

Molecular Identification and Pathological characteristics of native isolated NPV against *Spodoptera litura* (Fabricius) in Pakistan

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Abstract

The cotton army worm *Spodoptera litura* Fabricius (Lepidoptera: Noctuidae) is a destructive pest of various field crops and vegetables in Pakistan. Development of bio pesticide is an attractive strategy to minimize the problems of pest resistance, environmental pollution and human health concerns. The isolates of *S. litura* Nucleopolyhedroviruses (SlNPV) were collected from infected larvae fed on natural cotton crops. The NPV was isolated from the larvae and viral occlusion bodies (VOBs) were detected using a light microscope. The toxicity of native isolates against *S. litura* also studied by testing different concentrations (1×10^2 POB (Polyhedral occlusion bodies) mL^{-1} - 1×10^{10} POB mL^{-1}) from the occlusion bodies produced from NPV isolates against 2nd, 3rd, 4th and 5th instar larvae of *S. litura*. The rapid and sensitive polymerase chain reaction (PCR) technique was used for the molecular detection of NPV gene from native NPV diseased insect. Multiple sequence alignment and phylogenetic analysis were performed to compare SlNPV- FSD15 based on *Lef-8* with other *Lef-8* genes sequences clearly showed that our SlNPV-FSD15 isolate belongs to *Spodoptera litura* associated NPVs. The biological activities of this NPV isolates were investigated under laboratory condition. The highest mortality of *S. litura* was observed at early instars. Against second instars of *S. litura*, LC_{50} values of NPV isolate ranged from 1.92×10^3 to 3.64×10^3 OB/ml with LT_{50} values of 69.30 hrs. to 72.80 hrs. respectively. This study showed highly effectiveness and provides an opportunity to cut down the use of synthetic approaches and develop safe biological/microbial insecticides from NPV isolates, which in future may effectively control *S. litura*.

35 **Keywords:** *Spodoptera litura*, PCR, NPV, Bio pesticide, DNA barcoding

36

37 INTRODUCTION

38 *Spodoptera litura* Fabricius (Lepidoptera: Noctuidae) is a cosmopolitan and polyphagous pest
39 which cause severe losses in southern and northern districts of Pakistan (Ahmed *et al.*, 2016;
40 Saleem *et al.*, 2016). It is widely distributed throughout Asia, Africa and Europe (Nathan *et al.*,
41 2005; El-Helaly, 2013) causing damage to numerous economically important cash crops such as
42 cotton, groundnut, soybean, tomato, sweet potato, onion, clover chili, cauliflower and cabbage
43 (El-bendary and El-Helaly, 2013; Saleem *et al.*, 2016). Current methods to control this pest are
44 based on the use of conventional insecticides which causes the development of resistance in the
45 pest and further has a negative environmental and human impact. Extensive use of synthetic
46 insecticides has led to outbreaks of insecticide resistance in *S. litura* (Bhatti *et al.*, 2013; Ahmed
47 *et al.*, 2015). The development of resistance in *S. litura* against organochlorine,
48 organophosphates and synthetic pyrethroids has been reported in the areas of cotton belt of south
49 Punjab, Pakistan (Ahmed *et al.*, 2015). An attractive and alternate tool for *S. litura* control is the
50 use of entomopathogens. Several species of insect viruses, bacteria, fungi and protozoa were
51 isolated and investigated for control of *S. litura* (Çakici *et al.*, 2014). In recent years, more than
52 600 insect species belonging to order Lepidoptera, Hymenoptera, Diptera, Orthoptera,
53 Coleoptera, Neuroptera, Thysanura, and Trichoptera infected with baculovirus have been
54 isolated (Haase *et al.*, 2015). Baculoviruses are insect-specific, diverse group of double-stranded
55 DNA circular viruses. Baculoviruses belong to the family Baculoviridae which is further divided
56 into two genera, the Nucleopolyhedroviruses (NPVs) and Granuloviruses (GVs) (Hu *et al.*, 2003;
57 Jehle *et al.*, 2006; Barreto *et al.*, 2005). The NPVs are cuboidal shaped having occlusion body of
58 0.4 to 2.5 µm in size visible under electron microscope (Moser *et al.*, 2001; Shapiro *et al.*, 2004).
59 Lepidopteran pests, *Spodoptera exigua* (Murillo *et al.*, 2001; Wu *et al.*, 2012; khattab *et al.*,
60 2013). *S. litura* (Lavina *et al.*, 2001; Martins *et al.*, 2005; Laarif *et al.*, 2011), *Helicoverpa*
61 *armigera* (Lepidoptera: Noctuidae) (Mehrvar 2007, Kumar *et al.*, 2012; Nouné and Hauxwell,
62 2015) and *Malacosoma americanum* (Demir, 2014) have shown susceptibility to several isolates
63 of NPV. Horizontal transmission of baculoviruses from one host to another occurs when a
64 susceptible insect ingests food contaminated with occlusion bodies (OBs) (Takahashi *et al.*,
65 2015). Several studies have reported the isolation of NPVs from *S. litura* (Lavina *et al.*, 2001;

