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Detection of Tilapia Lake Virus (TiLV) in Clinical Samples by **Culturing and Nested RT-PCR**

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- Detection of Tilapia Lake Virus (TiLV) in Clinical Samples by Culturing and
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ABSTRACT

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28	Tilapia are an important group of farmed fish that serve as a significant protein
29	source, worldwide. In recent years, substantial mortality of wild tilapia has been
30	observed in the Sea of Galilee and in commercial ponds in Israel and Ecuador. We
31	have identified the etiological agent of these mass die-offs as a novel orthomyxo-like
32	virus and named it tilapia lake virus (TiLV). Here we provide conditions for efficient
33	isolation, culturing and quantification of the virus, including the use of susceptible
34	fish cell lines. Moreover, we describe a sensitive nested RT-PCR assay, allowing the
35	rapid detection of TiLV in fish organs. This assay revealed, for the first time, the
36	presence of TiLV in diseased Colombian tilapia, indicating a wider distribution of this
37	emerging pathogen and stressing the risk that TiLV poses for the global tilapia
38	industry. Overall, the described procedures should provide the tilapia aquaculture
39	industry important tools for the detection and containment of this pathogen.
40	
41	
42	INTRODUCTION
43	
44	Tilapines, a generic term for edible fish belonging to the family Cichlidae, are fast
45	growers, efficient food convertors and relatively disease-resistant. These assets render
46	them most suitable for farming; indeed, tilapines are one of the most significant
47	groups of farmed fish worldwide and serve as an important protein source, especially
48	in developing countries (1-6). Common ectoparasites and the few bacterial pathogens
49	of tilapines are well controlled by pharmacotherapy. Few viral diseases have been

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Recently, a novel RNA virus termed Tilapia Lake Virus (TiLV) has been identified and recovered from episodes of massive mortalities of wild and pond-cultured tilapia all over Israel (10). High mortalities were also observed in naïve tilapia, exposed to an isolate of TiLV (10). Tilapia mortality, suspected of having a viral etiology, has also been described in Ecuador (11, 12). Although variations in pathological presentation have been described (where lesions were focused in the central nervous system or in the liver, in Israel or Ecuador, respectively), sequencing the whole genome of TiLV

reported for tilapia and these are of limited impact (7-9).

26

59 revealed that tilapia in the two countries were infected with almost identical viruses

- 60 (4). This analysis also revealed that this pathogen is a novel orthomyxo-like virus with
- 61 a 10-segment, negative-sense RNA genome (4). Segment 1 contains an open reading
- 62 frame (ORF) with weak sequence homology to the polymerase subunit (PB1) of
- 63 influenza C virus, while the other nine segments showed no homology to other
- 64 viruses.
- 65

TiLV outbreaks are characterized by high mortalities and economical losses (10, 11) 66 and no vaccines against TiLV are currently available. Thus, there is a great need for 67 68 the implementation of prompt control measures: culling of infected stocks, setting 69 quarantine, restricting trades and control of possible vectors. This calls for 70 development of fast and sensitive detection methods and improved culturing techniques. Here we show that the presently available reverse transcription (RT)-PCR 71 assay (10), although highly specific, is of limited sensitivity when applied to clinical 72 73 samples. Accordingly, we now describe a highly sensitive, nested RT-PCR assay for TiLV detection from clinical specimens. In addition, TiLV-sensitive cell lines, other 74 than the reported E-11 cells (10), are described and the optimal parameters for TiLV 75 76 culturing are defined.

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MATERIALS AND METHODS

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Cell cultures and infection of cells with TiLV. E-11 (13), TO-2 (14), OmB (15) and 81 82 TmB (16) cells were grown in Leibovitz (L-15) medium (Gibco, USA), supplemented with 10% inactivated FCS (Gibco), L-glutamine (300 mg/liter), HEPES (pH 7.3; 1%), 83 penicillin (40 U/ml), streptomycin (40 µg/ml), and Nystatin (5 µg/ml). Primary brain 84 cells were prepared and grown as described before (10). For TiLV infections, E-11 85 monolayers in 25cm² flasks (~90% confluence, washed twice with PBS before 86 infection) were incubated with TiLV preparations at 25 °C for 1 h; cells were then 87 88 washed with PBS and incubated at 25 °C in L-15 medium (supplemented with 10% FCS) and monitored for CPE for up to 14 days. TO-2, OmB and TmB cells were 89 infected with TiLV as described for E-11 cells (see below). 90

