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Comparative performance evaluation of double-stranded RNA high-throughput sequencing for the detection of viral infection in temperate fruit crops

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in memoriam

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1 ABSTRACT

2 There is limited information on the compared performance of currently used biological,
3 serological and molecular assays with high-throughput sequencing (HTS) for viral indexing in
4 temperate fruit crops. Here, using a range of samples of predetermined virological status, we
5 compared two performance criteria (inclusivity and analytical sensitivity) of ELISA, molecular
6 hybridization, RT-PCR, and double-stranded RNA (dsRNA) HTS for the detection of a total of
7 14 viruses (10 genera) and four viroids (three genera). Using undiluted samples from individual
8 plants, ELISA had the lowest performance, with an overall detection rate of 68.7%, followed
9 by RT-PCR (82.5%) and HTS (90.7%, and 100% if considering only viruses). The lower
10 performance of RT-PCR reflected the inability to amplify some isolates as a consequence of
11 point mutations affecting primer-binding sites. In addition, HTS identified viruses that had not
12 been identified by other assays in close to two-thirds of samples. Analysis of serial dilutions of
13 fruit tree samples allowed to compare analytical sensitivity for various viruses. ELISA showed
14 the lowest analytical sensitivity, but RT-PCR showed higher analytical sensitivity than HTS for
15 a majority of samples. Overall, these results confirm the superiority of HTS over biological
16 indexing in terms of speed and inclusivity and show that while the absolute analytical sensitivity
17 of RT-PCR tends to be higher than that of HTS, PCR inclusivity is affected by viral genetic
18 diversity. Taken together, these results make a strong case for the implementation of HTS-based
19 approaches in fruit tree viral testing protocols supporting quarantine and certification programs.

20 **Keywords:** Fruit tree, Prunus, Malus, Pyrus, virus, viroid, Indexing, High-throughput
21 sequencing, dsRNA.

22 INTRODUCTION

23 The control of plant viruses for vegetatively propagated species, such as temperate fruit crops,
24 relies heavily on the use of virus-indexed planting materials (Martin et al. 2000; Hadidi et al.
25 2011). Efficient and sensitive diagnostic techniques constitute a key pillar of control efforts,
26 including quarantine measures and certification programs aiming to make available to growers
27 certified or virus-tested propagation materials (Martin et al. 2000, 2016; Reed and Foster 2011).
28 Biological indexing by grafting on sensitive woody indicators (Thompson et al. 2011) has been
29 extensively used for quarantine and certification programs for temperate fruit crops. However,
30 serological and molecular diagnostic assays, such as ELISA, molecular hybridization, or RT-
31 PCR (Martin et al. 2000; Mumford et al. 2006) have been gradually integrated for virus
32 diagnosis. Because of its broad scope (inclusivity) and perceived analytical sensitivity,
33 biological indexing is still routinely used in association with available laboratory tests, despite
34 its long turnover and high costs linked to the months or years sometimes needed for symptoms
35 expression (Rowhani et al. 2005; Thompson et al. 2011, Al Rwahnih et al. 2015; Rott et al.
36 2017).

37

38 Since their first application for plant virus discovery and characterization in 2009 (Kreuze et al.
39 2009; Adams et al. 2009; Al Rwahnih et al. 2009) high-throughput sequencing (HTS)
40 approaches have demonstrated a remarkable potential and indeed revolutionized several fields,
41 including virus discovery, etiology and, more broadly, metagenomics and virus ecology
42 (Malmstrom et al. 2011; Roossinck et al. 2015; Maliogka et al. 2018; Zhang et al. 2019;
43 Villamor et al. 2019; Maclot et al. 2020). The potential of HTS in the diagnostics field was
44 recognized very early (Adams et al. 2009; Massart et al. 2014) and stems from several factors,
45 including its ability to provide an unbiased and potentially complete picture of the sanitary
46 status of a sample in a single experiment (Olmos et al. 2018; Maree et al. 2018). It was also

47 recognized that a number of hurdles would need to be overcome for HTS widespread adoption
48 in routine diagnostic laboratories, including the availability of internationally recognized
49 guidelines, robust protocols and standard operating procedures, reliable bioinformatics tools for
50 sequence data analysis, and strategies to define positive detection thresholds (Massart et al.
51 2014; Maree et al. 2018; Olmos et al. 2018). Many of these challenges have now been
52 addressed, including the definition of international standards or recommendations (Lebas et al.
53 2021; Massart et al. 2022; OEPP/EPPO, 2022) or the development and benchmarking of
54 appropriate bioinformatics pipelines (Massart et al. 2018). Another key element for the
55 adoption of HTS in diagnostic laboratories that was identified early is the availability of
56 information on the performance of HTS-based diagnostics and direct comparisons with
57 currently used biological, serological, or molecular assays (Massart et al. 2014; Maree et al.
58 2018).

59
60 A few such direct comparisons are available for some herbaceous hosts (see, for example,
61 Hagen et al. 2012; Rolland et al. 2017; Santala and Valkonen 2018). However, low viral titers,
62 uneven virus distribution, and the potential presence of inhibitory substances frequently
63 complicate virus detection in woody hosts (Wetzel et al. 1992; Knapp et al. 1995, Maliogka et
64 al. 2018, Wright et al. 2021), so that direct comparisons of HTS with existing assays is
65 specifically needed in such hosts. Comparisons with biological indexing are available for
66 grapevine (Al Rwahnih et al. 2015), small fruits (Villamor et al. 2022) or temperate fruit crops
67 such as apple (*Malus*), pear (*Pyrus*) or *Prunus* (apricot, peach, plum or cherry) (Rott et al. 2017).
68 Broadly speaking, these studies concluded that HTS is superior to biological indexing for
69 detection purposes due to its speed, lower cost and comprehensiveness, and to HTS ability to
70 detect novel agents. For small fruits, the comparison also included RT-PCR assays, but no
71 attempts were made to compare analytical sensitivities (Villamor et al. 2022). The results

72 obtained showed that for the testing of individual plants, HTS and RT-PCR provided nearly
73 parallel results but that HTS allowed the detection of a broader range of isolates.

74 As a further step towards the widespread adoption of HTS assays, we report here the results of
75 a direct comparison of the performance criteria (OEPP/EPPO 2021) of biological indexing,
76 ELISA, RT-PCR and double-stranded RNA (dsRNA) based HTS, for the detection of a wide
77 range of viruses and viroids in temperate fruit trees, including a comparison of the limits of
78 detection for the latter three approaches.

