isolates originating from North America and Western Europe formed a cluster with the highest bootstrap support values, indicating strong genetic similarity among these populations (Moonan and Mirkov, 2002). In contrast, isolates from Australia and Brazil indicated positions on separate branches and exhibited relatively lower bootstrap support values, suggesting higher evolutionary divergence within these populations (Martin *et al*., 2005).

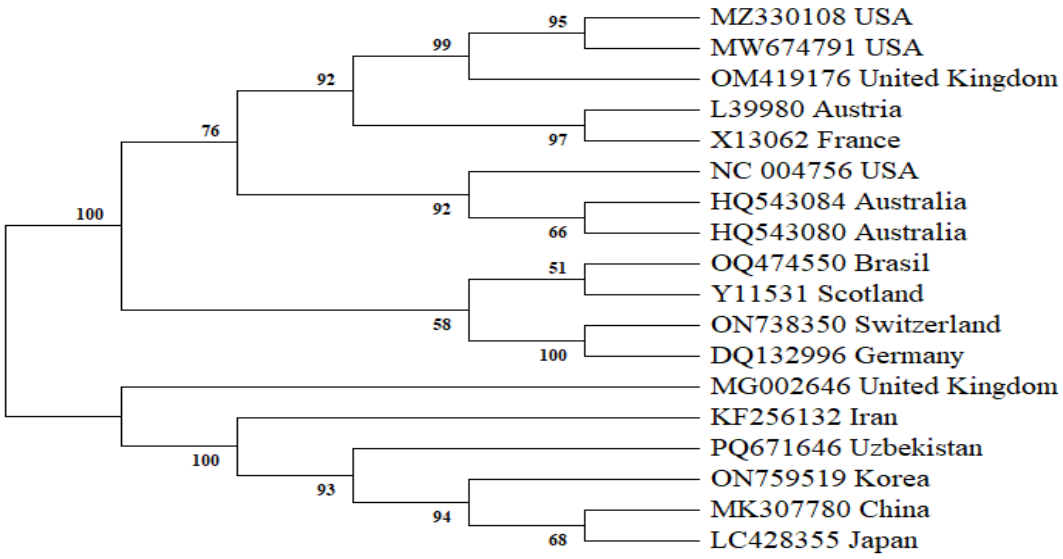

Figure 3. Phylogenetic tree of the Beet western yellows virus TS-1 isolat.

Asian isolates formed a distinct phylogenetic cluster. Notably, the Uzbek BWYV isolate demonstrated close phylogenetic affinity with Iranian isolates, indicating a possible regional evolutionary lineage within Central Asia. This cluster signified sequential connection with East Asian isolates, suggesting potential interregional dissemination of BWYV between Central and East Asia (Xiang *et al*., 2010). Similar evolutionary relationships between BWYV and closely related viruses, such as CABYV, turnip yellows virus (TuYV), and barley yellow mosaic virus (BMYV), have also appeared in in previous studies (Beuve *et al*., 2008; Xiang *et al*., 2010).

Overall, the phylogenetic analysis demonstrated the evolutionary structure and genetic diversity of BWYV isolates have strong influences from geographical factors. The clustering of isolates from different ecological regions suggests the existence of region-specific evolutionary lineages and potential gene flow between continents (Moonan and Mirkov, 2002; Pagán and Holmes, 2010). Such genetic variability may increase the risk of the emergence of novel viral variants capable of infecting additional host species, including economically important crops, such as chickpea.

CONCLUSIONS

The results confirmed that the chickpea (*Cicer arietinum* L.) cultivated in Uzbekistan incurs natural infections from poleroviruses belonging to the family *Solemoviridae*, including beet western yellows virus (BWYV) and cucurbit aphid-borne yellows virus (CABYV). These findings indicate that chickpea serves as an important host for these viruses under local agroecological conditions. Phylogenetic analysis of the BWYV-TS1 isolate obtained from chickpeas revealed the highest genetic similarity to isolates reported from Iran and Korea, as well as a close evolutionary relationship with East Asian isolates from Japan and China. Despite the wide geographical distribution and regional diversification of the BWYV, the coat protein (*CP*) gene remained highly conserved among chickpea-infecting isolates. These results highlight the importance of continuous monitoring of viral infections in chickpeas and provide a molecular basis for developing resistant cultivars and implementing integrated plant protection strategies.