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- 92 Quantification of temperature-dependent TiLV growth. E-11 cell line and cultures of primary tilapia brain cell (10) (90% confluency in 24-well plates) were infected 93 with TiLV [isolate 4/2011, (10); 10^{3.6} TCID₅₀/well] and incubated at 15, 20, 25 or 30 94 95 °C for up to 19 days. Cells were harvested at the indicated days post-infection and lysed by three freeze-thaw cycles. Total RNA was extracted with peqGOLD Trifast 96 97 (Peqlab; 30-2010) and levels of TiLV and cellular β -actin RNAs were quantified by 98 quantitative RT-PCR (qRT-PCR). Reverse transcription was performed using Verso 99 1-step RT-PCR ReddyMix kit (Thermo, Lithuania; AB-1454/LD/A); complemented with primers specified below. Quantification was accomplished by real-time PCR 100 101 using the ABsolute Blue qPCR SYBR Green Rox Mix (Thermo scientific; AB-102 4163/A) according the manufacturer's instructions with the following specifications: 103 each reaction contained 3 µl cDNA; TiLV-specific primers [ME1 5'GTTGGGCACAAGGCATCCTA3' and clone 7450/150R/ME2 104 105 5'TATCACGTGCGTACTCGTTCAGT3', 300 nM each, amplifying a 250-bp fragment (10)]; annealing and extension were performed at 60 °C for 1 min. To detect 106 β -actin RNA, we used the primers described in (17) (F β -actin 107 5'GGGTCAGAAAGACAGCTACGTT3' and R β-actin 108 109 5'CTCAGCTCGTTGTAGAAGGTGT3', amplifying 143 bp fragment). Continuous fluorescence measurements were achieved with StepOne apparatus (Applied 110 111 Biosystems). Positive and negative controls consisted of TiLV cDNA and no-template 112 control, respectively. Relative quantification (RQ) was calculated according to (18) 113 with the StepOne software (Applied Biosystems). 114 115 Quantification of TiLV growth by end-point dilution assays. E-11, TmB or OmB cell lines were cultured in 96-well plates in 100µl/well of Leibovitz (L-15) medium 116
- (Gibco, USA), supplemented with 10% inactivated fetal calf serum (FCS, Gibco, 117
- 118 USA). Serial dilutions of TiLV were prepared in the above serum-supplemented
- medium and 100 µl from each dilution were added to each well (~ 80% confluency). 119
- Altogether, 10 wells of each cell line were infected for each dilution. The 120
- 121 development of CPE was monitored on a daily basis through 14 days post-infection,
- when cultures were washed with PBS and stained with crystal 122
- violet/formaldehyde/methanol solution. TCID50 values were calculated by the method 123
- 124 of Reed and Muench (19).
- 125

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cui	126	RT- PCR
IUS I	127	PCR for d
an	128	TiLV clor
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p b	131	pJET1.2/b
N	132	used (at va
Ă	133	following
	134	491 bp fra
	135	(5'GTTGO
	136	(5'TATCA
	137	embedded
	138	of these tv
	139	(15 µl eac
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Micr	144	of the exte
	145	ReddyMix
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	147	steps were
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ne 7450 (GenBank Accession No. KJ605629), was amplified with primers

xt-1' (5'TATGCAGTACTTTCCCTGCC3') and 'Nested ext-2'

[CTGAGCAAGAGTACC3') (10). The resulting fragment was cloned into

plunt (Thermo Fisher Scientific), which was purified, serially diluted and

arious known concentrations) as a template for PCR. For these reactions, the

pairs of primers were used: Nested ext-1 and Nested ext-2 (amplifying the

gment in a reaction called 'external PCR'); 'ME1'

GGCACAAGGCATCCTA3') and '7450/150R/ME2'

