Primerdesign™ Ltd

Taylorella equigenitalis

DNA gyrase subunit B (gyrB) gene

genesig® Advanced Kit

150 tests

For general laboratory and research use only

DNA testing

Everything...
Everyone...
Everywhere...

Introduction to Taylorella equigenitalis

Taylorella equigenitalis is a Gram-negative bacterium of the genus Taylorella, and the causative agent of Contagious Equine Metritis (CEM) in horses.

T. equigenitalis was first described in the United Kingdom in 1977, after which it was diagnosed in a number of countries world-wide. Infected stallions are asymptomatic and act as the principal source of infection as they mate with numerous mares and the carrier status may persist for many months or even years.

The approximate size of t.equigenitalis' genome is 1,695,860 bp long (for the MCE9 strain), with an overall G+C content of 37.42%. There are ~1,556 protein-coding genes, with an average length of 1,007 bp. There are 38 tRNA genes for all amino acids and three copies of the 16S-23S-5S rRNA operon, three putative transposase genes, and four putative phage-related genes.

The disease caused by T. equigenitalis, Contagious Equine Metritis is an inflammatory disease of the reproductive tract of the mare which usually results in temporary infertility. It is a nonsystemic infection, the effects of which are restricted to the reproductive tract of the mare.
When present in the mare, clinical signs include endometritis, cervicitis and vaginitis of variable severity and vaginal discharge.

Direct venereal contact during natural mating presents the highest risk for the transmission of T. equigenitalis from a contaminated stallion or an infected mare.
Many primary cases of infection with T. equigenitalis in the mare are subclinical, and a frequent indicator of infection is a mare returning in oestrus prematurely after being bred to a putative carrier stallion.

Carrier mares and stallions act as reservoirs of T. equigenitalis, but stallions, because they mate with numerous mares, play a much more important role in dissemination of the bacterium. The urogenital membranes of stallions become contaminated at coitus, leading to a carrier state that may persist for many months or years. Failure to observe appropriate hygienic measures when breeding mares and stallions may also spread the organism.

Other sites of the horse's body are not known to harbour T. equigenitalis.

Taylorella equigenitalis is not known to infect humans.

Diagnosis of CEM is achieved by PCR or culturing the organism from samples of animals with suspected infection. Real-Time PCR provides the most rapid and reliable method of detecting the causative agent of CEM.

Specificity

The Primerdesign™ genesig® Kit for Taylorella equigenitalis (T.equigenitalis) genomes is designed for the in vitro quantification of T.equigenitalis genomes. The kit is designed to have the broadest detection profile possible whilst remaining specific to the T. equigenitalis genome.

The primers and probe sequences in this kit have 100% homology with a broad range of T.equigenitalis sequences based on a comprehensive bioinformatics analysis.

If you require further information, or have a specific question about the detection profile of this kit then please send an e.mail to enquiry@primerdesign.co.uk and our bioinformatics team will answer your question.

Kit Contents

- **T.equigenitalis specific primer/probe mix (150 reactions BROWN)**
  FAM labelled
- **T.equigenitalis positive control template (for Standard curve RED)**
- **Internal extraction control primer/probe mix (150 reactions BROWN)**
  VIC labelled as standard
- **Internal extraction control DNA (150 reactions BLUE)**
- **Endogenous control primer/probe mix (150 reactions BROWN)**
  FAM labelled
- **RNAse/DNAse free water (WHITE)**

Reagents and equipment to be supplied by the user

Real-Time PCR Instrument

DNA extraction kit

This kit is recommended for use with genesig EASY DNA/RNA Extraction kit. However, it is designed to work well with all processes that yield high quality DNA with minimal PCR inhibitors.

oasig™ Lyophilised or PrecisionPLUS™ 2x qPCR Mastermix

This kit is designed to work well with all commercially available Mastermixes. However, we recommend the use of oasig™ or PrecisionPLUS™ 2x qPCR MasterMix.

Pipettors and Tips

Vortex and centrifuge

Thin walled 1.5 ml PCR reaction tubes

Kit storage and stability

This kit is stable at room temperature but should be stored at -20ºC on arrival. Primerdesign does not recommend using the kit after the expiry date stated on the pack. Once the lyophilized components have been re-suspended, unnecessary repeated freeze/thawing should be avoided. The kit is stable for six months from the date of resuspension under these circumstances.

Suitable sample material

All kinds of sample material suited for PCR amplification can be used. Please ensure the samples are suitable in terms of purity, concentration, and DNA integrity (An internal PCR control is supplied to test for non specific PCR inhibitors). Always run at least one negative control with the samples. To prepare a negative-control, replace the template DNA sample with RNAse/DNAse free water.

Dynamic range of test

Under optimal PCR conditions genesig® T.equigenitalis detection kits have very high priming efficiencies of >95% and can detect less than 100 copies of target template.