66 Martins *et al.*, 2005; Lucien *et al.*, 2009, Laarif *et al.*, 2011; Kumar *et al.*, 2011), *H. armigera*
67 (Figueiredo, 1999; Ogembo *et al.*, 2007; Mehrvar ,2008 Kumar *et al.*, 2012; Noune and
68 Hauxwell, 2015), *S. exigua* (Murillo *et al.*, 2001; Wu *et al.*, 2012; khattab *et al.*, 2013),
69 *Trichoplusia ni* (Erlandson *et al.*, 2007) *Diaphania pulverulentalis* (Pachippan *et al.*, 2012),
70 turnip moth (Jakubowska *et al.*, 2005) and *Chrysodeixis includens* (Alexandre *et al.*, 2010).

71 All NPVs have molecularly been characterized by restriction endonuclease mapping of viral
72 DNA, showing that they can be distinguished from each other by one or more DNA restriction
73 enzyme fragments. At biological level, some of these strains have presented better insecticidal
74 activities, which make them more suitable to *S. litura* (Martins *et al.*, 2005; Laarif *et al.*, 2011),
75 *H. armigera* (Ogembo *et al.*, 2007; Mehrvar, 2008) and *S. exigua* control (khattab *et al.*, 2013).
76 The present study was planned to identify NPVs as a biological control agent for *S. litura* from
77 local Spodoptera NPV infected population. Therefore, a simple molecular procedure suitable for
78 diagnosis of viruses in their natural hosts was adopted and report the evaluation of its biological
79 activity against different instars is reported.

80 **MATERIALS AND METHODS**

81 **NPV diseased insect collection**

82 The original virus isolates were obtained from diseased *S. litura* larvae collected from cotton
83 field of PARS-UAF. The larvae that showed baculovirus infection symptoms were brought to
84 laboratory (Fig. 1A) and examined to confirm the presence of virus by light microscope with
85 Giemsa staining according to Mustafa *et al.* (2001). A thin smear of infected worm tissue was
86 mounted and air dried. The smear was immersed for 1-2 min in Giemsa, rinsed under running tap
87 water for 5-10 sec then the smear was stained for two hours in 10% Giemsa stain (10g of Giemsa
88 dissolved in 100ml distilled water). The dye was rinsed off in running tap water for 5-10 sec and
89 allowed to air dry, then examined under a light microscope to detect the occlusion bodies (OBs).
90 After the examination, the diseased larvae were kept at -20°C until the purification of OBs
91 (polyhedra)

92 **Light microscope examination**

93 Moribund larvae showing specific disease symptoms were individually examined for the
94 presence of polyhedral inclusion bodies using light microscope. A wet smear of the homogenized
95 liquid using a drop of haemolymph or a small part of larval tissue was spread on a glass slide and
96 stained in 10% Giemsa's stain for 10 min. The excess stain was then washed with running water

97 for 5-10 second (Wigley, 1976). The prepared smear was examined using the oil immersion of
98 phase contrast microscope. The smear test would allow recognition of the occlusion bodies of
99 nuclear polyhedrosis viruses NPV.