ACGTGCGTACTCGTTCAGT3') (10), amplifying a 250 bp fragment,

in the above sequence (in a reaction called 'internal PCR'); or combination

wo pairs in a nested PCR reaction. For the external or internal PCR reactions

ch), the Verso 1-step RT-PCR ReddyMix kit (Thermo, Lithuania; AB-

A) was used with 200 nM (final concentration) of each of the above primers

but the enhancer (DNase). Amplification steps included: 1 cycle of 50 °C, 15

imic the reverse transcription step); 1 cycle of 95 °C, 2 min; 25 cycles of 95

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60°C, 60 s / 72 °C, 60 s and 1 cycle of 72 °C, 7 min. For nested PCR, 3 ul

ernal reaction were re-amplified by a PCR reaction (total of 15 µl) of 2X

x PCR Master Mix (Thermo Scientific; AB-0575/DC/LD/A), using primers

7450/150R/ME2 (each at a final concentration of 200 nM). Amplification

e as above but without the 50 °C, 15 min step. PCR products were separated

garose gel by electrophoresis.

e external and internal PCR reactions of the plasmid dilutions were also quantified by qPCR, using the Fast SYBR Green Master Mix (Applied Biosystems, 151 152 4385612) and the cognate set of primers described above (final concentration of 500 nM of each primer, per reaction). To quantify the nested PCR by qPCR, the external 153 PCR reaction was performed with the Verso 1-step RT-PCR ReddyMix kit, as 154 155 described above; 1 µl of this reaction was then re-amplified with the Fast SYBR Green Master Mix, using primers ME1 and 7450/150R/ME2 (500 nM each). For all 156 qPCR reactions the following steps were used: 1 cycle of 95°C, 20 s; 40 cycles of 157 158 95°C, 3 s / 60°C, 30 s. Fluorescence was monitored with StepOnePlus apparatus (Applied Biosystems). Ct values were calculated by the StepOne software. 159

5

161	TiLV RNA detection by nested RT-PCR. Total RNA was extracted from cell
162	cultures, or from liver organs (preserved in RNAlater reagent; QIAGEN; 76104), with
163	EZ-RNA Total RNA Isolation Kit (Biological Industries; 20-400-100) according to
164	the manufacturer's instructions. Reverse transcription and first round (external) PCR
165	were performed using Verso 1-step RT-PCR ReddyMix kit (Thermo, Lithuania; AB-
166	1454/LD/A), essentially according to the manufacturer's instructions but with the
167	following modifications: total volume of the reaction was 15 μ l, with primers 'Nested
168	ext-1' and 'Nested ext-2' (see above; 200 nM each). Thermal cycling program
169	included: a cDNA synthesis step (50 °C, 15 min); an inactivation step (95 °C, 2 min);
170	a denaturation step (95 °C, 30 s); 25 cycles of annealing (60 °C, 30 s) - extension (72
171	°C, 1 min); and a final extension step (72 °C, 7 min). 3 μl from the first round PCR
172	were then subjected to re-amplification by a second (nested) PCR of 2X ReddyMix
173	PCR Master Mix (Thermo Scientific; AB-0575/DC/LD/A), essentially according to
174	the manufacturer's instructions but with the following modifications: total volume of
175	the reaction was 15 $\mu l,$ using primers ME1 and 7450/150R/ME2 (see above; 200 nM
176	each). Thermal cycling program included: an initial denaturation step (95 °C, 2 min);
177	35 cycles of denaturation (95 °C, 1 min) - annealing (60 °C, 1 min) - extension (72
178	°C, 1 min); and a final extension step (72 °C, 5 min). PCR products were analyzed by
179	electrophoresis in 1% agarose gels.
180	
181	Amplification of Nervous Necrosis virus (NNV) RNA. RT-PCR was used to
182	amplify NNV RNA with conditions described above for TiLV RNA, using EZ-RNA
183	Total RNA Isolation Kit and Verso 1-step RT-PCR ReddyMix kit, but with primers
184	F1 (5'GGATTTGGACGTGCGACCAA3') and VR3
185	(5'TGGATCAGGCAGGAAGC3') and annealing temperature of 54 °C. The length of
186	the amplified product is 254 bp (20).
187	
188	Processing of clinical samples. Brain samples were collected in Israel between 2011
189	and 2013, from pond-raised tilapia (Oreochromis niloticus x Oreochromis aureus

hybrids), suspected to have been infected with TiLV. Brains from two ornamental
African cichlids, grown in an ornamental fish breeding farm and which showed
symptoms of TiLV infection, were also included in this study. Samples from mid2012 onwards were processed immediately upon arrival; earlier samples were

processed from archived materials (whole fish) stored at -80 ^oC. Negative control fish
were collected from fish ponds with no apparent disease.