79 **MATERIALS AND METHODS**

80 **Plant samples and virus isolates**

81 A total of 36 fruit tree samples belonging to six species [apricot (*Prunus armeniaca*), sweet
82 cherry (*P. avium*), plum (*P. domestica*), peach (*P. persica*), apple (*Malus domestica*) and pear
83 (*Pyrus communis*)] were included in the present study. For each species, one uninfected control
84 sample (sampled from certified germplasm collections) and between three and six samples
85 infected by various viruses and/or viroids were used Table 1. With the exception of five peach
86 samples, which were obtained following chip-budding inoculation on GF305 peach seedlings,
87 all other samples were obtained from trees that are part of the collections of viral isolates held
88 by the various partners. Depending on their regulatory status, plants were either grown in high-
89 containment greenhouses or under insect-proof screenhouses. Quarantine pests were held and
90 shared between partners under the appropriate letter of authority. For all infected samples,
91 between six and ten grams of leaves were collected in spring 2017 (except for one apricot
92 sample growing in a greenhouse, which was collected in early spring 2018). Leaves were cut
93 in small slivers using scissors to homogenize the sample and aliquots (1g fresh weight)
94 lyophilized before being distributed to partners. Healthy samples were similarly processed,
95 except that a total of 25g of leaves were processed for each healthy sample.

96 For the determination of analytical sensitivity, a sample was selected for each of the six fruit
97 species. For each of these samples, serial ten-fold dilutions in a healthy control homogenate of
98 the same species were prepared and tested as described below.

99 **Double-stranded RNA purification, HTS analysis and bioinformatic sequence data**
100 **analysis**

101 Double-stranded RNAs (dsRNAs) were purified by a first round of CC41 cellulose
102 chromatography followed by nucleases treatment and a second round of cellulose
103 chromatography as described (Marais et al. 2018). Purified dsRNAs were used for cDNA
104 synthesis, followed by a random PCR amplification step (Marais et al. 2018). In order to limit
105 intersample cross-talk, individual libraries were prepared for each sample, which were then
106 sequenced on an Illumina HiSeq 3000 (2x150 nt) at the GetPlaGe (INRAE Toulouse, France)
107 platform. Following quality trimming using CLC Genomics Workbench (CLC-GW version 15
108 or later, Qiagen), HTS reads obtained from the various samples were analyzed using CLC-GW
109 and the VirAnnot pipeline (Lefebvre et al. 2019). If needed, number of reads for different
110 samples was normalized by random reads sampling using CLC-GW. Reads were mapped using
111 CLC-GW against reference genomes downloaded from GenBank for all viruses known to infect
112 the tested fruit tree species. This mapping was performed at a reduced stringency level (length
113 fraction 100%, minimal similarity fraction 75%) in order to take viral intraspecific diversity
114 into account so that reads from divergent isolates would still be identified.

115 In addition, following *de novo* assembly performed with CLC-GW (word size, 50; bubble size,
116 300), contigs were annotated by BlastN and BlastX analyses against the GenBank database to
117 detect novel viruses or highly divergent variants of known viruses.

118 To take into account inter-sample crosstalk due to index jumping (Illumina 2017; van der Valk
119 et al. 2019), a threshold of positive detection was computed for each viral molecule by
120 calculating the average plus 3 standard deviations (SD) of background virus reads observed in

121 libraries generated for the six healthy samples. Assuming a normal distribution of background
122 reads, the use of such a positivity threshold would provide a <1% risk of reporting a false
123 positive detection (https://en.wikipedia.org/wiki/68%E2%80%939395%E2%80%939399.7_rule).

124 **Testing of fruit tree samples using ELISA assays**

125 All ELISA tests were performed using commercial kits and following the recommendations of
126 the kit providers. For apple chlorotic leaf spot virus (ACLSV), apple mosaic virus (ApMV),
127 apple stem grooving virus (ASGV), apple stem pitting virus (ASPV), prune dwarf virus (PDV),
128 prunus necrotic ringspot virus (PNRSV), plum pox virus (PPV), strawberry latent ringspot virus
129 (SLRSV) and tomato ringspot virus (ToRSV), BIOREBA kits (Reinach, Switzerland) were
130 used, while a kit from AGDIA (Elkhart, IN, USA) was used for American plum line pattern
131 virus (APLPV). Each sample was assayed using two ELISA wells and the analysis was repeated
132 twice. For the interpretation of the results, samples were considered positive if their average
133 absorbance value at 405 nm was above two times the average absorbance of the uninfected
134 control of the same plant species.

135 **Testing of fruit tree samples by molecular hybridization**

136 Peach latent mosaic viroid (PLMVd) was detected by molecular hybridization using non-
137 radioactive *in vitro* transcribed RNA probes labeled with digoxigenin. The protocol used
138 broadly follows that of Turturo et al. (1998). Each sample was spotted in duplicate on the
139 hybridization membrane.

140 **Testing of fruit tree samples using RT-PCR assays**

141 Testing of fruit tree samples by RT-PCR was performed using RT-PCR conditions and primers
142 that are either according to published protocols or have been developed in the frame of the
143 present study. A detailed list of the protocols used is provided in Supplementary Table S1.

144

RESULTS

145 Detection of viruses and viroids in temperate fruit tree samples using various techniques

146 Infection by a range of viruses and viroids in a total of 36 temperate fruit tree (apricot, peach,
147 sweet cherry, plum, apple, and pear) samples, including one healthy control per tree species,
148 were tested in parallel by ELISA, RT-PCR, and double-stranded RNA (dsRNA) based high-
149 throughput sequencing (HTS). The virological status of the samples had previously been
150 determined by biological indexing using recommended protocols and woody indicators
151 (Jelkmann 2003) and/or by targeted serological or molecular analyses combined with symptoms
152 observation. The samples (from three to six per species) were selected to cover a broad diversity
153 of fruit tree viruses and viroids, including agents of quarantine or certification significance in
154 single or mixed infections. In total, the 30 infected samples analyzed represent 14 viruses
155 belonging to 10 genera and four viroids belonging to three genera (Table 1).

156 For each virus, only samples previously found infected by a given virus and negative controls
157 were tested using the corresponding ELISA assay. Detection of peach latent mosaic viroid
158 (PLMVd) was similarly performed by molecular hybridization using digoxigenin-labeled RNA
159 probes on healthy controls and on two PLMVd-infected peach samples (Table 1).

160 The presence of all viruses and viroids, with the exception of PLMVd, was similarly assessed
161 in controls and in relevant samples using virus-specific validated RT-PCR or qRT-PCR assays
162 or using assays specifically developed for the present project (Supplementary Table S1). Lastly,
163 all samples were indexed by the Illumina HTS analysis of randomly amplified cDNAs produced
164 from highly purified dsRNAs (Marais et al. 2018) (on average 2.58M +/-1.27M trimmed
165 reads/sample).