100 **NPV production and Purification**

101 The diseased larvae of 3rd to 5th instar of *Spodoptera litura* were collected from cotton fields in
102 Faisalabad, Pakistan, in 2013. The infected larvae showing baculovirus presence symptoms were
103 brought to IGCDB laboratory and stored at -20 °C until the isolation of OBs (polyhedra).
104 Isolation and purification of the NPV was performed in 4th instar of *S. litura*. Using
105 haemocytometer (Hausser Scientific), NPV viral concentrations were quantified under a light
106 microscope with six counts per hemocytometer. A stock suspension of NPV was prepared from
107 *S. litura* which was diluted to various concentrations 1×10^2 - 1×10^9 OBs/ml. Twenty-five larvae
108 were placed in 50 ml tube containing 25 ml 0.5% SDS and homogenized in conical tubes using
109 T-25 basic ULTRA-TURRAX set. Homogenates were filtered through 5 layers of cheesecloth
110 set in a funnel fitted with a wire mesh. Then, filtrate was transferred to 50 ml round bottom
111 polyb carbonate tubes.. POBs were settled at bottom of tube by centrifugation at 2700 rpm for 10
112 min at room temperature in 50 ml round bottom centrifuge tubes. Before final isolation, the
113 pellets were re-suspended in 0.1% SDS and re-suspension was repeated with 0.5 M NaCl. Then
114 the OBs were finally re-suspended in distilled water containing 0.02% sodium azide. Following
115 the protocol of Cheng et al. (1990), POBs were further purified according to sucrose gradient
116 centrifugation method.

117 **DNA extraction and PCR**

118 DNA was extracted from NPV infected larvae of *S. litura* with DNeasy Tissue kit (Qiagen,
119 Hilden, Germany) according to manufacturer protocols. Quantity and quality of extracted virus
120 DNA was estimated using UV spectrophotometer (Pico200) and by the ethidium bromide 1.5%
121 agarose gel electrophoresis respectively. The DNAs obtained were stored at -20°C until used.
122 The primer nucleotide sequences based on Nucleopolyhydroviruses (NPV) conserved gene late
123 expression factor (Lef-8) was carried out for PCR in a reaction volume of 48 µl. The reaction
124 volume contains ddH₂O (33 µl), 10Xreaction buffer (5 µl), 1 mM dNTPs (5 µl), 200 µM of each
125 forward and reverse primers (1 µl), and 1 µl of purified DNA (~ 50 ng). The lef-8 specific
126 degenerate primers (prL8-1 and prL8-2) developed by Lange et al. (2004) was used in PCR. The
127 amplification of DNA was accomplished with a PCR thermal cycler (PeqStar, Germany) under

128 following PCR cycling conditions. DNA samples were preheated to 95 °C for 4 min, followed
129 by 35 cycles with denaturation temperature of 95 °C for 2 min, annealing temperature of 46 °C
130 for 2 min, and extension temperature at 72 °C for 1 min. Then, final extension at 72 °C for 2 min
131 was included for final amplification. In the first step of PCR, 0.2 µl of Taq polymerase and 1.8µl
132 its dilution buffer was added in each tube making final reaction volume up to 50 µl.. The PCR
133 product was analyzed by 1% agarose gel electrophoresis at 80 V for 1 h. After the PCR, gels
134 were stained in solution of ethidium bromide (2µg/mL) and were visualized under UV light
135 using fisher scientific gel documentation system (Syngene™ IG3) for the confirmation of virus
136 presence.

137 **Nucleotide Sequencing and Phylogenetic Analysis**

138 Polymerase chain reaction product (745 bp) was purified using commercial kit and sequencing
139 was performed and analyzed on AbiPrism 3100 Genetic Analyzer apparatus (Applied
140 Biosystems, USA). The resulting Lef-8 sequence has been deposited in international database
141 (NCBI). NPV Lef-8 sequences identified by Blast sequence homology were downloaded from
142 Genbank database (<http://www.ncbi.nlm.nih.gov>). All Lef-8 sequences were aligned with
143 ClustalW and phylogenetic analysis was performed under MEGA6 software (Tamura et al. 2013)