REFERENCES

Abduvaliev B, Akhmadaliev B, Adilov B, Abdikarimov B (2025). First report of soybean mosaic virus on soybean (*Glycine max* L.) in Uzbekistan. *J. Plant Pathol.* 107: 775.

Abraham AD, Varrelmann M, Vetten HJ (2008). Molecular evidence for the occurrence of two new luteoviruses in cool season food legumes in Northeast Africa. *Afr. J. Biotechnol.* 7(4): 414–420.

Akhmadaliev B, Abduvaliev B, Adilov B, Aripova S, Kadirova Z, Abdikarimov B, Eshchanov B (2024). Preparation of polyclonal antiserum to Tomato mosaic virus and its application as a viral diagnostic test. *J. Plant Biotechnol.* 51(4): 265–272.

Akhmadaliev B, Abduvaliev B, Adilov B, Sherimbetov A, Abdikarimov B, Ruzmetov D (2025). First report of Tomato brown rugose fruit virus infecting sweet pepper (*Capsicum annuum*) in open fields in Uzbekistan. *Plant Dis.* 109(9): 2001.

Ali M, Anwar S, Shuja MN, Tripathi RK, Singh J (2018). The genus *Luteovirus*: From infection to disease. *Eur. J. Plant Pathol.* 151(4): 841–860.

Ali M, Hameed S, Tahir M (2014). *Luteovirus*: Insights into pathogenicity. *Arch Virol.* 159(11): 2853–2860.

Beuve M, Stevens M, Liu HY, Wintermantel WM, Hauser S, Lemaire O (2008). Biological and molecular characterization of an American sugar beet-infecting Beet western yellows virus isolate. *Plant Dis.* 92: 51–60.

Byrne MJ, Steele JF, Hesketh EL, Walden M, Thompson RF, Lomonossoff GP, Ranson NA (2019). Combining transient expression and cryo-EM to obtain high-resolution structures of luteovirid particles. *Structure* 27(12): 1761–1770.

Domier LL, D'Arcy CJ (2008). Luteoviruses. In: B.W.J. Mahy and M.H.V. Van Regenmortel (Eds.) Encyclopedia of Virology. Elsevier, pp. 231–238.

Hauser S, Stevens M, Mougel C, Smith HG, Fritsch C, Herrbach E, Lemaire O (2000). Biological, serological and molecular variability suggest three distinct Polerovirus species infecting beet or rape. *Phytopathology* 90: 460–466.

Hema M, Sreenivasulu P, Patil BL, Kumar PL, Reddy DVR (2014). Tropical food legumes. *Adv Virus Res* 90: 431–505.

Hsu HT, Lawson RH (1991). Direct tissue blotting for detection of tomato spotted wilt virus in Impatiens. *Plant Dis.* 75: 292–295.

Kholmatova M, Fayziev V, Akhmadaliev B, Absamatov T, Temirov A, Tangriev T, Jovlieva D, Askarova M (2024). Molecular identification of potato leaf roll virus and its impact on important nutrients in tubers. *J. Wildl. Biodivers.* 8(3): 149–161.

Kumar N, Hong S, Zhu Y, Garay A, Yang J, Henderson D, Li Y (2025). Comprehensive review of chickpea (*Cicer arietinum*): Nutritional significance, health benefits, techno-functionalities and food applications. *Comp. Rev. Food Sci. Food Saf.* 24(2): 70152.

Kumari SG, Najar A, Attar N, Loh MH, Vetten HJ (2010). First report of Beet mosaic virus infecting chickpea (*Cicer arietinum* L.) in Tunisia. *Plant Dis.* 94: 1068.