166 Overall, of the 46 infections expected in the 30 infected samples, only three were not confirmed
167 by any of the assays. This concerns a peach sample (F586) in which an expected tomato ringspot
168 virus (ToRSV) infection was not detected by ELISA, RT-PCR and HTS and two pear samples
169 (PO13357 and PO1492) in which apple chlorotic leaf spot (ACLSV) infection was not

170 confirmed by ELISA, RT-PCR and HTS (Table 1). Since spring is the recommended sampling
171 period for these two viruses, these results might reflect the irregular distribution of the viruses
172 in the sampled tree, a loss of a viral isolate during propagation or possibly a misidentification
173 of a viral infection during biological indexing resulting from the mixed infection status of some
174 of the analyzed samples. In any case, due to the convergent results obtained using several
175 techniques, the three samples concerned were considered as free of infection by the relevant
176 virus/viroid and therefore not considered in all further data analyses. No virus or viroid
177 detection was obtained by any of the techniques for the negative controls.

178 Altogether, a positive ELISA detection result was obtained for 22 of the 32 expected infections
179 tested (68.7%), the 10 expected infections not detected concerning ACLSV [two infections in
180 plum (PR72 and PR3473) and two in apple (LX86 and X259)], apple stem pitting virus (ASPV)
181 [one infection in apple (LX86) and two in pear (PO13357 and PO161)] and all three tested
182 American plum line pattern virus (APLPV) infections in peach and plum (Table 1). The three
183 APLPV infections missed by ELISA were confirmed by both RT-PCR and HTS, together with
184 one ACLSV infection (X259 apple) and one ASPV infection (LX86 apple), while the other
185 ACLSV or ASPV infections not detected by ELISA were only confirmed by HTS.

186 RT-PCR assays confirmed 33 infections out of the 40 tested (82.5%). The seven negative results
187 concern a strawberry latent ringspot virus (SLRSV) infection in peach (LS27) confirmed by
188 ELISA and HTS, an ACLSV infection in peach (PR3473) similarly confirmed by ELISA and
189 HTS and three ACLSV infections (PR72 and PR3473 plums, LX86 apple) plus two ASPV
190 infections (PO13357 and PO161 pears), only confirmed by HTS.

191 Finally, HTS confirmed 39 of 43 tested infections (90.7%). The four infections not identified
192 by HTS concern three viroids confirmed by RT-PCR [apple scar skin viroid, (ASSVd) in X259
193 apple, hop stunt viroid (HSVd) in Roma1 apricot and PR72 plum, and pear blister canker viroid

194 (PBCVd) in PO2098 pear], so that the performance of HTS if considering only infections by
195 viruses reaches 100% detection (39/39).

196 **Unexpected viral infections detected by dsRNA-based HTS**

197 Of the 30 tested samples, 19 (63%) were found to be infected by viruses that had not been
198 previously detected by biological indexing or by targeted assays. Five of those 19 samples had
199 mixed infections involving two unforeseen viruses. All these infections detected by HTS and
200 that had not been previously identified by biological indexing were confirmed by specific RT-
201 PCR assays (Table 1).

202 Six of the unforeseen infections detected by HTS concern cherry virus A (CVA) in peach,
203 cherry and plum, a virus for which there is currently no known biological indicator. Other
204 detected infections for which no biological indexing assay is available concern mostly recently
205 described viruses such as Asian prunus virus 3 (APV3) in peach, nectarine stem pitting-
206 associated virus (NSPaV) in peach, plum bark necrosis stem pitting-associated virus
207 (PBNSPaV) in peach and plum, peach leaf pitting-associated virus (PeLPaV) in plum, prunus
208 virus F (PrVF) in cherry, citrus concave gum-associated virus (CCGaV) in apple and citrus
209 virus A (CiVA) in pear (Table 1). They also concern viruses whose presence in temperate fruit
210 trees was not expected, such as cucumber mosaic virus (CMV) in plum or grapevine cryptic
211 virus (GCV) in apricot. However, eight of the detected infections concern well-known fruit tree
212 viruses that should have been detected by biological indexing, such as little cherry virus 1
213 (LChV1) in apricot and cherry, apple stem grooving virus (ASGV) in apple and pear, ACLSV
214 in apple, ASPV in pear or apple rubbery wood viruses 1 and 2 (ARWV1 and ARWV2 in apple
215 and pear, respectively) (Table 1).

216 In parallel, several infections were identified by HTS but not confirmed by RT-PCR. Some of
217 these represent clear instances of false positive detection because the viruses involved are not
218 known to be able to infect the host in which they were identified. This concerns, for example,

219 the detection of plum pox virus (PPV) in a pear sample or the detection of ASPV in a peach
220 and a plum sample. In some other cases, the infections detected by HTS could not be discounted
221 on such biological bases. However, when analyzed, the isolates identified by HTS and not
222 confirmed by RT-PCR were found to be identical to other isolates included in the experiment
223 and that had yielded particularly high read counts. For example, the PPV isolate identified in
224 the PO13357 pear is identical to the GS apricot PPV isolate, which yielded in excess of 1.7
225 million (M) reads (65.7% of total reads), while that identified from the LS27 peach is identical
226 to the one that yielded over 1.2M reads (48.4% of total reads) from the D peach sample. These
227 comparisons thus indicate that HTS detections not confirmed by RT-PCR should be considered
228 as false positives resulting from laboratory or sequencing platform experimental
229 contaminations or inter-sample crosstalk during sequencing.

230 **Point mutations in primer-binding sites explain the failure to detect some viral isolates**
231 **by RT-PCR**

232 Given its known analytical sensitivity, the failure of RT-PCR to detect some viral isolates found
233 positive by ELISA and HTS came as a surprise and prompted efforts to see whether mutations
234 affecting primer-binding sites might be responsible for these results. Indeed, for several viral
235 isolates, such mutations could be identified. A particularly clear-cut case involves the SLRSV
236 isolate in peach LS27, which was detected by ELISA and by HTS (>35,000 reads above
237 threshold, nearly complete genome assembled) and yet was not detected by RT-PCR.
238 Inspection of the assembled genome revealed, respectively, four and five mutations affecting
239 the binding sites of primers SLRSV-F and SLRSV-R (Postman et al. 2004) (Figure 1A). In
240 particular, one of the mutations affects the 3' end of primer SLRSV-R, which is very likely to
241 limit amplification of the LS27 isolate. The assembled genome of this highly divergent isolate
242 has been deposited in GenBank (OR513894-OR513895) and shows an overall 29-32% nt
243 divergence with other GenBank SLRSV isolates. For ACLSV and ASPV isolates not detected

244 by RT-PCR and for which HTS genome coverage allowed the analysis of primers binding sites,
245 a similar pattern was observed (Figure 1B and 1C). In the case of ACLSV, respectively six and
246 five mismatches were identified with primer A52 (Candresse et al. 1995), including a mutation
247 affecting the primer 3' end, for isolates PR3473 from peach and LX86 from apple (Figure 1B),
248 while the corresponding region was not covered by HTS reads for pear isolates PO13357,
249 PO1492 and PO161. Between two and three mismatches were also found to affect the binding
250 site of primer A53 for all non-detected isolates (Figure 1B). It should be noted that the detection
251 of isolates PR3473 and LX86 by HTS was unambiguously positive, with respectively >69,000
252 reads and 1,390 reads above the threshold and genome coverages of 89% and 74%, respectively
253 (GenBank OR513892 for the PR3473 isolate, the fragmented assembly of the LX86 isolate was
254 not deposited).

