Molecular Diagnosis of Iris Yellow Spot Virus (IYSV) on Onion in Iran

N. Beikzadeh1*, B. Jafarpour1, H. Rouhani1, D. Peters2, and A. Hassani-Mehraban2

ABSTRACT

Viral symptoms indicative of Iris yellow spot virus (IYSV) were observed on onion in several fields near Chenaran in Khorasan Razavi Province. Mechanical inoculation of herbaceous hosts with onion sap extracts from symptomatic plants showed similar symptoms to those described for IYSV. The mechanically transmitted virus reacted only with antisera specific to IYSV in DAS-ELISA but not with antisera specific to seven other tospoviruses. In RT-PCR, a DNA fragment approximately 822 bp in size was amplified from infected Nicotiana benthamiana by using primers specific to the nucleocapsid (N) gene of IYSV. After cloning and sequencing, the deduced N protein sequence of two isolates (GenBank accession no. HQ148173 and HQ148174) showed 98% amino acid identity with a Sri Lankan isolate, 96% with a Dutch isolate and 92% with a Brazilian isolate. To our knowledge, this is the first molecular characterization of IYSV in Iran.

Keywords: Iran, Iris yellow spot virus, Molecular diagnosis, Onion.

INTRODUCTION

Tospoviruses are among the most destructive and widespread plant viruses, causing severe damage in a broad range of crops throughout the world, both in field and in greenhouses (Mumford et al., 1996). All tospoviruses are transmitted by thrips in a propagative-circulative manner and in recent years, several species have caused severe damage in tropical and subtropical regions (Persley, 2006). Today, 21 tospovirus species are approved or proposed based on serological and phylogenetic relationships of nucleoprotein (N proteins), host ranges and vector specificity (Persley et al., 2006). In tospoviruses, the most common gene sequenced is the nucleocapsid (N) gene and sequence comparisons have proven useful in the identification and classification of the viruses (Pappu et al., 2006).

Hall et al. (1993) first described a new tospovirus infecting onion (Allium cepa) in the USA. This virus was later isolated from iris (Iris hollandica) and leek (A. porrum) in the Netherlands and, after characterization, was named Iris yellow spot virus (IYSV; genus: Tospovirus; family: Bunyaviridae) (Cortéz et al., 1998; Smith et al., 2006). Today, IYSV has a worldwide distribution in onion and leek crops, and in various ornamentals, including iris, alstroemeria, lisianthus and amarilis (Kritzman et al., 2000; Mitsuru et al., 2005; Smith et al., 2006). The virus has been reported from several countries around the world (Pozzer et al., 1999; Bulajić et al., 2009; Gent et al., 2004; Ghotbi and Shahraeen, 2005; Pappu et al., 2006). Disease symptoms caused by IYSV include chlorotic and necrotic eye-like or diamond-shaped lesions on onion stalks (Gent et al., 2006). Once IYSV is established in an area, it spreads rapidly in

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onion crops. For example, in Colorado, its incidence increased from 6% in 2001 to 73% two years later (Gent et al., 2004).

In Iran, onion is one of the most important leafy vegetables. It is cultivated in open fields on approximately 50,000 ha with a production of 1.85 million tons per year (Anon., 2009). Using ELISA, the virus was first reported on onion in Iran in 2005 (Ghotbi and Sharaeen, 2005). Also, other studies reported the presence of IYSV in onion and some ornamentals in Iran using ELISA (Jafarpour et al., 2009). To date, no information is available on the nucleotide sequence of the N gene of IYSV isolates from Iran. In this study, the virus was diagnosed using molecular methods and its phylogenetic situation was determined.

MATERIALS AND METHODS

Plant Materials

Onion plants with characteristic symptoms of tospoviruses were collected and analysed for the infecting virus.

Bioassay

Infected onion leaves collected from the fields were used for sap inoculation on Nicotiana benthamiana, Petunia hybrida and Datura stramonium. Infected areas of the leaves were harvested and macerated using sterilized and chilled pestle and mortar adding 0.01 M phosphate buffer (pH 7) containing 0.1% sodium sulfite. The extracted sap was used for inoculation (Hassani-Mehraban et al., 2005; Bulajić et al., 2009) and applied directly by rubbing gently onto the leaves. The inoculated plants were then kept in an insect-proof glasshouse.