Makhmudov TK, Adilov BS, Kadirova ZN, Ziyayev ZM, Sherimbetov AG, Ruzmetov DR, Abdikarimov BQ, Chorshanbiev NE, Adegbola RO, Brown JK (2026). First report of Beet western yellows virus infecting wheat in Uzbekistan. *Plant Dis.* 110(1): 253.

Makhmudov TK, Kadirova ZN, Adilov BS, Abdikarimov BQ, Abduvaliev BA, Ziyaev ZM, Sherimbetov AG, Kurganov S (2023). Molecular identification based on coat protein sequences of barley yellow dwarf virus from Uzbekistan. *Pak. J. Phytopathol.* 35(1): 127–135.

Makkouk KM (2020). Plant pathogens which threaten food security: Viruses of chickpea and other cool season legumes in West Asia and North Africa. *Food Sec.* 12: 495–502.

Makkouk KM, Kumari SG, Hughes JA, Muniyappa V, Kulkarni NK (2003). Other legumes: Faba bean, chickpea, lentil, pigeon pea, mungbean, blackgram, lima bean, horse gram, bambara groundnut, and winged bean. In: Virus and Virus-like Diseases of Major Crops in Developing Countries. Kluwer Academic Publishers, Dordrecht, pp. 447–476.

Martin DP, Williamson C, Posada D (2005). RDP2: Recombination detection and analysis from sequence alignments. *Bioinformatics* 21(2): 260–262.

Mayo MA (2002). ICTV at the Paris ICV: Results of the plenary session and the binomial ballot. *Arch. Virol.* 147: 2254–2260.

Moonan F, Mirkov TE (2002). Analyses of genotypic diversity among North, South, and Central American isolates of Sugarcane yellow leaf virus. *J. Virol.* 76(3): 1339–1348.

Pagán I, Holmes EC (2010). Long-term evolution of the *Luteoviridae*: Time scale and mode of virus speciation. *J. Virol.* 84(12): 6177–6187.

Rashed A, Feng X, Prager SM, Porter LD, Knodel JJ, Karasev A, Eigenbrode SD (2018). Vector-borne viruses of pulse crops with emphasis on North American cropping systems. *Ann. Entomol. Soc. Am.* 111: 205–227.

Russell GE, Duffus JE (1970). Serological and host range evidence for the occurrence of Beet western yellows virus in Europe. *Phytopathology* 60: 1199–1202.

Rustam DRU, Sherimbetov AG, Adilov BS (2024). First report of *Macrophomina phaseolina* causing charcoal rot in soybean (*Glycine max*) in Uzbekistan. *Plant Dis.* 108(7): 2221.

Salam MU, Davidson JA, Thomas GJ, Ford R, Jones RAC, Lindbeck KD, MacLeod WJ, Kimber RBE, Galloway J, Mantri N (2011). Advances in winter pulse pathology research in Australia. *Australas. Plant Pathol.* 40: 549–567.

Sandhu JS, Tripathi S, Chaturvedi SK (2023). Chickpea nutritional status and value chain for sustainable development. In: S.A. Narula and S.P. Raj (Eds.). Sustainable Food Value Chain Development: Perspectives in Developing and Emerging Economies, pp. 175–183.

Sharman M, Appiah AS, Filardo F, Nancarrow N, Congdon BS, Kehoe M, Aftab M, Tegg RS, Wilson CR (2021). Biology and genetic diversity of Phasey bean mild yellows virus. *Arch. Virol*. 166: 1575–1589.

Sharman M, Lapbanjob S, Sebunruang P, Belot JL, Galbieri R, Giband M, Suassuna N (2015). First report of Cotton leafroll dwarf virus in Thailand. *Australas. Plant Dis. Notes.* 10: 24.

Xiang HY, Dong SW, Zhang HZ, Wang WL, Li MQ, Han CG, Yu JL (2010). Molecular characterization of two Chinese isolates of Beet western yellows virus infecting sugar beet. *Virus Genes* 41(1): 105–110.