196

197 Brains were removed aseptically, pooled (2-3 samples from each outbreak; except 198 from the two samples of ornamental fish that were processed separately) and split into 199 two tubes. The first aliquot was used for RNA extraction and subsequent PCR 200 reactions as described above. The second aliquot was utilized for virus isolation and 201 was manually homogenized with 9 volumes of phosphate-buffered saline (PBS) solution and centrifuged at 3000 x g for 10 min; supernatants were filtered through 202 203 0.22 µm membrane filters (Starsdet, Germany) and 200 µl were used to infect E-11 204 monolayers as specified below. For Sample No. 12, E-11 cells that were incubated 205 with brain homogenates and that showed no CPE, were freeze-thawed, and 200 µl of cleared extract was used to infect naïve E-11 cells. This procedure was repeated once 206 more till a clear CPE was observed. 207

208

Liver samples, diagnosed histopathologically as having lesions typical of syncytial
hepatitis (11), were collected from clinically sick fish, from Ecuador and Columbia.
Control livers were collected from unexposed, healthy tilapia (*Oreochromis niloticus*),
reared in St. George's University, Grenada. All liver samples were preserved in
RNAlater reagent (QIAGEN; 76104).

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216

215

RESULTS

Temperature-dependent viral growth. Being ectotherms (and cultured at 16-32 °C 217 range) (21), tilapia potentially may be infected over a relatively wide range of 218 temperatures; yet, the effect of temperature on TiLV replication and thus, on its 219 isolation, has not been studied. Hence, TiLV growth at various temperatures was 220 evaluated by infecting monolayers of E-11 and primary tilapia brain cells, with 221 subsequent incubation at various temperatures (15, 20, 25 and 30 °C) for up to 19 222 days. Infection was quantified by qRT-PCR reactions, measuring TiLV RNA 223 expression levels, with TiLV specific primers. Viral RNA levels were normalized to 224 cellular β-actin mRNA levels [Relative Quantification (RQ); Fig. 1 and Materials and 225 Methods]. In E-11 cells, the maximum increase in TiLV RNA levels was observed at 226

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25 0 C at day 9 post-infection (RQ = 1328; Fig. 1A). Higher (30 0 C) or lower (20 0 C) 227 temperatures resulted in reduced TiLV RNA levels (RQ = 191 and 490, respectively, 228 day 9 post-infection). At 15 °C, TiLV RNA production was dramatically reduced (RQ 229 = 35; day 9 post-infection) and reached maximal levels at day 15 post-infection. In 230 infected primary tilapia brain cells, 25 °C was also the optimal temperature for TiLV 231 replication (Fig. 1B); yet this replication peaked only at day 14 post-infection and 232 233 reached much lower levels (about 12%), compared to the one in E-11 cells. Altogether, E-11 cells at 25 °C provide optimal conditions for TiLV replication, thus 234 all isolations from clinical samples (see below) were carried out under these 235 236 conditions.

237

Quantification of TiLV growth in tilapia cell lines. In our former study (10), eight 238 established fish cell lines were tested for their permissiveness to TiLV infection and 239 240 only E-11 cells were found suitable for this purpose. We now extended this analysis to 241 three additional tilapia cell lines, derived from ovary [TO-2; (14)], brain [OmB; (15)] 242 and bulbus arteriosus [TmB; (16)]. Initial qualitative analyses revealed that OmB and TmB, but not TO-2, support TiLV replication (data not shown). We next compared 243 244 the use of the permissive cell lines (E-11, OmB and TmB) in the quantification of TiLV infection by endpoint dilution assays. The cell lines were infected with dilutions 245 of the virus, CPE was monitored for 14 days and TCID₅₀ values were calculated. The 246 247 results of three independent experiments are shown in Table 1. All three cell lines 248 showed comparable sensitivities to TiLV infection. Yet, E-11 cultures were superior 249 because the CPE development was clearly detected in a relative short time (~4, 6 or 8 250 days post-infection for E-11, TmB or OmB, respectively). OmB cells also provided 251 convenient way to monitor CPE at longer time post-infection (~14 days), as uninfected cells remained attached as monolayers while infected cultures completely 252 detached at this time point. TmB cells were sensitive to TiLV-induced CPE, yet we 253 254 found that detecting CPE in this line was more difficult compared to the other lines 255 because TmB cells did not support the formation of clear plaques and only a portion 256 of the infected cells detached from the plate over time.

