

Chinese Taipei's Comments on February 2020 Manual of Diagnostic Tests and Vaccine for Terrestrial Animals Text

30 June 2020

OIE draft	Proposed alternatives	Rationale
<p>Chapter 2.1.2</p> <p>3. Isothermal amplification Isothermal amplification technologies offer the advantage of omitting thermocycling, enabling DNA amplification at constant temperature.</p>	<p>Chapter 2.1.2</p> <p>3. Isothermal amplification Isothermal amplification technologies offer the advantage of omitting thermocycling, enabling DNA amplification at a constant temperature.</p>	<p>An indefinite article should be needed.</p>
<p>Chapter 2.1.2</p> <p>3. Isothermal amplification From a diagnostic point of view, the advantages and strengths of the isothermal amplification technologies are as follows:</p> <p>i) Enables amplification at constant temperature unlike A much simpler procedure than PCR;</p> <p>ii) Requires less complex and less expensive equipment;</p> <p>iii) Easy to adapt to “on-site” applications;</p> <p>iv) Simple diagnosis under the read-out suitable for field conditions; for an example see the review of Mansour <i>et al.</i> (2015).</p>	<p>Chapter 2.1.2</p> <p>3. Isothermal amplification From a diagnostic point of view, the advantages and strengths of the isothermal amplification technologies are as follows:-</p> <p>i) Enables amplification at constant temperature unlike A much simpler procedure than PCR;-</p> <p>ii) Requires less complex and less expensive equipment;-</p> <p>iii) Easy to adapt to “on-site” applications;-</p> <p>iv) Simple diagnosis under the read-out suitable for field conditions; for an example see the review of Mansour <i>et al.</i> (2015).-</p>	<p>These advantages and strengths were described in the previous two paragraphs.</p>
<p>Chapter 2.1.2</p> <p>4. Diagnosis by restriction fragment length polymorphisms (RFLP) and related DNA-based approaches The restriction fragment length polymorphisms (RFLP) method allows individual genomes to be identified based on unique</p>	<p>Chapter 2.1.2</p> <p>4. Diagnosis by restriction fragment length polymorphisms (RFLP) and related DNA-based approaches The restriction fragment length polymorphisms (RFLP) method allows individual genomes to be identified based on unique</p>	<p>RFLP usually works with pathogen subtyping and epidemiological approaches rather than clinical diagnosis.</p>

patterns caused by [restriction enzymes](#) cutting in specific regions of DNA. A restriction enzyme is an endonuclease that recognises and cleaves double-stranded DNA at specific nucleotide sequences called restriction sites (Loza-Rubio *et al.*, 1999). The RFLP approach is based on the fact that the genomes of even closely related pathogens are defined by variation in sequences. For example, the linear order of adjacent nucleotides comprising the recognition sequence of a specific restriction enzyme in one genome may be absent in the genome of a closely related strain or isolate. The RFLP procedure consists of digesting the pathogens' nucleic acid (DNA or PCR products) with one or a panel of restriction enzymes and then separating the DNA fragments by agarose gel electrophoresis to determine the number of fragments and their relative sizes. A restriction enzyme is an endonuclease that recognises and cleaves double-stranded DNA at specific nucleotide sequences called restriction sites (Loza-Rubio *et al.*, 1999).

Pulsed-field gel electrophoresis (PFGE) can be used for the separation of large (up to megabase size) fragments of DNA and can be a useful adjunct to the basic RFLP analysis. These technologies are extensively used in the official

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<p>programmes for detection and discrimination of food-borne pathogens (<i>Escherichia coli</i> O157:H7, <i>Salmonella</i>, <i>Shigella</i>, <i>Listeria</i>, or <i>Campylobacter</i>) worldwide (http://www.pulsenetinternational.org; https://www.cdc.gov/pulsenet/).</p> <p>RFLPs have a clear value for use in epidemiological studies, however, an RFLP difference may not be functionally significant. Although the RFLP and PCR-RFLP are much less powerful compared with the modern sequencing technologies, they are relatively inexpensive, easy to perform and sufficiently descriptive for epidemiological investigations of outbreaks and identification of individual strains of pathogens.</p>	<p>programmes for detection and discrimination of food-borne pathogens (<i>Escherichia coli</i> O157:H7, <i>Salmonella</i>, <i>Shigella</i>, <i>Listeria</i>, or <i>Campylobacter</i>) worldwide (http://www.pulsenetinternational.org; https://www.cdc.gov/pulsenet/).</p> <p>RFLPs have a clear value for use in epidemiological studies, however, an RFLP difference may not be functionally significant. Although the RFLP and PCR-RFLP are much less powerful compared with the modern sequencing technologies, they are relatively inexpensive, easy to perform and sufficiently descriptive for epidemiological investigations of outbreaks and identification of individual strains of pathogens.</p>	
<p>Chapter 2.1.2 5.1. Immunofluorescence (The last sentence of the second Paragraph.) The method is commonly used in diagnostic laboratories for the detection of antibodies raised against a wide range of pathogens, e.g., African swine fever virus (Cubillos <i>et al.</i>, 2013), Q fever (Roest <i>et al.</i>, 2013) and many other infectious agents in veterinary medicine.</p>	<p>Chapter 2.1.2 5.1. Immunofluorescence (The last sentence of the second Paragraph.) The method is commonly used in diagnostic laboratories for the detection of antibodies raised against a wide range of pathogens, e.g., African swine fever virus (Cubillos <i>et al.</i>, 2013), <i>Coxiella burnetii</i>, causative bacteria of Q fever (Roest <i>et al.</i>, 2013) and many other infectious agents in veterinary medicine.</p>	<p>Because Q fever is a name of disease, amend wording to the pathogen consistency with text grammar.</p>
<p>Chapter 3.3.4 A. INTRODUCTION (The last sentence of the second</p>		<p>Virologically, the term “influenza A virus” is composed of all viruses within the genus <i>influenzavirus A</i>,</p>

Paragraph.)

...and 3) influenza A as an infection with ~~by any HPAI or LPAI virus will be used. The latter indicates any influenza virus from birds that is H1-~~ H16.

which may infect a wide spectrum of animal species. As showed in the chapters “infection with influenza A virus of swine” and “equine influenza”, different wording about influenza viruses A in these chapters should be systemically reviewed and consistent. If not possible, keeping use “avian influenza viruses” may be better.