Serological Test

Double-antibody sandwich enzyme-linked immunosorbertent assay (DAS-ELISA) was performed to detect the infection of tospovirus in the collected onion samples. Polyclonal antibodies directed against the N protein of Tomato yellow ring virus (TYRV), Iris yellow spot virus (IYSV), Tomato spotted wilt virus (TSWV), Impatiens necrotic spot virus (INSV), Groundnut bud necrosis virus (GBNV), Groundnut ring spot virus (GRSV), Tomato chlorotic spot virus (TCSV) and Chrysanthemum stem necrosis virus (CSNV) that were previously prepared at Wageningen University were used to check the serological identity of the onion tospovirus isolates. Symptomatic leaf samples of N. benthamiana were extracted in extraction buffer (1:30 w/v). The immunoglobulin (IgG) and alkaline phosphatase conjugate (1 mg ml⁻¹) were diluted 1,000 times and the substrate solution was used in a concentration of 0.1 mg ml⁻¹. After incubating the substrate at room temperature for 1 hour, absorbance values were recorded at 405 nm using a plate reader (FLUOstar OPTIMA, BMG LABTECH GmbH, Germany), (Clark and Adams, 1977; de Ávila et al., 1990; Gent et al., 2004).

Total RNA Extraction and RT-PCR

Total RNA from healthy and infected N. benthamiana leaves was extracted using Trizol reagent (Invitrogen, USA) according to the manufacturer’s instructions. RT-PCR was used to characterize the IYSV N gene in samples that showed a positive reaction in DAS-ELISA. The first strand cDNA synthesis was performed in the presence of specific primers IY1 (5'-ATGGCTACCGTGTAAGG-3') and IY2 (5'-TAAATTATATCTATCTTCTTGGG-3') (Cortêz et al., 1998; Pozzer et al., 1999), total RNA, AMV Reverse Transcriptase (22 U µl⁻¹, Promega, USA), 5x buffer, RNase inhibitor (40 U µl⁻¹, Promega), dNTPs (10 mM) and sterile RNase-free water at 60°C for 1 hour after a 3 min denaturation at 85°C. PCR amplifications were carried out using a modification of a published method (Pozzer et al., 1999) in a 50 µl reaction...
mixture containing 5x GoTaq buffer, 25 mM MgCl₂, 10mM dNTPs, GoTaq polymerase (5 U µl⁻¹, Promega), primers and cDNA. All PCR reactions were performed in an automated thermal cycler (Peqlab, Primus 25) by pre-heating at 92°C for 2 minutes followed by 30 cycles of 30 seconds of denaturation at 92°C, 30 seconds of annealing at 55°C and 1 minute for extension at 72°C. Finally, the amplified DNA was incubated at 72°C for 7 minutes to accomplish a final extension. Amplified products were analyzed by 1% agarose gel electrophoresis in TAE buffer and stained with ethidium bromide.

**Cloning, Digestion and Phylogenetic Analysis**

DNA fragments of the IYSV N gene of the expected size were excised from the gel and extracted using the GFX™ PCR DNA and Gel Band Purification Kit (GE Healthcare UK Limited) according to the manufacturer’s instructions. The purified fragment was ligated into the pGEM-T Easy vector (Promega) and cloned in *Escherichia coli* DH5α. Isolation of recombinant plasmid DNA was done using GeneJET™ Plasmid Miniprep Kit (Fermentas, Germany) according to the manufacturer’s instructions. The presence of an insert in transformants was confirmed by restriction enzyme *NotI* digestion. Finally, the selected recombinant clones were sequenced at the automatic DNA sequencing facility (Sanger et al., 1977) using SP6 primer. The nucleotide sequences were translated to N protein sequences using Expasy software (http://expasy.org/tools/dna.html). The sequence data were compiled, analyzed, and compared with those available in the GenBank using NCBI/BLAST.

Data from a Clustal W alignment (Thompson et al., 1994) of N protein sequences were used as input for phylogenetic tree construction using MEGA 4.0 software (Tamura et al., 2007). Genetic distances (the average number of nucleotide substitutions between two randomly selected sequences in a population) between IYSV isolates from Asia, Europe, Oceania, and America continents were calculated using MEGA 4.0 based on the Kimura two parameter model. The average number of non-synonymous substitutions per non-synonymous site (dN) and the average number of synonymous substitutions per synonymous site (dS) were estimated using DnaSP (Rozas and Rozas, 1999; Yang and Bielawski, 2000; Wei et al., 2009). The dN/dS ratio was used to estimate natural selection pressure.