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258 Sensitivity and specificity of TiLV detection by PCR. A sensitive RT-PCR
259 detection method for TiLV is required for rapid and accurate diagnosis of this threat

260 to tilapine aquaculture. We have described TiLV detection by RT-PCR (10); however, 261 assays were not optimized. To optimize this procedure, we first prepared a standard curve for this assay. Specifically, a 491 bp long PCR fragment, derived from TiLV 262 263 clone 7450 (GenBank Accession No. KJ605629) (10), was cloned into a plasmid and 264 dilutions of the resulting plasmid DNA were used in the following PCR/gel 265 electrophoresis (Fig. 2A) and qPCR (Fig. 2B) reactions. Different sets of primers were 266 used to amplify either the 491 bp fragment ('external PCR'; Fig. 2A, Upper Panel) or 267 an internal 250 bp fragment ('internal PCR'; Fig. 2A, Middle Panel). Additional reaction ('nested PCR'; Fig. 2A, Lower Panel) consisted of the external PCR, 268 269 combined with the internal PCR (Materials and Methods). This analysis showed that 270 as expected, the external and internal PCR reactions were less sensitive than the 271 nested PCR: the highest dilution in which the TiLV sequence was clearly detected by the external or the internal PCR reactions was 10⁻⁶ (Fig. 2A, Lane 2, Upper and 272 Middle Panels); relating to detection of ~70,000 TiLV copies. The nested PCR 273 274 showed much higher sensitivity, enabling the detection of as low as 7 copies of TiLV sequence (Fig. 2A, Lane 6, Lower Panel). Amplification of the above diluted plasmid 275 DNA by qPCR also demonstrated the higher sensitivity of the nested PCR over the 276 277 non-nested PCR reactions as much lower threshold cycle (Ct) values were obtained 278 for the former reaction (Fig. 2B). Of note, the detection limit of the nested qPCR (70 279 copies, Fig. 2B), was higher than that of the nested PCR (7 copies, Fig. 2A). These 280 differences likely result from the different reagents and conditions used for these two 281 types of reactions (Materials and Methods).

282

The specificity of the developed nested PCR was further demonstrated by the amplification of TiLV sequences from cDNAs that were prepared from TiLV-infected E-11 cells; but not from negative samples composed of cDNAs of NNV-infected, or naïve E-11 cells (Fig. 2C).

287

TiLV detection in diseased tilapia from Israel. Based on the optimal conditions for TiLV growth and detection defined above, we next set out to isolate TiLV from clinical specimens obtained from 13 different outbreaks between 2011 and 2013 in nine different commercial farms, distributed over Israel (Galilee, Jordan valley and Mediterranean coastal areas). In all these outbreaks, diseased fish showed typical symptoms related to TiLV infection (10). Brain samples were obtained from

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lournal of Clinical Microbiology 294 commercial pond-raised tilapia for human consumption (Oreochromis niloticus x Oreochromis aureus hybrids; Specimens No. 1-11, Table 2), and ornamental African 295 cichlids (Specimens No. 12 and 13, Table 2). Brain was chosen for these analyses 296 297 because this tissue is relatively confined and susceptible to TiLV infection (10). The brains were homogenized (pools of 2-3 brains for each outbreak for Samples No. 1-298 11; Samples No. 12 and 13, each consisted of a single brain) and added to E-11 cells, 299 cultured at 25 °C. This procedure resulted in the appearance of CPE at 5 to 6 days 300 301 post-inoculation, in 12 out of the 13 cases (Table 2). For Specimen No. 12, two additional passages in E-11 cell cultures were required before CPE became apparent 302 303 (Materials and Methods). No CPE was observed for a negative control group, 304 consisting of 15 fish that were collected from ponds showing mortalities due to either 305 environmental conditions (low oxygen levels or high ammonia concentrations) or other infectious diseases (i.e. streptococci) (data not shown). 306