255 In the case of ASPV, while no sequence information could be obtained for pear isolate PO161,
256 analysis of the reads for pear isolate PO13357 showed the binding sites for primers ASPV-F
257 and ASPV-R (Menzel et al. 2002) to be respectively affected by three- and four-point mutations,
258 including an insertion in the case of ASPV-R (Figure 1C). Similar to the situation with ACLSV,
259 the detection by HTS of ASPV in PO13357 was unambiguous, with 21,500 reads above the
260 threshold and ~86% of genome coverage (GenBank OR513893).

261 **Comparative analytical sensitivity evaluation of ELISA, RT-PCR and HTS on fruit tree** 262 **samples**

263 In a second step, using serial dilutions of a set of temperate fruit tree samples, we tried to assess
264 the analytical sensitivity of the three techniques by means of the limit of detection (LOD)
265 determination using a set of serial dilutions. For this experiment, we selected one sample for
266 each of the six fruit species addressed in the present work. For each of those samples, 10-fold
267 serial dilutions of a homogenate were prepared in a healthy control homogenate of the same
268 species. The serial dilutions were tested directly by ELISA or used for total nucleic acids

269 extraction prior to RT-PCR assays or for dsRNA extraction prior to HTS analysis, which
270 yielded an average of 2.06 +/-0.76M trimmed reads per sample.

271 The results obtained are presented in Table 2. Of the 10 viruses thus analyzed, three (CVA,
272 ARWV1 and ARWV2) could not be assayed by ELISA because no commercial kits are
273 available for their detection. Only three of the seven tested viruses could be detected by ELISA
274 in diluted samples: PNRSV in plum with a LOD of 10^{-1} , PDV in peach with a 10^{-2} LOD and
275 PPV in apricot, which was still weakly detected at the 10^{-3} dilution. In addition, ASPV was
276 detected with a LOD of 10^{-2} in apple but was only detected in pear in the undiluted sample. All
277 other viruses (ApMV, ACLSV, ASGV) could only be detected in undiluted samples. In two
278 cases (plum PR3473 and apple LX225), ACLSV was not detected by ELISA, even in undiluted
279 samples (Table 2).

280 Although there was a lot of variability in the LOD for different viruses and for different
281 virus/host combinations, RT-PCR generally proved much more sensitive than ELISA. LODs
282 of 10^{-5} to 10^{-7} were, for example, obtained for ACLSV (in apple LX225), CVA, PDV, ApMV,
283 PPV, and ASPV (in apple LX225). The lowest analytical sensitivity was observed for ARWV2
284 and ACLSV in cherry (LOD of 10^{-1}) and ARWV1, ASPV in pear and PNRSV (LOD of 10^{-2}).
285 For its part, dsRNA-based HTS generally showed an analytical sensitivity intermediate between
286 ELISA and RT-PCR. Two viruses, ARWV1 and ARWV2 could only be detected from
287 undiluted samples. ACLSV showed a LOD of 10^{-1} to 10^{-3} depending on the host/sample and
288 ApMV a LOD of 10^{-2} , while the other six viruses (CVA, PDV, PNRSV, PPV, ASGV and
289 ASPV) showed LODs of 10^{-3} or better, the most sensitive detection being observed for PPV
290 with a LOD of 10^{-5} . In the case of PDV and PNRSV, analytical sensitivity higher by a 10 to
291 100-fold factor was observed if considering RNA3 reads than those for RNA1 or RNA2 (Table
292 2).

293 Since sequencing depth is obviously a factor affecting analytical sensitivity using HTS
294 approaches (Bester et al. 2021; Schönegger et al. 2023), HTS datasets for the various samples
295 and controls were randomly subsampled at different depth (1M, 300K, 100K, 33K and 10K
296 reads) and detection performance evaluated by mapping the reads on reference genomes. The
297 same threshold (average of negative controls plus three standard deviations) was used to
298 determine positive detections and all resamplings were performed three times in order to
299 evaluate repeatability of results. For this analysis, the detection of CCGaV in the LX225 apple
300 sample, of CiVA in the PO1492 pear sample and of PLMVd in the Gotheron 94/6 peach sample
301 were also taken into consideration so that the overall rate of detection of 13 agents (12 viruses
302 plus one viroid) as affected by sequencing depth and sample dilution is shown in Figure 2.

303 As expected, performance evaluated in terms of the proportion of viral agents detected was
304 generally reduced as sequencing depth decreased, whatever the tested samples' dilution rate.
305 Similarly, for a given sequencing depth, the fraction of viral agents detected was reduced as
306 more and more diluted samples were analyzed (Figure 2).

307 Detection of all 13 tested viruses and viroids was only achieved using undiluted samples, with
308 the agents most frequently lost when resampling the 10^{-1} dilution dataset being PLMVd and the
309 four negative-stranded viruses ARWV 1 and 2, CCGaV and CiVA. On the other hand, using
310 undiluted samples, all viral agents could be reproducibly detected using as little as 300K reads,
311 while variability in performance was observed when using only 100K reads (Figure 2), with a
312 failure to detect, in some of the resampling, one or two of the agents frequently lost using the
313 10^{-1} dilution.

314 **DISCUSSION**

315 Very few studies have attempted so far to directly compare the performance of currently used
316 biological, serological, or molecular assays with that of HTS-based approaches for woody plant
317 materials (Al Rwahnih et al. 2015; Rott et al. 2017; Villamor et al. 2022). Viral diagnosis in

318 woody perennial hosts often poses specific difficulties that are linked to the uneven distribution
319 and low titers observed for many viruses in these hosts (Knapp et al. 1995; Maliogka et al.
320 2018; Morvan and Castelain 1976; Wetzel et al. 1992; Wright et al. 2021). These problems can
321 also be compounded by the frequent presence in these hosts of inhibitory substances, such as
322 polysaccharides or polyphenolics, that may interfere with detection assays. Using samples of
323 the six most common temperate fruit crops, we report here efforts at a direct performance
324 comparison of a dsRNA-based HTS approach with not only biological indexing as done in
325 previous publications but also ELISA and RT-PCR.