144 **Insect Rearing and Bioassay study**

145 The *S. litura* larvae used in this experiment derived from cotton fields of Punjab and reared on
146 artificial diet consisting of chickpea flour 150g, sorbic acid 0.75 g, yeast powder 24g, linseed oil
147 6 ml, agar 8.4 g, vitamin mixture 0.02 g, ascorbic acid 2.35 g, methl-4-hydroxy benzoate 1.5 g, d
148 H₂O 550 ml and streptomycin 0.75 g. The rearing was done under controlled laboratory
149 condition (25± 2^oC, 70± 5 RH, 14:10 h light: dark photoperiod). The diet was stored at 4°C until
150 use. About fifty 2nd and 3rd instar *S. litura* larvae were transferred in individual plastic vials
151 containing 0.5 -1.5 g thin layer of artificial diet until they reached at fourth larval stage. Then,
152 they were transferred to boxes containing 3 cm thick layer of vermiculite (<0.5 mm grain size)
153 for pupation. Additional artificial diet was provided shortly before pupation. Pupae were
154 collected and incubated at 25 ^oC. All the larvae were maintained at 25±2°C, 75% r.h and 16:10
155 (D:L) photoperiod (Jehle et al., 2013).

156 All the bioassays were performed according to Lucien et al. (2009) with slight
157 modification. Briefly, Virulence of NPV was tested against 2nd, 3rd 4th and 5th instar larvae of *S.*
158 *litura*. Molted larvae were distinguished by their head capsule slippage and transferred to

159 individual vials for 12 h. Different NPV suspensions (1×10^2 ; to 1×10^9 POB mL^{-1}) were
160 prepared and 5-10 μl of each viral concentration was soaked with fresh piece of artificial (2mm^2)
161 in vials. Molted Larvae were allowed to feed on the treated artificial diets until complete
162 consumption. After consuming artificial diet, 25 larvae were individually shifted on diet without
163 virus suspension. Larvae served with virus free diet constituted the healthy controls. LC50 and
164 LT50 values were determined from data observed every day. Concentrations of OBs were
165 determined with haemocytometer under phase contrast microscopy at 400X magnification. All the
166 treatments were replicated thrice and maintained at $25 \pm 2^\circ\text{C}$, 75% r.h. and L16: D8 h
167 photoperiod.

168 **Statistical analysis**

169 The data were analyzed using Probit analysis software to arrive at lethal concentration of
170 virus required to cause 50% mortality (LC_{50}) and lethal time required to cause 50% mortality
171 (LT_{50})

172 **RESULTS**

173 **Symptoms of viral infection**

174 The native *Spodoptera litura* nucleopolyhydrovirus (NPV) isolate was obtained from infected
175 larvae collected from cotton field of Post graduate Agriculture Research Station (PRAS) of
176 University of Agriculture Faisalabad. The symptoms of viral infection on *S. litura* collected from
177 the cotton field were liquefied ruptured larval body (Fig. 1-A), and slow motion swollen larvae
178 with red color cuticle (Fig. 1-B). The field collected virus isolate was cultured in a *S. litura*
179 laboratory colony (Fig. 1-C-F). Then infected propagated colony was then purified and kept at -
180 80°C for further studies.

181 **Microscopic Examination**

182 The viral occlusion bodies (VOBs) from diseased larvae were observed under a light as well as
183 inverted microscope. A thin smear of infected larvae fluid was stained with drop of Giemsa,
184 VOBs appearing as polyhedral and negatively stained particles. Under light and inverted
185 microscope, NPV associated occlusion bodies were observed (Fig.2)

186 **PCR of NPV specific gene**

187 The infected samples collected from Faisalabad district were analyzed for PCR detection.
188 The partial codons sequence of the late expression factor-8 (Lef-8) gene was amplified using

189 specific PCR primers. Gel electrophoresis analysis of the PCR product showed an amplification
190 of single fragment at correct length (~745 bp)(Fig. 3).