**RESULTS AND DISCUSSION**

**Plant Samples**

In July 2009, symptoms indicative of tospovirus infection such as chlorotic and necrotic eye-like or diamond-shaped lesions on onion stalks were observed in several fields near Chenaran in Khorasan Razavi Province. Symptoms were similar to those caused by IYSV. Leaves and stalks with well pronounced symptoms were used in our study to confirm the presence of IYSV.

**Bioassay**

Bioassay studies revealed that the tospovirus from symptomatic onion plants could be mechanically transmitted to indicator plants. Necrotic local lesions were observed on the inoculated leaves of *P. hybrida*. The inoculated leaves of *N. benthamiana* showed chlorotic spots followed by systemic necrosis on newly developed upper leaves and branches. The symptoms were similar to those of other IYSV isolates (Pozzer et al., 1999; Kritzman et al., 2001). Mechanical inoculation on *D. stramonium* induced necrotic local lesions on the inoculated leaves. The symptoms caused by our IYSV isolates on *D.
stramonium were identical to those described by Gera et al. (2002). The various IYSV isolates cause different symptoms on D. stramonium. Some of them cause systemic infections (Cortêz et al., 1998; Pozzer et al., 1999), whereas some cause only local infection (Gera et al., 2002). However, Bulajić et al. (2009) did not observe symptoms on plants of this species. These differences may be related to different IYSV strains, environmental conditions, or differences in the susceptibility of the D. stramonium accessions (Pozzer et al., 1999). These data suggested that the pathogen causing the observed symptoms was likely IYSV. However, attempts to verify Koch’s postulates and back-inoculate the virus onto onion failed. Similar observations were also made earlier for IYSV (Pozzer et al., 1999).

Serology

Of the eight polyclonal antisera directed against the N protein of different tospoviruses, onion samples reacted only to IYSV antiserum in DAS-ELISA (Figure 1). No reaction was observed with antisera raised against the other seven tospoviruses tested. The onion tospovirus isolate was designated IYSV-O based on the serological data.

RT-PCR

According to the DAS-ELISA data, only specific primers designed in the IYSV N gene were used in RT-PCR to characterize the virus in symptomatic N. benthamiana. A fragment of approximately 822 bp in size was obtained from samples O5, O9, and O18. No DNA bands were observed from healthy tissue (Figure 2). Primer IY1 was complementary to the first 16 nucleotides at the 5’-end of the N gene of a Dutch IYSV isolate (GenBank accession no. AF001387) and primer IY2 was identical to the first 23 nucleotides at the 3’-end (Cortêz et al., 1998). The IYSV identity of the PCR products was confirmed by cloning and sequencing.

Cloning and Phylogenetic Analysis

PCR amplicons were cloned and sequenced. The sequence of IYSV isolates from onion samples O5 (GenBank accession no. HQ148173) and O18 (GenBank accession no. HQ148174) was determined. Comparative sequence analyses revealed that the two IYSV isolates shared 98% sequence identity with a Sri Lankan IYSV isolate (GenBank accession no. GU901211), 96% sequence identity with a Dutch IYSV

![Figure 1](https://example.com/figure1.png)

**Figure 1.** Serological reactions between eight tospoviruses and the onion tospovirus isolate showing amount of relatedness using polyclonal antisera against their respective N proteins. Infected plant extracts were used as antigen sources.
Molecular Diagnosis of Iris Yellow Sport Virus

Figure 2. RT-PCR amplification of the IYSV N genes of onion samples: Lane M: Lambda DNA/PstI marker; Lane N: Healthy control, Lanes O5, O9 and O18: Samples of three different symptomatic onion samples.

Table 1. IYSV isolates and their GenBank accession number.