326 The results reported here confirm previous efforts in woody perennials, showing that the main
327 advantage of HTS is its ability to detect a broader range of viruses than biological indexing (Al
328 Rwahnih et al. 2015; Rott et al. 2017; Villamor et al. 2022). Three infections expected from
329 previous biological indexing or targeted assays were not identified using HTS, but these
330 infections were also not detected using ELISA or RT-PCR, which suggests that they either
331 represent erroneous anterior indexing results, are the results of virus loss during virus source
332 propagation or are due to uneven viral distribution in the sampled trees. All other infections
333 expected from biological indexing results (43/46, Table 1) were confirmed by one or more
334 assays.

335 On the other hand, a total of 24 unexpected infections were detected in 19 of the 30 tested fruit
336 tree samples (63%), indicating that biological indexing had failed to identify a viral infection
337 in almost two-thirds of samples. Remarkably, eight of these unexpected infections (33%)
338 involved well-known viruses for which biological indexing assays are available (LChV1,
339 ASGV, ASPV, rubbery wood viruses). It should, however, be stressed that not all samples had
340 gone through a complete biological indexing scheme as used in certification programs and
341 which involves the use of multiple indicators and samples over an extended period. In this
342 respect, it is noteworthy that no infections were detected in the healthy samples obtained from

343 certified germplasm collections, which rules out, for example, the possibility that detection of
344 these agents might represent pollen contamination of the samples rather than real viral
345 infections. None of these four viruses has known vectors or is known to be mechanically
346 transmissible in woody hosts and their transmission is therefore believed to be mostly through
347 vegetative propagation of their hosts (Jelkmann and Eastwell 2011; Massart et al. 2011;
348 Jelkmann and Paunovic 2011; Yaegashi et al. 2011). This makes it highly unlikely that their
349 detection may reflect new infections of sampled hosts that developed between biological
350 indexing and sampling. Likewise, the fact that all these infections were confirmed by RT-PCR
351 rules out the possibility that they may represent false positive HTS detections. On the other
352 hand, symptom observations can be difficult, particularly in situations of mixed infection, such
353 as in many samples used for this study. Together with the fact that not all samples used here
354 had gone through a complete biological indexing scheme involving grafting on multiple
355 indicators to extend the range of viruses detected, the impact of mixed infections on symptoms
356 observation and the lack of biological indicators for some viruses likely explain the results
357 reported here.

358 When comparing the performance of ELISA, RT-PCR, and HTS on undiluted plant samples in
359 the first experiment, ELISA had an overall detection rate of 69% (22/32), RT-PCR of 82.5%
360 (33/40) and HTS of 90.7% (39/43) (Table 1). However, if considering only viruses, the HTS
361 detection rate increases to 100% (37/37, Table 1). The low performance with viroids (only
362 PLMVd detected out of the four viroids tested) of the dsRNA purification protocol used here
363 (Marais et al. 2018) is already known and possibly results from the nuclease treatment included
364 between the two cellulose chromatography steps. Indeed, PLMVd was only detected with low
365 sensitivity since it was among the agents that could not be reliably detected from 10-fold diluted
366 samples. The efficient detection of PLMVd using a dsRNA-based HTS approach has, however,
367 been reported previously (Kesanakurti et al. 2016; Rott et al. 2017).

368 The overall low performance of ELISA should not come as a surprise since some low titer
369 viruses, such as ASGV, ASPV, or ACLSV are notoriously difficult to detect by this technique
370 in woody hosts (Massart et al. 2011; Yaegashi et al. 2011). Isolate variability, which is known
371 to be large for these viruses, may further complicate detection of all isolates. On the other hand,
372 the relatively poor performance of RT-PCR, with an overall detection rate of 82.5%, appears to
373 be mostly (if not fully) linked to point mutations affecting primer binding sites in some isolates
374 rather than to a lack of analytical sensitivity of the technique or other artefactual causes. Despite
375 the use of validated assays known to show broad analytical specificity (Candresse et al. 1995;
376 El Morsy et al. 2017 ; Menzel et al. 2002; Postman et al. 2004; Tang et al. 2013), these limits
377 in the ability of the RT-PCR assays to amplify all the isolates of a given virus resulted in an
378 overall better performance of HTS if considering only viruses. It is, however, clear that the use
379 of different primer pairs may have modified the ability to detect some isolates (Katsiani et al.
380 2018a). An added benefit of HTS is that by providing access to the genomic sequence of viral
381 isolates, it offers a direct route to the evaluation and, if needed, the improvement of the
382 inclusivity of detection primers (Katsiani et al. 2018a; Marais et al. 2014).

383 When comparing the three techniques using 10-fold dilutions of samples, ELISA proved once
384 again to be the technique with the lowest analytical sensitivity (Figure 3), while RT-PCR
385 outperformed HTS by allowing the detection of all viruses tested using a 10^{-1} dilution of
386 samples. This indicates that the dsRNA-based HTS approach used should not be performed on
387 pooled samples unless a sequencing depth significantly deeper than 1M reads per sample is
388 used (Figure 2). In particular, the performance of this approach on the minus-stranded RNA
389 viruses analyzed (ARWV1 and 2, CCGaV, and CiVA) was not as good as on positive RNA
390 viruses. This confirms other observations on a lower performance of dsRNA-based approaches
391 with negative-stranded viruses (Schönegger et al. 2023). If needed, the use of a different nucleic
392 acids target population, such as ribodepleted total RNAs, could provide for more efficient

393 detection of minus-stranded viruses and viroids but would necessitate deeper sequencing of
394 samples since it does not benefit from the enrichment of viral sequences brought by dsRNA
395 purification.

396 Significant variability of the LOD was observed between viruses but also between fruit tree
397 samples infected by the same virus, despite the fact that the sampling was performed during the
398 spring period, which is generally regarded as the most appropriate for virus detection (Cambra
399 et al. 2011; Katsiani et al. 2018b). This might reflect a range of factors, including uneven virus
400 distribution, the variability of viral isolates, their level of adaptation to different fruit tree
401 species, or the impact of mixed infections on viral concentrations. This implies that LOD values
402 reported here should be considered as providing indications limited to the analyzed samples
403 that should not be generalized without caution. There similarly was variability in the compared
404 performance of RT-PCR and HTS, with RT-PCR having a lower LOD in 61.5% of comparisons
405 (8/13) but HTS showing the same or a lower LOD than RT-PCR in 38.5% of comparisons (2/13
406 equal performance and 3/13 better performance, Table 2). This might reflect viral variability
407 and the impact of mutations in primer-binding sites, possibly reducing amplification efficiency.
408 In this context of viral variability, it is interesting to notice that as little as 300K reads per single
409 plant sample allowed the detection of all viruses, thus providing a baseline for future use of this
410 technique for fruit tree indexing by sequencing.