307

308 The above 13 brain tissues were also tested for the presence of TiLV sequences by the internal and nested PCR reactions described above. For this, total RNA was extracted 309 from portions of the brains, reverse transcribed using random primers and PCR 310 311 amplified with TiLV-specific primers (Materials and Methods). The internal PCR detected TiLV sequences in only three samples (23%), in contrast to the nested PCR 312 313 that detected the virus in 12 samples (92%, Table 2). The amplification of TiLV 314 sequences was also verified by sequencing the PCR products (data not shown). None of the negative controls scored positive when examined by the nested PCR, further 315 316 demonstrating the specificity of this assay (data not shown).

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TiLV detection in diseased tilapia from South America. To further examine the 318 developed nested RT-PCR, we applied it to detect TiLV RNA in liver samples, 319 preserved in RNAlater reagent, that were taken from South American tilapia, showing 320 321 signs of syncytial hepatitis (11, 12), or from healthy controls. This test was performed in a blinded way using the following procedure: the presence or absence of TiLV 322 RNA in the samples was tested by RT-PCR (12), in St. George's University, Grenada. 323 324 The samples were then coded and shipped, preserved in an RNAlater reagent, to Tel 325 Aviv University, where RNA was extracted and nested RT-PCR was performed without knowing the samples' identities. Fig. 3A shows the results of this procedure 326 327 for Ecuadorian samples: six examined samples scored positive (Lanes 1-6) while six samples scored negative (Lanes 7-12). This fully matched the classification made ofthe samples, before shipment.

330

331 Tilapia with syncytial hepatitis were also observed in farms in Colombia and liver samples were examined for the presence of TiLV RNA, as above. This analysis 332 333 revealed that out of the six samples that were scored positive for TiLV, four samples 334 also scored positive after their shipment (Fig. 3B, Lanes 1-4), while the two other 335 samples scored negative (Fig. 3B, Lanes 5-6). This discrepancy likely resulted from the degradation of TiLV RNA in these samples. Indeed, attempts to amplify TiLV 336 337 RNA from these two samples using different sets of primers that were derived from 338 another segment of TiLV genome, failed too (data not shown). For the negative 339 samples, no PCR products were observed (Fig 3B, Lanes 7-12).

340

Overall, these results demonstrate that the developed nested RT-PCR can be applied for detection of TiLV strains in Israel and South America and suggest that preserved material can be analyzed too. Importantly, these results further show for the first time that TiLV is present also in tilapia farmed in Colombia, and confirm the global distribution of this newly recognized pathogen.

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DISCUSSION

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TiLV, a recently identified pathogen, causes recurrent outbreaks in wild and cultured
tilapia. These outbreaks are characterized by significant mortality and morbidity,
resulting in massive losses to tilapia industry both in Israel and South America (4, 1012). Thus, efficient methods for TiLV isolation and detection are required.

353

354 Temperature is the first parameter that we examined for optimization of TiLV

355 culturing, since outbreaks of viral diseases of fish are typically temperature-dependent

356 (22). Of note, the temperature at which a disease occurs does not necessarily reflect

357 the optimal temperature for the *in vitro* growth of the cognate pathogen. For example,

358 deadly outbreaks of viral hemorrhagic septicemia (VHS) in farmed Japanese flounder,

- 359 caused by viral hemorrhagic septicemia virus (VHSV), occurred when water
- 360 temperatures were between 8 and 15 °C, while the isolated VHSV strain replicated

361 most rapidly at 20 °C (23). Similarly, spring viremia of carp (SVC), caused by

- temperatures of 10 to 17 °C, while the optimum temperature for the *in vitro*
- replication of SVCV is 20 °C (24). In the case of TiLV, the broad range of water
- temperature (~ 24 to 33 °C) that occurs during the hot season (May to October) (10),
- 366 calls for determination of the optimal temperature for efficient virus growth, *in vitro*.
- 367 Our results (Fig. 1) clearly demonstrate that 25° C allows maximal growth of TiLV.
- 368

