



Occurance of fall armyworm, *Spodoptera frugiperda* on maize (*Zea mays*) in higher altitudes of Kashmir, India: First report

ISHTIYAQ AHAD¹, ARSHIMA SHAJI V¹, DANISHTA AZIZ^{1*}, ARADHANA PANDA¹,
ISHFAQ MAJEED SHAH¹, ZAKIRH KHAN¹, VENKATESAN T² and BAJYA D R³

Sher-e-Kashmir University of Agricultural Sciences and Technology, Kashmir, Jammu Kashmir

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The polyphagous fall armyworm, *Spodoptera frugiperda* (J.E. Smith), invaded India which is a major danger for maize (*Zea mays* L.) (Ankush *et al.* 2019) and other crops like rice, sorghum, cruciferous crops, cowpea, Solanaceous crops, soybean, groundnut, ginger, besides some wild grasses and sugarcane (Suby *et al.* 2020). Given the destructive nature of FAW, the financial harm caused globally is high enough to be ignored. This pest thrives on over 353 host crop spp. but feeds insatiably on every stage of the developing maize (Montezano *et al.* 2018) becoming its significant pest. Early larval instars create an extended, papery window by scraping the epidermis of leaf (Sharanabasappa *et al.* 2018). Conversely, 3rd instar onwards, larvae settle in leaf whorl and feed inside. In rainfed maize, the harm and severity caused by invasive *S. frugiperda* ranged from 22.13–46.83% and 3.0–4.9 on a 0–9 scale (Omprakash *et al.* 2021). The fall armyworm being native to America, not only damages crop, but has spread to many countries including its invasion in India from 2018 (Srikanth *et al.* 2018, Maruthadurai and Ramesh 2020) in states like Karnataka, Tamil Nadu, Andhra Pradesh, Telangana and Maharashtra (Srikanth *et al.* 2018). Suby *et al.* (2020) has mentioned the presence and spread of fall armyworm in all maize growing regions of Indian subcontinent, however no report in Himachal Pradesh and Jammu and Kashmir were found till so far.

Collection of samples: A study was carried out during 2022, at Sher-e-Kashmir University of Agricultural Sciences and Technology, Kashmir (34°20'54"N; 74°24'02"E and 1606 msl), Jammu Kashmir for the collection and survey of

pest complexes from maize experimental plots. Among the collected samples, the identity of few samples was suspicious and were resembling more to fall armyworm, which is a pest of invasive origin. The active larvae (Fig. 1A) were collected from field and brought to laboratory for rearing and studying adult morphology. The newly formed pupae were transferred to 12 well plate (one pupa/well) for adult emergence (Fig. 1B), and then adult morphology (Fig. 1C) was studied. At the same time, the type of damage done by this pest in maize crop (Fig. 2A, B, C) was also monitored to make the identity clearer.

Morphometry and microscopy of samples: The laboratory reared insect pest specimens, resembling fall armyworm were prepared for microscopy. The general, identification marks were observed on larva as well as adults. In adults, the morphometric data of head, thorax, abdomen and wings was taken from an average of 10 insect samples.

Statistical analysis: The data obtained from 10 insect samples were subjected to standard statistical analysis using R software, and the length of different body parts under study was calculated and expressed as mean and the range was also calculated.

Molecular characterization: In the meantime, samples collected from Wadura, were sent to ICAR-National Bureau of Agricultural Insect Resources, Bengaluru, Karnataka for molecular characterization. For this purpose, DNA was isolated from insect samples using Dneasy® Qiagen's blood and tissue kit as per protocol. A phylogenetic tree (Fig. 3) was contributed to evaluate evolutionary similarities and intraspecific distance was also calculated in MEGA 11 software (Table 1).

Occurrence of pest and damage symptoms: For the 1st time, FAW incidence was noted during 2022–2023 in the Western Himalayan region in maize fields of FoA, Wadura, Sher-e-Kashmir University of Agricultural Sciences and Technology, Kashmir, Jammu Kashmir, causing a heavy damage in maize crop during early October, 2022. The active early instars were observed consuming leaves by scrapping

¹Sher-e-Kashmir University of Agricultural Sciences and Technology, Kashmir, Jammu Kashmir; ²ICAR-National Bureau of Agricultural Insect Resources, Bengaluru, Karnataka; ³Sri Karan Narendra Agriculture University, Jobner, Jaipur, Rajasthan. *Corresponding author email: daniaziz9974@gmail.com