191 **DNA sequencing and Phylogenetic analysis**

192 The evolutionary history was inferred by using the Maximum Likelihood method based on the
193 Tamura-Nei model (Tamura and Nei, 1993). Phylogenetic analyses were conducted in MEGA6
194 (Tamura et al., 2013) for the comparison of the SINPV-FSD15-lef-8 gene sequences with the
195 sequences of other lef-8 genes of various nucleopolyhydroviruses (NPVs) available in GenBank.
196 The nucleotide sequence of the native NPV isolate (Slt NPV-FSD15) is composed of 745bp,
197 submitted at GenBankNCBI. This sequence was aligned using ClustalW with the NCBI available
198 nucleotide sequences of NPVs associated with different insects. The molecular phylogeny of
199 nucleotide sequence of the SINPV-FSD15-lef-8 showed maximum homology (99-100%) with
200 nucleotide sequence of SpliNPV from *Spodoptera litura* of Germany, (AY706581.1), Japan
201 (AB326103.1, AB583682.1, AB581187.1)), and Indian origin, (JF2760358.1),. The *Helicoverpa*
202 *armigera* associated NPV formed separate clade clearly distinguished from *Spodoptera litura*
203 NPV isolates with lowest similarity percentage index (Fig. 4) which was observed between 82-
204 90%.

205 **Biological activity of native SpltNPV-FSD15 isolate**

206 Bioassay of isolated strain of SpltNPV against 2nd, 3rd, 4th and 5th instars larvae of *S.*
207 *litura* under laboratory condition show a wide range of variation in its biological activity. The
208 LC50 values in three experiments of SpltNPV were inversely correlated with the age of the
209 larvae, LC50 values being the highest for fifth instars. Similarly, LT50 was as low as 69-72
210 hours for second instar larvae and regularly increased to reach at 144 to 146 hours for fifth larvae
211 instars. LT50 values were not significantly different between the different independent
212 experiments. Bioassay result revealed that the SpltNPV strain isolated from *S. litura* was highly
213 effective especially against 2nd, 3rd instar larvae. In first experiment, LC50 values for 2nd, 3rd, 4th
214 and 5th instar larvae were 2.64×10^3 , 2.92×10^4 , 2.94×10^5 , and 2.15×10^6 OBs/ml respectively.
215 Briefly, in the third experiment, for 2nd instars, the most virulent LC₅₀ value (1.92×10^3 POB
216 mL⁻¹) was observed, followed by 2nd and 1st experiment (Table 1). The order of LC₅₀ value in the
217 case of three experiments of SpltNPV was second < third < forth < fifth instar. Similarly, LT₅₀
218 value of 3rd spltNPV experiment was the lowest (59 hours) followed by 2nd and 1st experiment
219 (Table 2).

220

221 **DISCUSSION**

222 *S. litura* (Lepidoptera: Noctuidae) also called armyworm is one of the most destructive
223 and notorious phytophagous insect pests on cotton, vegetables and other field crops. Microbial
224 bio-pesticides based on native baculoviruses have great potential in agriculture with better
225 insecticidal characteristics and higher safety' for environment. The NPV virus isolates was
226 obtained from diseased *S. litura* collected cotton. The diseased larvae exhibited viral-like
227 symptoms such as swollen bodies, moribund appearance when field collected and also when
228 laboratory NPV treated. . Similarly, because of deposition of occluded viruses (OVs), infected
229 larval bodies become pale and their cuticle ruptured discharging body fluid and ultimately killing
230 the insect. Similar results were reported by Toprak *et al.* (2005). The viral occlusion bodies
231 (VOBs) of the Pakistani nucleopolyhedrovirus isolates (SINPV-FSD15) were detected using a
232 light microscope by staining thin smear of infected larvae and drop of VOBs with Giemsa stain
233 which appeared polyhedral and negatively stained particles. The developed bio informative tools
234 and application of latest genomic data facilitated the identification of viruses because of good
235 primer designing. Here, we also used molecular techniques to characterize native *S. litura*
236 associated NPVs that were found identical to SpltNPVs from other countries and clearly
237 different from *Helicoverpa armigera* and *Mythimna separata* NPVs (Kouassai *et al.*, 2009).
238 Further, LC50 values against 2nd -5th instars with LT50 values of this NPV isolate (SltNPV-
239 FSD15) indicated a significant effective control against *S. litura*. Result obtained by Laarif *et*
240 *al.* (2011) indicated that amino acid and nucleotide sequences of *S. littoralis* (Tun-SINPV)
241 nucleopolyhedrovirus strain was almost identical with different GenBank deposited sequences of
242 NPVs (Clem *et al.*, 2013; Ikeda *et al.*, 2013).