369 We also determined TiLV growth in several types of fish cells. When comparing primary tilapia brain cells to E-11 cells, TiLV replication generated much higher viral 370 371 RNA in the latter cells, despite the fact that E-11 cells are derived from the snakehead 372 fish (Ophicephalus striatus) (13, 25) - a freshwater perciform fish (family 373 Channidae), which is distant from tilapines (family Cichlidae). Our present study identified two additional tilapia cell lines that support TiLV growth: the OmB; (15) or 374 375 TmB (16) cells, derived from tilapia brain or bulbus arteriosus, respectively. In 376 respect to CPE development, E-11 and OmB were superior compared to TmB. Plaques where readily detected in E-11 cells, whereas TiLV-infected OmB cultures 377 were characterized by almost complete detachment from the plate. Thus, E-11 cells 378 379 are convenient for plaque assays and OmB cultures are useful in end-point dilution 380 (TCID₅₀) assays. E-11 cells, which are derived from a species distant from the natural 381 host, should also be useful in studies involving TiLV attenuation. Yet, E-11 cells also 382 produce the snakehead retrovirus (SnRV) (13) and this may hamper the development of pure vaccine strains for TiLV. Since OmB and TmB cells are SnRV-free (our 383 384 unpublished results), these cells should be useful in generating pure TiLV strains.

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- $\label{eq:weight} \textbf{We demonstrated that TiLV culturing is a sensitive method for detection of the virus.}$
- 387 Yet, this methodology is time consuming and labor intensive; thus, it is inadequate
- 388 when prompt and accurate control measures are required (i.e. culling of infected
- 389 stocks). Hence, we developed RT-PCR-based techniques that are fast and sensitive.
- 390 We demonstrated that the nested RT-PCR protocol, described here, detects only few
- 391 molecules of TiLV genome and can be applied in detecting TiLV RNA in fresh and
- 392 preserved organs of diseased fish. The protocol is based on amplification of consensus
- 393 regions that were identified by analyzing high-throughput sequencing data, obtained
- from TiLV samples collected in Israel and Ecuador. This analysis revealed high
- 395 sequence homology between the Israeli and Ecuadorian samples across TiLV genome

396	(4) and thus, all TiLV segments can be used as templates in RT-PCR reactions. The
397	four primers used in our protocol are derived from Segment 3 of the Israeli isolate of
398	TiLV (4, 10). Three primers (Nested ext-1, Nested ext-2 and ME1) fully match
399	sequences of TiLV obtained from 12 Ecuadorian samples. The fourth primer
400	(7450/150R/ME2) fully matches eight of the 12 Ecuadorian samples, but has a single
401	mismatch in its second position, compared to the other four samples (sequences of the
402	latter contain a G instead of an A). This 5' mismatch should not interfere with
403	amplification and the described set of primers readily amplified TiLV sequences from
404	samples obtained from disease outbreaks in both Israel and Ecuador. Moreover, the
405	power of this RT-PCR-based assay was exemplified when it detected TiLV in organs
406	of diseased tilapia, obtained from yet another country - Colombia.
407	
408	This is the first report of TiLV occurrence in Colombian aquaculture, which adds to
409	the reports of TiLV outbreaks in Israel and Ecuador. This substantiates TiLV as an
410	emerging pathogen and highlights the risk that TiLV poses for the global tilapia
411	industry. The methods described here should detect the virus through early onset of
412	TiLV infection, assisting its containment.
413	
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425	

of

E.B., A.E., N.M., T.B., and W.I.L. have applied for patents in the fields of TiLV 426 diagnostics and vaccines. 427

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FIGURE LEGENDS

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502 Figure 1. TiLV replication at different temperatures. E-11 (A) and primary brain

(B) cultures in 24-well plates were infected with TiLV and incubated at the indicated 503

temperatures. Total RNA was extracted from infected cells at the indicated time 504

505 points postinfection and TiLV and cellular β-actin RNA levels were quantified by

506 qRT-PCR. The results show the relative quantification (RQ) of TiLV RNA levels,

507 relative to β -actin RNA levels (means of duplicates \pm standard deviations).