<table>
<thead>
<tr>
<th>Acc. No.</th>
<th>Host</th>
<th>Geographical Origin</th>
</tr>
</thead>
<tbody>
<tr>
<td>AF001387</td>
<td>Iris</td>
<td>Netherlands</td>
</tr>
<tr>
<td>EU287943</td>
<td>Onion</td>
<td>Canada</td>
</tr>
<tr>
<td>FJ785835</td>
<td>Onion</td>
<td>Greece</td>
</tr>
<tr>
<td>FJ713700</td>
<td>Onion</td>
<td>America</td>
</tr>
<tr>
<td>FJ514257</td>
<td>Garlic</td>
<td>America</td>
</tr>
<tr>
<td>GU901211</td>
<td>Leek</td>
<td>Sri Lanka</td>
</tr>
<tr>
<td>AB378751</td>
<td>Allium tuberosum</td>
<td>Japan</td>
</tr>
<tr>
<td>EU750697</td>
<td>Onion</td>
<td>Serbia</td>
</tr>
<tr>
<td>DQ838590</td>
<td>Onion</td>
<td>Guatemala</td>
</tr>
<tr>
<td>DQ150107</td>
<td>Onion</td>
<td>Chile</td>
</tr>
<tr>
<td>AY377428</td>
<td>Leek</td>
<td>Slovenia</td>
</tr>
<tr>
<td>AY345226</td>
<td>Onion</td>
<td>Australia</td>
</tr>
<tr>
<td>AF067070</td>
<td>Onion</td>
<td>Brazil</td>
</tr>
<tr>
<td>EU477515</td>
<td>Onion</td>
<td>New Zealand</td>
</tr>
<tr>
<td>AB121026</td>
<td>Lisianthus</td>
<td>Japan</td>
</tr>
<tr>
<td>AB181370</td>
<td>Alstroemeria</td>
<td>Japan</td>
</tr>
<tr>
<td>FJ185142</td>
<td>Onion</td>
<td>Italy</td>
</tr>
<tr>
<td>EU310299</td>
<td>Onion</td>
<td>India</td>
</tr>
<tr>
<td>HQ148173</td>
<td>Onion</td>
<td>Iran</td>
</tr>
<tr>
<td>HQ148174</td>
<td>Onion</td>
<td>Iran</td>
</tr>
</tbody>
</table>

isolate (GenBank accession no. AF001387) and 92% sequence identity with a Brazilian IYSV isolate (GenBank accession no. AF067070). To consider a tospovirus isolate as a distinct species, N protein amino acid sequence identity (%) should be below 90% (de Ávila et al., 1990) compared to other described tospovirus N proteins, therefore, both IYSV-O5 and IYSV-O18 could not be considered as a distinct species.

To determine the phylogenetic relationship of the two IYSV isolates with tospovirus species, the amino acid sequences of both isolates and 19 tospovirus sequences available in the GenBank were aligned using Clustal W (Thompson et al., 1994). Moreover, amino acid sequences of the IYSV-O5 and IYSV-O18 isolates and 18 IYSV isolates in GenBank (Table 1) were aligned. Data from the multiple sequence alignment of N protein sequences were used for the construction of a phylogenetic tree (consensus phylogenetic tree) using the neighbor-joining method of MEGA 4.0 software. Bootstrap values are shown as percentages derived from 500 replicates (Tamura et al., 2007) (Figures 3 and 4). The results clearly showed that the tospoviruses were distributed in two major clades (Figure 3). One clade (American tospovirus clade) contained all tospovirus species that were isolated and primarily distributed in American countries, while the second clade (Eurasian tospovirus clade) contained all species that were isolated and primarily distributed in Eurasian countries (Hassan-Mehrabani et al., 2010). IYSV-O5 and IYSV-O18 clustered with IYSV within the second clade, as expected. This analysis is in agreement with the close relationship of
Figure 3. Cluster dendrogram based on the amino acid sequences deduced from the complete N gene sequences of tospovirus species: (Abbr. ASNV: Alstroemeria necrotic streak virus; CCSV: Calla lily chlorotic spot virus; CaCV: Capsicum chlorosis virus; MeSMV: Melon severe mosaic virus; MYSV: Melon yellow spot virus; PCFV: Peanut chlorotic fan-spot virus; PYSV: Peanut yellow spot virus; TZSV: Tomato zonate spot virus; WBNV: Watermelon bud necrosis virus; WSMoV: Watermelon silver mottle virus; and ZLCV: Zucchini lethal chlorotic virus).

Figure 4. Cluster dendrogram based on the amino acid sequences deduced from the complete N gene sequences of IYSV isolates.
Table 2. Genetic distances within districts for N gene. Standard error (SE) was calculated by using a bootstrap of 500 replicates.