243 In bioassay, increasing value of LC50 and LT50 with the age of the host showed the
244 susceptibility of the different larval stages; decline in *S. litura* susceptibility to NPV is due to
245 dilution effect because larval weight increased as the insect grows (Briese *et al.*, 1986). Lucein *et*
246 *al.* (2009) and Bhutia *et al.* (2012) also found that LC50 and LT50 values were increased as
247 larval age increased showing - against SpltNPVN. However, Trang *et al.* (2002) reported that
248 older larvae of *S. litura* were not affected through ingestion, but intra haemocoelic infection of
249 NPV in mature insect resulted in insect death (Rao *et al.*, 2015). SpltNPV isolate from
250 Biocontrol research laboratory (BCRL) was found to be virulent against 3rd instar larvae of *S*

251 *litura* larvae with LT₅₀ value (122.16 d) at 1×10⁶ OB's/ ml (Bhutia *et al.*, 2012). Subramanien *et*
252 *al.* (2005) described that LT₅₀ values for larvae of *S. litura* was dose-dependent. The LC₅₀ value
253 for the larvae of *S. litura* increases 15,000 times in 2 day-old larvae as compared to 8th day larvae
254 (Trang *et al.*, 2002). Similar trend for LC50 of SpltNPV isolate against 2nd and 3rd were (3.5 9
255 ×10⁴ and 2.4 9× 10⁵ OBs/ml) observed (Kumar *et al.*, 2011). In summary, increasing dose of
256 NPV caused significant reduction in the survival times of Lepidoptera larvae. This pattern was
257 also observed in instar of *Mythima separata* and third instars of *S. litura* larvae (Koussoi *et al.*,
258 2009). Minimum lethal time (LT50) (96-216 hrs) of different instars of *S. litura* suggests that
259 application of SpltNPV isolate as bio insecticide would be economic and attractive strategy for
260 the control of *S. litura*. (Lucein *et al.*, 2009) .Contradictory results were found by Koussoi *et al.*
261 (2009) who observed that high LC50 of MSNPV (180 hrs) and Indian NPV isolates (240 hrs)
262 against *M. separata* made clear that their sole application would not be an efficient strategy for
263 insect control, but should become effective bio insecticides when combined with enhancers. In
264 our case, the very good results of LC50 and LT50 showed highly effectiveness of Slt NPV-
265 FSD15 isolate against all tested instars of *S. litura* as compared to other reported SltNPV
266 isolates. The biological activity of this isolate is under progress against other important
267 lepidopterous pest of major agriculture crops.

268 CONCLUSION

269 The indigenous NPV strain associated to *S. litura* (SltNPV-FSD15) collected from Faisalabd
270 cotton fields was successfully isolated from NPV infected larvae of *S. litura* and characterized
271 and evaluated against this important insect pest. The results confirmed that this native isolate
272 (SltNPV FSD-15) was highly effective against *S. litura* showing high mortality with reduced
273 LT50 values as compared to other SltNPVs reported from other countries. We have also
274 developed NPV based microbial insecticide using this native NPV isolate. The efficacy
275 evaluation of some other native SltNPV isolates collected from various regions of Punjab is
276 under process,

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282 **Conflict of interest statement**

283 The authors have no conflict of interest.

284

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434 Fig.1. NPV infected *S. litura* (A) Typical NPV symptom of NPV ruptured infected larvae,
435 usually die 4–9 days after infection, disintegrate and release a virus-laden fluid (B) Slow move
436 NPV infected swollen malformed pale brown larva; C- Slow move NPV infected swollen
437 malformed dark larva from 5th Instar (D-E) Malformed pre-pupae (F) Laboratory propagative
438 NPV infected larva (G) Healthy larva

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440 Fig.2. (A) NPV infected *S. litura* viral occlusion body's polyhedra under light microscopy (B)
441 degenerating (ruptured) infected *S. litura* cell.