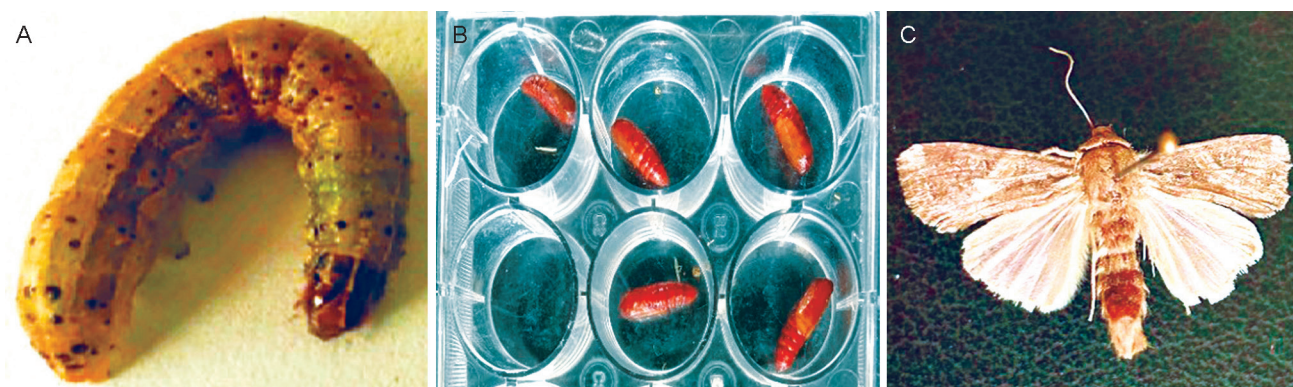


Fig. 1 Various life of stages of insect pest under investigation. (A) Larva; (B) Pupa; (C) Adult.



Fig. 2 Damage symptoms in maize leaves and inflorescence. (A) Whitish patches on leaves; (B) Faecal pellets on leaves; (C) Larva excreta on tassels.

chlorophyll, forming whitish long patches (Fig. 2A) and later on, making their way into tassels. The wounded plants had the typical characteristics of ragged leaves and shot holes. There were tiny holes and leaf margin damage on the same leaves. The feeding was confirmed by the presence of fresh faecal pellets (Fig. 2B) on the leaves and tassels (Fig. 2C) beside the larvae. Damasias *et al.* (2020) found the similar damage by the early and late instar larvae. Our findings were supported by Deole and Paul (2018), who reported similar fall armyworm damage in maize during vegetative and reproductive stage where the larvae scrape the leaf tissue, forming window pane like structures on leaf along with its faecal material at feeding areas. Similar damage type was reported in maize by Goergen *et al.* (2016), where larvae were feeding on maize crop at all growth phases causing heavy damage at early stages.

Morphometric identification: The larvae's morphological examination confirmed the morphological identity by displaying an inverted Y-shaped mark (Fig. 1A) on the head capsule and four square-shaped spots at the posterior segment (Fig. 1A). Similar description of both early and late instar larva was given by Hardke *et al.* (2015), Deole and Paul (2018) and Herlinda *et al.* (2022). The adult forewings were shaded in grey and brown, with triangular white dots towards the middle and at its tip. In both sexes, the hind wings had a short dark border and an iridescent silver-white color (Fig. 1C). Our findings are in line with that of Deole and Paul (2018) and Herlinda *et al.* (2022), quoting fall

armyworm having brown to grey forewing in both sexes with a white blotch at tip of forewing, and white colored hind

Table 1 Intraspecific genetic distance between *Spodoptera frugiperda* isolate from Wadura and COX1 sequences retrieved from GenBank

Place	Accession no.	Intra-specific genetic distance (%)	Reference
West Sumatra, Indonesia	MW876211	0.00152	Nelly <i>et al.</i> (2021a)
West Bengal, India	OK178016	0.00152	Barman <i>et al.</i> (2021)
Giza, Egypt	OQ150895	0.00153	El-Sayed (2023)
Faisalabad, Pakistan	MT180097	0.00153	Ahmad <i>et al.</i> (2020)
Giza, Egypt	OQ920981	0.00153	El-Sayed <i>et al.</i> (2023)
Maharashtra, India	MW561313	0.00153	Swathi and Venkatesan (2022)
Karnataka, India	MW561310	0.00153	Swathi and Venkatesan (2022)
Karnataka, India	MW561305	0.00153	Swathi and Venkatesan (2022)
Karnataka, India	MW561302	0.00153	Swathi and Venkatesan (2022)

Table 2 Morphometrics of different body parts of fall armyworm samples collected from infested maize field

Parameter	*Length (cm)	Range (cm)
Head	0.2	0.18–1.24
Antenna	0.9	0.83–1.03
Proboscis	0.8	0.77–0.87
Thorax	0.4	0.32–0.52
Abdomen	0.9	0.81–0.96
Forewing	1.5	1.4–1.65
Hindwing	1.2	1.1–1.3

*Mean of 10 replications.

wings in both sexes. The average (n=10) length (Table 2) of head, antenna, proboscis, thorax and abdomen was 0.2 mm, 0.9 mm, 0.8 mm, 0.4 mm and 0.9 mm, respectively. Forewing and hindwing measured as 1.5 cm and 1.2 cm, respectively with a total wing expansion of around 3.5 cm. The wing span of both sexes was in the range of 30–40 mm as per reports by Huesing *et al.* (2018). Navasero and Navasero (2020) also reported the adult body length as 13.33 mm with a total wingspan of 32.66 mm. Further, the larval head capsule length ranging between 0.22 mm in first instar to 2.03 mm in last instar. Similarly, Rakholiya *et al.* (2024) reported a wingspan of 32.77 mm in males and 32.15 mm in females of fall armyworm moths. Another report by Jena *et al.* (2024) also showed a wing span of adult males and females as 31.87 and 32.81 mm, respectively.