411 Overall, the results reported here confirm previous findings showing the superiority of HTS
412 approaches over biological indexing in terms of speed and inclusivity (Al Rwahnih et al. 2015;
413 Rott et al. 2017; Villamor et al. 2022). They also show that while the absolute analytical
414 sensitivity of RT-PCR assays tends to be higher, their inclusivity is often incomplete as a
415 consequence of viral variability and of mutations affecting primer-binding sites. Taken
416 together, these elements make a strong case for the implementation of HTS-based approaches

417 in fruit tree diagnostics protocols supporting quarantine and certification programs for which
418 the speed and inclusivity of these approaches represent clear benefits.

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	Cerasifera#2	2017	APLPV	-	nt	+	+	CVA, CMV
	Negative control	-	-	-	-	-	-	-
	LX86	2017	ACLSV	-	nt	-	+	-
			ASPV	-	nt	+	+	-
	X259	2009	ACLSV	-	nt	+	+	ASGV
			ASSVd	nt	nt	+	-	
Apple	LX225	2017	ACLSV	+	nt	+	+	ARWV1, CCGaV
			ASPV	+	nt	+	+	
			ASGV	+	nt	+	+	
			ApMV	+	nt	+	+	
	J2959	2017	ApMV	+	nt	+	+	-
	LX223	2017	ASPV	+	nt	+	+	ACLSV
ASGV			+	nt	+	+		
	Negative control	-	-	-	-	-	-	-
	PO13357	2016	ACLSV	-	nt	-	-	-
ASPV			-	nt	-	+		
ARW			nt	nt	nt	+		
Pear	PO1492	2017	ACLSV	-	nt	-	-	ASGV, CiVA
			ASPV	+	nt	+	+	
			ARW	nt	nt	+	+	
			PO2098	2006	PBCVd	nt	nt	
	PO161	2013	ASPV	-	nt	-	+	-
	P160	2010	ASPV	+	nt	+	+	ARWV2
	Negative control	-	-	-	-	-	-	-

%; viruses expected to be present in the source based on previous biological indexing and virus testing (for example for CVA, AVCaV, PBNSPaV, HSVd). ACLSV: apple chlorotic leaf spot virus; APLPV: American plum line pattern virus; ApMV: apple mosaic virus; APV3: Asian prunus virus 3; ARW: apple rubbery wood virus; ARWV1: apple rubbery wood virus 1; ARWV2: apple rubbery wood virus 2; ASGV: apple stem grooving virus; ASPV: apple stem pitting virus; ASSVd: apple scar skin viroid; AVCaV: apricot vein clearing-associated virus; CCGaV: citrus concave gum-associated virus; CiVA: citrus virus A; CMV: cucumber mosaic virus; CNRMV: cherry necrotic rusty mottle virus; CVA: cherry virus A; GCV: grapevine cryptic virus; HSVd: hop stunt viroid; LChV1: little cherry virus 1; NSPaV: nectarine stem pitting-associated virus; PBCVd: pear blister canker viroid; PBNSPaV: plum bark necrosis stem pitting-associated virus; PDV: prune dwarf virus; PeLPaV: peach leaf pitting-associated virus; PLMVd: peach latent mosaic viroid; PNRSV: prunus necrotic ringspot virus; PPV: plum pox virus; PrVF: prunus virus F; SLRSV: strawberry latent ringspot virus; ToRSV: tomato ringspot virus. nt: not tested.

ASGV	Apple	LX225	ELISA	X	-	-	-	-	-	nt	nt	nt
			HTS	X	X	X	X	X	-	nt	nt	nt
			RT-PCR	X	X	X	X	X	-	-	nt	nt
	Pear	PO1492	HTS	X	X	X	X	-	-	nt	nt	nt
			RT-PCR	X	X	X	X	-	-	-	nt	nt
	ASPV	Apple	LX225	ELISA	X	X	X	-	-	-	nt	nt
HTS				X	X	X	X	-	-	nt	nt	nt
RT-PCR				X	X	X	X	X	X	-	-	nt
Pear		PO1492	ELISA	X	-	-	-	-	-	nt	nt	nt
			HTS	X	X	X	X	-	-	nt	nt	nt
			RT-PCR	X	X	X	-	-	-	-	-	nt
ARWV1	Apple	LX225	ELISA	nt	nt	nt	nt	nt	nt	nt	nt	nt
			HTS	X	-	-	-	-	-	nt	nt	nt
			RT-PCR	X	X	X	-	-	-	nt	nt	nt
ARWV2	Pear	PO1492	ELISA	nt	nt	nt	nt	nt	nt	nt	nt	nt
			HTS	X	-	-	-	-	-	nt	nt	nt
			RT-PCR	X	X	-	-	-	-	nt	nt	nt

a: only PNRSV or PDV RNA3 detected at these dilutions

LEGENDS TO THE FIGURES

Fig. 1. Multiple nucleotide sequence alignments showing detection primers and their binding sites on the genome of strawberry latent ringspot virus (SLRSV, **A**), apple chlorotic leaf spot virus (ACLSV, **B**) and apple stem pitting virus (ASPV, **C**). Primers are indicated in bold italics and, for each, the reverse complement sequence is shown for reverse primers. For each virus, the sequence of a reference isolate known to be amplified is shown immediately below primer sequences with its GenBank accession number, followed by sequences for viral isolates that were not detected by RT-PCR but were detected by HTS. Mutations affecting primer-binding sites are in bold and highlighted in light grey. Dashes represent an insertion, while question marks are used to represent missing information not available from HTS sequencing reads.

Fig. 2. Overall rate of detection of 12 viruses and one viroid (PLMVd) in undiluted and in 10-fold serial dilutions of temperate fruit tree extracts as a function of Illumina sequencing depth. For each sequencing depth, three random subsamplings of the original dataset were performed. A detection is considered positive if the number of reads mapping on the reference genome used for each pathogen is superior to the average of mapped reads for the six negative controls plus three times the standard deviation. For viruses with a divided genome, mapped reads number above threshold for any one of the genomic RNAs were considered as positive detection.

Fig. 3. Percentage of detection of the viral agents present in the six tested fruit tree samples as a function of the rate of dilution of those samples in uninfected samples of the same species.