<table>
<thead>
<tr>
<th>District</th>
<th>Sequence No.</th>
<th>( \text{Pi(s)} ) and C (( \text{dS} ))</th>
<th>( \text{Pi(a)} ) and C (( \text{dN} ))</th>
<th>( \text{dN/dS} )</th>
<th>Genetic distance within each district</th>
<th>SE</th>
</tr>
</thead>
<tbody>
<tr>
<td>World</td>
<td>20</td>
<td>0.33670</td>
<td>0.03829</td>
<td>0.1137</td>
<td>0.094</td>
<td>0.007</td>
</tr>
<tr>
<td>American</td>
<td>6</td>
<td>0.22229</td>
<td>0.02384</td>
<td>0.1072</td>
<td>0.0621</td>
<td>0.0055</td>
</tr>
<tr>
<td>Asian</td>
<td>7</td>
<td>0.23077</td>
<td>0.02659</td>
<td>0.1152</td>
<td>0.0667</td>
<td>0.0057</td>
</tr>
<tr>
<td>European</td>
<td>5</td>
<td>0.41754</td>
<td>0.05407</td>
<td>0.1294</td>
<td>0.1211</td>
<td>0.0096</td>
</tr>
<tr>
<td>Oceanian</td>
<td>2</td>
<td>0.53842</td>
<td>0.05647</td>
<td>0.1048</td>
<td>0.1444</td>
<td>0.0147</td>
</tr>
</tbody>
</table>

TYRV and IYSV (Hassani-Mehraban et al., 2005) and the fact that IYSV is more closely related to the Asian tospovirus species GBNV and WSMoV than to any of the other tospovirus species (Cortêz et al., 1998).

Phylogenetic relationships of IYSV-O5 and -O18 with other 18 IYSV isolates are shown in Figure 4. The IYSV isolates from four geographic origins i.e. America, Asia, Europe and Oceania (Table 2) grouped into two major clades. Clade 1 contained several Asian isolates, two European isolates, one Oceanian isolate (from Australia) and an American isolate (from Northern America). Nine isolates were found in clade 2 containing several American isolates, two European isolates, one Oceanian isolate (from New Zealand) and one Asian isolate. The Slovenia isolate (GenBank accession no. AY377428) was equally distant from the isolates in clade 1 and 2. Southern American isolates only clustered within clade 2. As shown in a previous study on Rice stripe virus (RSV) (Wei et al., 2009), IYSV isolates clustering within two distinct clades (e.g. Japanese and Oceanian isolates) are more diverse than other isolates. IYSV-O5 and IYSV-O18 isolates reported from Iran (Iranian isolates) in Asia clustered within clade 1 and showed a distant phylogenetic relationship with the Southern American isolates. Both Iranian isolates were more closely related to a recent published Sri Lankan isolate and clustered together. The phylogenetic relationship shown in Figure 4 confirmed amino acid sequence identities of the N proteins of the both Iranian isolates with that of Sri Lankan (98%), Dutch (96%) and Brazilian isolates (92%). Also, the analyses indicated that both Iranian isolates and Sri Lankan isolate shared a common ancestor, providing a clue to the origin of the Iranian isolates, although more sequences data are needed. Furthermore, the analyses raise a question over the taxonomic status of the Slovenian isolate (Smith et al., 2006) because it did not fit in any of the two clades and its amino acid identities with those of other IYSV isolates had a wider difference of 84-87%.

The results shown in Table 2 indicate that the mean genetic distance within all IYSV isolates is 0.094 and the maximum and minimum genetic diversity can be found within the Oceanian and American isolates, respectively. The geographical origin of a virus can be inferred from the extent of its genetic diversity. If a viral population shows a high genetic diversity, it is usually considered to be more ancient (Wei et al., 2009). Although a larger number of isolates should be analyzed for a more accurate estimation of IYSV genetic diversity, based on our data, we can conclude that the Oceanian isolates are older than the American isolates. The historical record of disease may or may not be consistent with the extent of genetic diversity. For example, the genetic diversity of the Indonesian Rice tungro bacilliform virus (RTBV) population is higher than its population in the Philippines. The virus was reported in 1840 in Indonesia and in 1940 in the Philippines. Therefore, its genetic diversity is consistent with historic records of rice tungro disease. On the other hand, RSV was initially reported in eastern China, but southwest China could be the geographical origin of the virus in China due to its higher genetic diversity in that region (Wei et al., 2009).
IYSV was initially reported in Australia and New Zealand in 2003 and 2008, respectively (Ward et al., 2008), but its genetic diversity is higher than the American and European isolates. In spite of iris yellow spot disease being initially described in 1993 (Hall et al., 1993) and then its cause designated Iris yellow spot virus in the Netherlands in 1998 (Cortêz et al., 1998), Oceania could be considered as IYSV geographical origin due to its high genetic diversity in the continent.