Molecular identification: After running the BLASTn tool of NCBI, it was found that the query sequence of current study, OQ352635 showed maximum resemblance with sequences MW561302, MW561305, MW561310, MW561313, OQ920981, MT180097 and OQ150895 and was sharing a common intra-specific distance of 0.00153% with all sequences. The same observations were revealed in phylogenetic tree also. All the sequences to which query

sequence was resembling more was that of fall armyworm from different localities, which makes our findings more evident. Thus, morphometric as well as molecular characterization of pest species infesting maize in Wadura,

Jammu and Kashmir, India is fall armyworm, *Spodoptera frugiperda*, which was previously not found in the Western Himalayan region of country. This being the first report, there is a lot to study on the infestation range and seriousness of damage across the Kashmir valley. So, to tackle this terrible pest, further research is needed to determine optimal management tactics, and an integrated approach combining biological, chemical, and cultural methods is needed.

SUMMARY

Maize queen of cereals is almost grown in every part of India, particularly under hilly areas as a mixed crop. However, this crop is prone to damage from various insect pests and diseases due to frequently changing weather conditions. One such invasion of an insect pest in India which within a year of invasion, made its way throughout maize-growing regions of India, endangering the maize crop growing area is the fall armyworm. The first occurrence of fall armyworm, in the western Himalayan region, with similar nature of infestation was noticed during 2022–23 in the maize fields of Sher-e-Kashmir University of Agricultural Sciences and Technology, Wadura, Sopore, Jammu and Kashmir. Both early and late instar larvae were found to form holes in maize plants, eating on the edges of the leaves with newly excreted debris suggesting their establishment on their host. During the investigation at morphological level, it was seen that the pest under study was fall armyworm. Later on the molecular characterization of this pest, done at ICAR-National Bureau of Agricultural Insect Resources, Bengaluru, Karnataka also confirmed it. The query sequences were showing much resemblance with the sequences retrieved from GenBank,

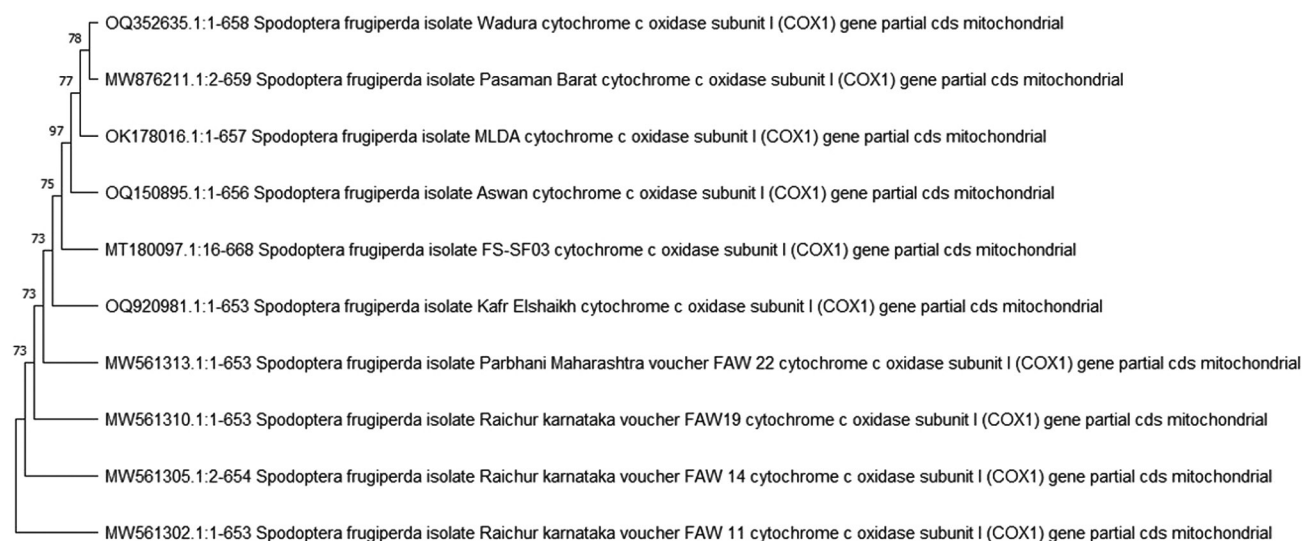


Fig. 3 Phylogenetic tree (Neighbor-joining) depicting evolutionary similarities between the query sequence and sequences retrieved from GenBank through BLASTn.

MW561302, MW561305, MW561310, MW561313, OQ920981, MT180097 and OQ150895 and was sharing a common intra-specific distance of 0.00153% with all the sequences. Hence, morphomolecular characterization of this pest confirmed the first report of the occurrence of fall armyworm in maize crops of Kashmir region of Jammu and Kashmir, India.

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