Figure 1**A**

	SLRSV-F	SLRSV-R
	<i>CCTCTCCAACCTGCTAGACT</i>	<i>//...AGTTACACCTTCATGCGCTT</i>
NC_006965	CCTCTCCAACCTGCTAGACT...	//...AGTTACACCTTCATGCGCTT
X77466	CCTCTCCAGCCTGCTAGACT...	//...AGTTACACCTTCATGCGCTT
LS27	CCT T T G CAACCTGC AC GACT...	//... G GTTAC CGG TTCATGCG G TT

B

	A52	A53
	<i>TTCGACTTCAATAAGGGTCTG</i>	<i>// GGCAACCCTGGAACAGA</i>
M58152	TT T GATTTCAATAAGGGTCTG...	//...GGCAACCCTGGAACAGA
PR3473	TT T GATTT T AAC A AGGG C CT C ...	//...GG T AAT C CTGGAACAGA
LX86	TT T GATTT T AATAAGGG C CT A ...	//...GGCA T TCTGGAACAGA
PO13357	????????????????????	// GG T AAT C CTGGAACAGA
PO1492	????????????????????	// GGCA T CCTGGAACAGA
PO161	????????????????????	// GG T AAT C CT A GAACAGA

C

	ASPV-F	ASPV-R
	<i>ATGTCTGGAACCTCATGCTGCAA</i>	<i>//...TTATGCTTTTT-AGTAAAGTTGATCCCAA</i>
KY490039	ATGTCTGGAACCTCATGCTGCAA...	//...TTATGCTTTTT G - AA TAAAGTTGATCC GA
P013357	ATGT T TGGA A T C T G ATGCTGCAA...	//...TTATGCTTTTT AAA TAAAGTTGATCC GC

Figure 2

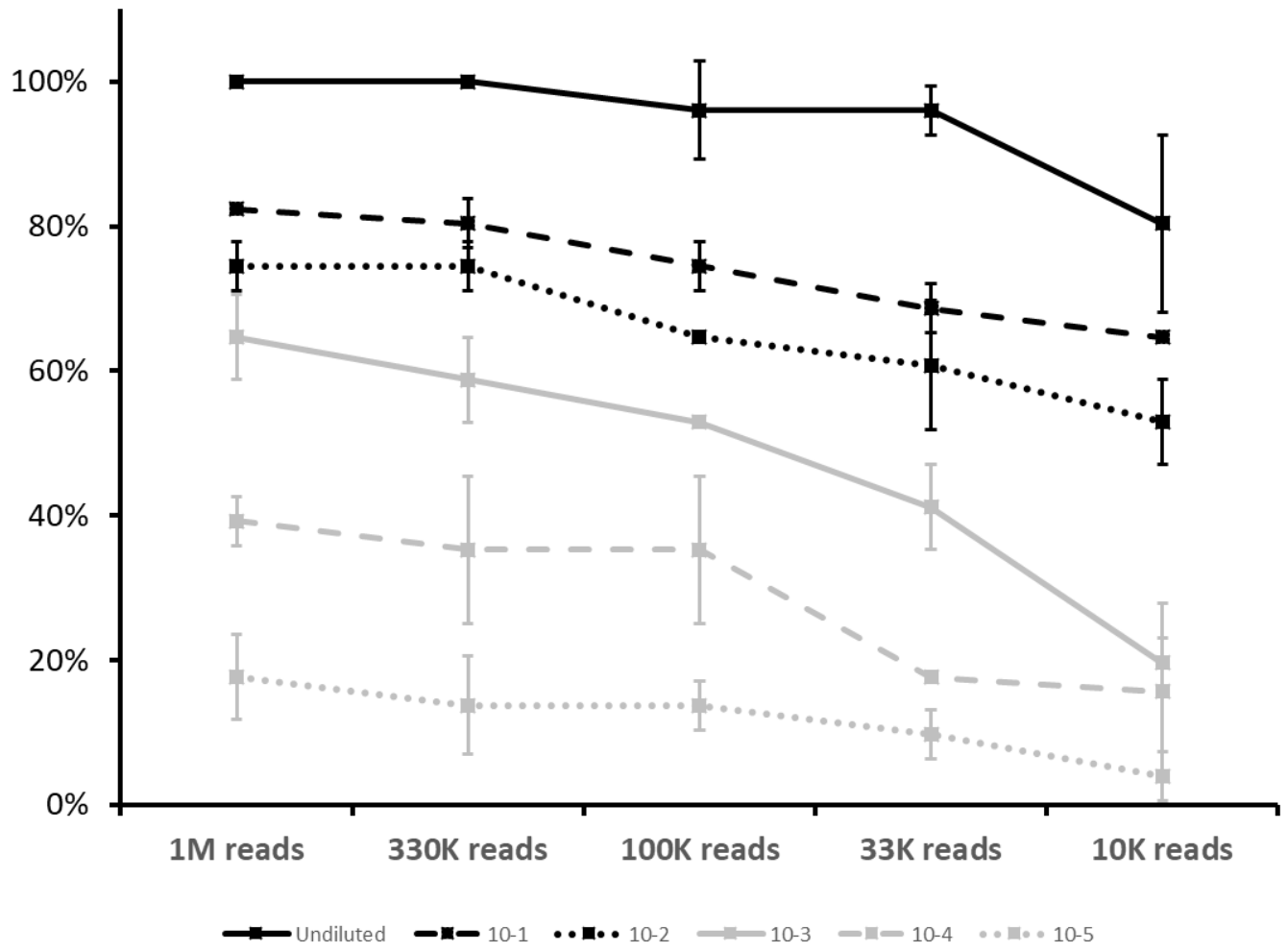
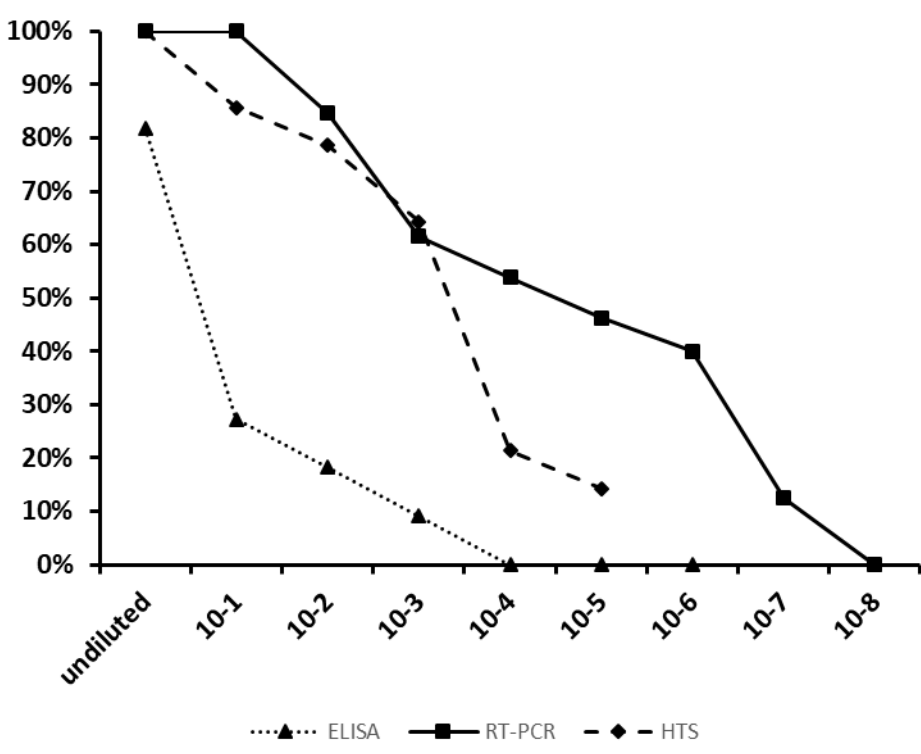


Figure 3



Supplementary table title

Supplementary TABLE S1. RT-PCR assays used for the detection of the various viruses in the present study.