Genetic distances between four districts of IYSV isolates (i.e. American, Asian, European and Oceanian) were calculated (Table 3). According to the results, genetic diversity varied between the districts, ranging from 0.0801 to 0.1052. Host-virus interaction, vector-virus interaction, and transmission by mechanical ways may explain the high or low genetic diversity in plant virus populations (Wei et al., 2009). IYSV infects monocotyledonous and dicotyledonous plants (Kritzman et al., 2000) and can be transmitted by mechanical inoculation and by Thrips tabaci in a persistent/propagative manner (Cortêz et al., 1998). Therefore, the host range, insect-vector, and transmission by mechanical ways of IYSV may explain the observed high genetic diversity in some districts in this study. T. tabaci is the only known vector of IYSV (Gent et al., 2006), but since the specificity of virus-vector interaction impose significant constraints on the evolution of plant viruses rather than the specificity of virus-host plant interactions (Wei et al., 2009), transmission of IYSV by other thrips species may also explain the high genetic diversity. Also, low genetic diversity of IYSV in some districts in the study may be due to founder effect, which is often invoked to explain the low genetic diversity of certain populations of various plant viruses (Wei et al., 2009).

Nucleotide diversity and dN/dS ratio is cited in Table 2. The mean ratio is 0.1137 for all IYSV isolates. The ratio is maximum and minimum within European and Oceanian isolates, respectively. For most coding genes, the dN/dS ratio is below unity, which is consistent with negative selection against protein change. In contrast, a ratio above unity may be an indication that adaptive or positive selection is driving gene divergence (Yang and Bielawski, 2000; Nei and Gojobori, 1986). In this study, the dN/dS ratio is below unity, implying that N gene in the IYSV isolates is under negative selection. High dS in Oceanian isolates indicates that IYSV is under a strong negative selection pressure in this region and older than other IYSV isolates. However, more nucleotide sequences should be analyzed for a more accurate estimation of the selection effect on IYSV evolution.

Multiple sequences alignment between N protein amino acid sequences of IYSV-O5 and IYSV-O18 isolates revealed that the isolates differed by 6 amino acids at positions 46 (Thr/Met), 121 (Tyr/His), 254 (Ala/Val), 267 (Ser/Pro), 269 (Lys/Glu) and 270 (Asp/Arg). The significance of these amino acid substitutions is not known. To get a better insight in the genetic diversity of IYSV in Iran, a large number of isolates from different onion producing regions have to be analyzed.

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REFERENCES


شناختی مولکولی ویروس لکه زرد زنبیل (Iris yellow spot virus) روی پیاز در ایران


چکیده

علائم ویروسی شیب آلوگری های ناشی از ویروس لکه زرد زنبیل (Iris yellow spot virus, IYSV) در جنوب مرزه پیاز در شهرستان چخماق از استان خراسان رضوی مشاهده گردید. تحقیق ماکائیکی برخی گیاهان آزمون با استفاده از عصاره تهیه شده از نمونه های یافت در استان ایلام نشان داد که علائم ایجاد شده شیب علائم توصیف شده برای این ویروس هستند. در آزمون آنالیز ویروس که به طریق ماکائیکی نقل شده بود، فقط با یک سرم اختصاصی ویروس لکه زرد زنبیل واکش مشابه ناکام و در پاران سرم اختصاصی 7 گونه توسیعی ناگهانی هیچ گونه واکش مشابه نداشت. در آزمون RT-PCR، ناقصی 1 گونه توسیعی ناگهانی هیچ گونه واکش مشابه نداشت. در حضور براهمی اختصاصی برای تکیه زن تونکلوپروتئین (Nucleoprotein; N) زنبیل، یک چشمه DNA با اندامه تقریباً 82 حاصل از بیشتر مراکز آلوگری زنبیل گردید که بعد از همسانی سازی و تبعیض توالی آن با رویسیدی در N آنتی-Body (لیبق داده در GenBank توسط رش شماره374 و H1481874 نشان داد که توسط دو رویسی آنتی-Body هر دو نژاد داده در آنتی-Body 1 نژاد داده با رویسی H1481874 و H1481874 نژاد داده با رویسی 98 درصد با یک چشمه مشابه در هنده و 92 درصد با یک چشمه دارد. این اولین شناسایی مولکولی این ویروس در ایران می باشد.