Figure 2. Sensitivity and specificity of PCR, nested PCR and qPCR in the 508 509 amplification of TiLV. (A) Ten-fold dilutions of a plasmid containing a 491 bp long 510 PCR fragment, derived from TiLV clone 7450 (GenBank Accession No. KJ605629), were subjected to PCR with primers, amplifying either a 491 bp (Upper Panel) or 250 511 bp (Middle Panel) fragments. A nested PCR, using the above two sets of primers was 512 also performed (Lower Panel). Lanes 1 to 9 show the PCR products for 10⁻⁵ to 10⁻¹³ 513 514 dilutions range, respectively, separated on a 1% agarose gel by electrophoresis. The PCR reaction that amplified the 10⁻¹⁰ dilution (Lane 6) contained 7 copies of TiLV 515 sequence. (B) qPCR reactions were also applied to the dilutions and primer pairs 516 517 described in (A). The values of the threshold cycle (Ct) were plotted against calculated TiLV copies and trendlines were added using Excel software. Reactions 518 519 were run in triplicates and only the linear range is shown. (C) cDNAs of TiLVinfected E-11 cells (Lane 1), Naïve E-11 cells (Lane 2) or NNV-infected E-11 cells 520 (Lane 3) were subjected to Nested PCR with TiLV-specific primers as in (A), to 521 detect TiLV sequences. Amplification of TiLV sequences from the plasmid described 522 523 in (A) was used as a positive control (Lane 4). Amplification reaction with no DNA template served as a negative control (Lane 5). The absence or presence of NNV 524 sequences in cDNAs, prepared from naïve (Lane 6) or NNV-infected (Lane 7) E-11 525 cells, respectively, was confirmed by PCR with NNV-specific primers. M, denotes 526 527 size markers.

528

529 Figure 3. Detection of TiLV RNA in preserved tilapia livers from Ecuador and 530

Columbia. Nested RT-PCR was used to determine the presence or absence of TiLV

531 RNA in liver samples, preserved in RNAlater reagent. (A) Samples from Ecuador of

diseased (Lanes 1-6) or healthy fish (Lanes 7-12). Reaction with no RNA served as a 532

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- 533 negative control (Lane 13). (B) Samples from Columbia of diseased (Lanes 1-6) or
- healthy fish (Lanes 7-12). M marks DNA size markers.
- 535

TABLES

536 537

538 TABLE 1. ^aComparison of TCID₅₀ values for three TiLV-susceptible cell lines

	Cell Lines			
Experiment No.	E-11	TmB	OmB	
1	3.2x10 ⁵	5x10 ⁵	1.6×10^5	
2	$4x10^{6}$	4x10 ⁵	5x10 ⁵	
3	1.6×10^5	$2x10^{5}$	1.6×10^5	

^aThe same stock of TiLV (grown in E-11 cells) was quantified in three independent

540 endpoint dilution assays. Values are in $TCID_{50}/ml$.

541

TABLE 2. TiLV detection in clinical specimens by culturing, RT-PCR and nested RT-PCR.

Specimen No.	Location	^a CPE	RT-PCR	Nested RT-PCR
1	Farm 1, Galilee	+	+	+
2	Farm 1, Galilee	+	-	+
3	Farm 2, Jordan	+	-	+
	Valley			
4	Farm 2, Jordan	+	-	+
	Valley			
5	Farm 3, Jordan	+	+	+
	Valley			
6	Farm 4, Jordan	+	+	+
	Valley			
7	Farm 4, Jordan	+	-	+
	Valley			
8	Farm 5, Jordan	+	-	+
	Valley			
9	Farm 6, Coastal	+	-	+

MOL

	region			
10	Farm 7, Jordan Vallev	+	-	+
	5			
11	Farm 8, Galilee	+	-	-
12	Farm 9, Jordan	ь+	-	+
	Valley			
13	Farm 9, Jordan	+	-	+
	Valley			
%	Positives	100	23	92

^aCPE was detected in E-11 cells, incubated with the brain specimens.

⁵⁴⁵ ^bCPE visible only after two additional passages on E-11 cell cultures.

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