Supplementary TABLE S1. RT-PCR assays used for the detection of the various viruses in the present study.

Targeted virus	Reference of the RT-PCR assay used or primer pair used
ACLSV	Candresse <i>et al.</i> (1994). <i>Acta Hort.</i> 386, 136-147.
APLPV	Primers APLPV196 5GGTGCCCGTTTAATTCAGG3' and et APLPVc420 5'TATTGCTGCCTCACAAAGTGG3' (Tm 55°C, amplicon 224 nt), Villamor (2012), PhD dissertation. https://rex.libraries.wsu.edu/esploro/outputs/99900581654701842
ApMV	Candresse <i>et al.</i> (1997). <i>Acta Hort.</i> 472, 219-226.
APV3	Marais <i>et al.</i> (2006). <i>Virus Res.</i> 120, 176-183.
ARWV1	Rott <i>et al.</i> (2018). <i>Plant Dis.</i> 102, 1254-1263.
ARWV2	Rott <i>et al.</i> (2018). <i>Plant Dis.</i> 102, 1254-1263.
ASGV	Roy <i>et al.</i> (2005). <i>J. Virol. Meth.</i> 129, 47-55.
ASPV	Menzel <i>et al.</i> (2002). <i>J. Virol. Meth.</i> 99, 81-92.
ASSVd	This work. Primers ASSf 5'GAGAAAGGAGCTGCCAGC3' and ASSr 5'CCCGCCGCTGCGTCAAA3' (Tm 60°C, amplicon 193 nt)
AVCaV	Marais <i>et al.</i> (2015). <i>PLoS One</i> , 10, e0129469.
CCGaV	This work. Primers CCGaV-F1 5'CTAGAGATGGTGATGACGGGCAA3' and CCGaV-R1 5'CTGTTTGGCCCTCAGTAGACAAC3' (Tm 60°C, amplicon 327 nt).
CiVA	Svanella-Dumas <i>et al.</i> (2019). <i>Plant Dis.</i> 103, 2703.
CMV	Primers CMV-C1 5'CCAGGACGGCGTACT3' and CMV-C1' 5'CCTGATTCAGTCACGG3' (Tm 46°C, amplicon 300 nt). Eric Verdin (INRAE, Avignon, France) personal communication.
CNRMV	Rott & Jelkmann (2001). <i>Arch. Virol.</i> 146, 395-401.
CVA	Marais <i>et al.</i> (2012). <i>Plant Pathol.</i> 61, 195-204.
GCV	This work. Primers GCryV-F 5'ACGGAACGACCCCGACAAGATG3' and GCryV-R 5'CAAACCCAATGGCTTGTGCCAT3' (Tm 60°C, amplicon 854 nt).
HSVd	Bernad & Duran-Vila (2006). <i>Mol. Cell. Probes</i> 20, 105-113.
LChV1	Katsiani <i>et al.</i> (2018). <i>Plant Disease</i> 102, 899-904.
NSPaV	Khalili <i>et al.</i> (2023). <i>Phytopathology</i> 113, 345-354.
PBCVd	This work. Primers PBCf 5'CCCCTGACCTGCRITCC3' and PBCr 5'TTACTCACAGCCGCGCGC3' (Tm 60°C, amplicon 116 nt)
PBNSPaV	Marais <i>et al.</i> (2014). <i>Phytopathology</i> 104, 660-666.
PDV	Parakh <i>et al.</i> (1994). <i>Acta Hort.</i> 386, 421-430.
PeLPaV	This work. Primers PeLPaV-F 5'GCACATGCATGAGCTTGTTAGA3' and PeLPaV-R 5'CACTCCTTCCAATGCACACAA3' (Tm 60°C; amplicon 347 nt).
PLMVd	Ambrós <i>et al.</i> (1998). <i>J. Virol.</i> 72:7397-7406.
PNRSV	Candresse <i>et al.</i> (1997). <i>Acta Hort.</i> 472, 219-226.
PPV	Olmos <i>et al.</i> (2005). <i>J. Virol. Meth.</i> 128, 151-155.
PrVF	This work. Primers PrVF-F 5'TTGAGTGGCACTTGGAAACTC3' and PrVF-R 5'AGTCTGGTCTTAGGCTTACCA3" (Tm 58°C; amplicon 526 nt).
SLRV	Tang <i>et al.</i> (2013). <i>Plant Dis.</i> 97, 662-667.
ToRSV	Tang <i>et al.</i> (2014). <i>J. Virol. Meth.</i> 201, 38-43.

ACLSV: apple chlorotic leaf spot virus; APLPV: american plum line pattern virus; ApMV: apple mosaic virus; APV3: asian prunus virus 3; ARW: apple rubbery wood virus; ARWV1: apple rubbery wood virus 1; ARWV2: apple rubbery wood virus 2; ASGV: apple stem grooving virus; ASPV: apple stem pitting virus; ASSVd: apple scar skin viroid; AVCaV: apricot vein clearing-associated virus; CCGaV: citrus concave gum-associated virus; CiVA: citrus virus A; CMV: cucumber mosaic virus; CNRMV: cherry necrotic rusty mottle virus; CVA: cherry virus A; GCV: grapevine cryptic virus; HSVd: hop stunt viroid; LChV1: little cherry virus 1; NSPaV: nectarine stem pitting-associated virus; PBCVd: pear blister canker viroid; PBNSPaV: plum bark necrosis stem pitting-associated virus; PDV: prune dwarf virus; PeLPaV: peach leaf pitting-associated virus; PLMVd: peach latent mosaic viroid; PNRSV: prunus necrotic ringspot virus; PPV: plum pox virus; PrVF: prunus virus F; SLRV: strawberry latent ringspot virus; ToRSV: tomato ringspot virus.