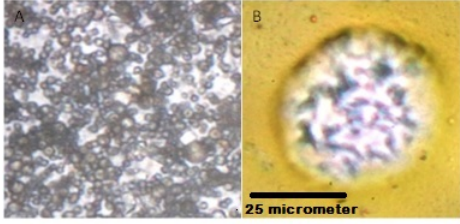
442
443 Fig.3. PCR detection of NPV from *S. litura* infected samples from Pakistan by using NPV LEF8-
444 specific primers: Lane1-3 Non infected *S. litura* Larva, Lane 4-8 NPV infected *S. litura* larva
445 (Pak-15 Faisalabad strain), M- 1 kb DNA Marker (Invitrogen).

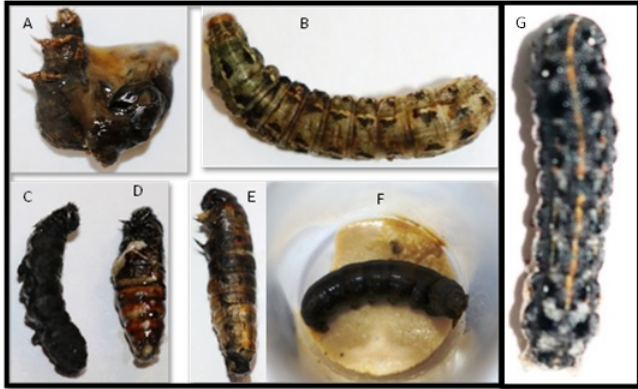
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448 Fig.4. Molecular Phylogenetic analysis by Maximum Likelihood method of Pakistani isolate
449 SltNPV-FSD15 strain based on nucleotide sequences with the corresponding partial late
450 expression factor-8 (Lef-8) gene of 12 nucleopolyhydroviruses associated with *S. litura* (NPVs).
451 *S. litura* associated NPV isolates origin and GenBank accession numbers used in the sequence
452 analysis and phylogenetic tree construction; AY706581.1 S37 (Germany), JF276035.1
453 (Banglore, India), AB451187.1 (AB326103.1, AB451187.1, AB583682.1 (Japan). The numbers
454 represent bootstrap percentage values based on 1,000

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463 Table 1.- LC50 (95% CL) values of SPLtNPV-FSD15 Isolate against 2nd, 3rd and 4th instar of *Spodoptera litura*.

Instars	SPLtNPV-1					SPLtNPV-2					SPLtNPV-3				
	LC50	Slope	X ²	Df	P	LC50	Slope	X ²	Df	P	LC50	Slope	X ²	Df	P
Second	2.64×10 ³	10298210	3.02009	1	0.082	1.94×10 ³	10672645	3.07360	1	0.080	1.92×10 ³	10672645	3.05460	1	0.081
Third	2.92×10 ⁴	9727687	3.87286	1	0.049	1.66×10 ⁴	10301158	4.45550	1	0.874	1.91×10 ⁴	9898068	5.46667	1	0.019
Fourth	2.94×10 ⁵	248157064	0.173039	1	0.677	2.68×10 ⁵	69371413	0.0973090	1	0.755	3.9×10 ⁵	55947328	0.09-3141	1	0.764
Fifth	2.15×10 ⁶	65593222	0.449124	1	0.503	2.34×10 ⁶	56888296	0.294854	1	0.587	3.96×10 ⁶	54577160	0.295128	1	0.587

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465 Table 2.- LT50 (95% CL) value of SPLtNPV-FSD15 isolate against 2nd, 3rd, 4th and 5th instar of *Spodoptera litura*.

Instars	SPLtNPV-1					SPLtNPV-2					SPLtNPV-3				
	Lt50 (hr)	Slope	X ²	Df	P	Lt50(hr)	Slope	X ²	Df	P	Lt50(hr)	Slope	X ²	Df	P
Second	72.50	0.917231	0.304227	1	0.581	70.4	0.948467	0.587796	1	0.443	69.30	0.953284	0.657373	1	0.417
Third	95.76	0.802226	0.117478	1	0.732	98.4	0.786250	1.49456	1	0.222	93.6	0.839378	1.10078	1	0.294
Fourth	121.6	0.713918	0.0030889	1	0.956	125.2	0.700997	0.0038591	1	0.950	123.5	0.693892	0.118227	1	0.731
Fifth	144.64	0.654180	0.0038249	1	0.951	146.8	0.660854	0.0632983	1	0.801	145.8	0.676337	0.0005908	1	0.981

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