Notices and disclaimers

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Trademarks

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Principles of the test

Real-time PCR

A T.equigenitalis specific primer and probe mix is provided and this can be detected through the FAM channel.

The primer and probe mix provided exploits the so-called TaqMan® principle. During PCR amplification, forward and reverse primers hybridize to the T.equigenitalis DNA. A fluorogenic probe is included in the same reaction mixture which consists of a DNA probe labeled with a 5`-dye and a 3`-quencher. During PCR amplification, the probe is cleaved and the reporter dye and quencher are separated. The resulting increase in fluorescence can be detected on a range of real-time PCR platforms.

Positive control

For copy number determination and as a positive control for the PCR set up, the kit contains a positive control template. This can be used to generate a standard curve of T. equigenitalis copy number / CT value. (n.b. A new standard curve should be prepared from the positive control template on each occasion rather than freeze/thawing.) Alternatively the positive control can be used at a single dilution where full quantitative analysis of the samples is not required. Each time the kit is used, at least one positive control reaction must be included in the run. A positive result indicates that the primers and probes for detecting the target T.equigenitalis gene worked properly in that particular experimental scenario. If a negative result is obtained the test results are invalid and must be repeated. Care should be taken to ensure that the positive control does not contaminate any other kit component which would lead to false-positive results. This can be achieved by handling this component in a Post PCR environment. Care should also be taken to avoid cross-contamination of other samples when adding the positive control to the run. This can be avoided by sealing all other samples and negative controls before pipetting the positive control into the positive control well.

Negative control

To validate any positive findings a negative control reaction should be included every time the kit is used. For this reaction the RNAse/DNAse free water should be used instead of template.

Internal DNA extraction control

When performing DNA extraction, it is often advantageous to have an exogenous source of DNA template that is spiked into the lysis buffer. This control DNA is then co-purified with the sample DNA and can be detected as a positive control for the extraction process. Successful co-purification and real-time PCR for the control DNA also indicates that PCR inhibitors are not present at a high concentration.

A separate primer and probe mix are supplied with this kit to detect the exogenous DNA using real-time PCR. The primers are present at PCR limiting concentrations which allows multiplexing with the target sequence primers. Amplification of the control DNA does not interfere with detection of the T.equigenitalis target DNA even when present at low copy number. The Internal control is detected through the VIC channel and gives a CT value of 28+/-3.

Endogenous control

To confirm extraction of a valid biological template, a primer and probe mix is included to detect an endogenous gene. Detection of the endogenous control is through the FAM channel and it is NOT therefore possible to perform a multiplex with the T.equigenitalis primers. A poor endogenous control signal may indicate that the sample did not contain sufficient biological material.

Carry-over prevention using UNG (optional)

Carry over contamination between PCR reactions can be prevented by including uracil-N-glycosylase (UNG) in the reaction mix. Some commercial mastermix preparations contain UNG or alternatively it can be added as a separate component. UNG can only prevent carry over from PCR reactions that include deoxyuridine triphosphate (dUTP) in the original PCR reaction. Primerdesign recommend the application of 0.2U UNG per assay with a 15 minute incubation step at 37°C prior to amplification. The heat-labile UNG is then inactivated during the Taq polymerase activation step (95°C for 10 minutes).

Reconstitution Protocol

To minimize the risk of contamination with foreign DNA, we recommend that all pipetting be performed in a PCR clean environment. Ideally this would be a designated PCR lab or PCR cabinet. Filter tips are recommended for all pipetting steps.

1. **Pulse-spin each tube in a centrifuge before opening.**
   This will ensure lyophilised primer and probe mix is in the base of the tube and is not spilt upon opening the tube.

2. **Reconstitute the kit components in the RNase/DNase-free water supplied, according to the table below:**
   To ensure complete resuspension, vortex each tube thoroughly.

Component	Volume
Pre-PCR pack	
T.equigenitalis primer/probe mix (BROWN)	165 µl
Internal extraction control primer/probe mix (BROWN)	165 µl
Endogenous control primer/probe mix (BROWN)	165 µl
Pre-PCR heat-sealed foil	
Internal extraction control DNA (BLUE)	600 µl
Post-PCR heat-sealed foil	
Positive Control Template (RED) *	500 µl

* This component contains high copy number template and is a VERY significant contamination risk. It must be opened and handled in a separate laboratory environment, away from the other components.

DNA extraction

The internal extraction control DNA can be added either to the DNA lysis/extraction buffer or to the DNA sample once it has been resuspended in lysis buffer.

DO NOT add the internal extraction control DNA directly to the unprocessed biological sample as this will lead to degradation and a loss in signal.

1. **Add 4µl of the Internal extraction control DNA (BLUE) to each sample in DNA lysis/extraction buffer per sample.**

2. **Complete DNA extraction according to the manufacturers protocols.**

Real-time PCR detection protocol

1. **For each DNA sample prepare a reaction mix according to the table below:**
   Include sufficient reactions for positive and negative controls.

Component	Volume
oasig™ or PrecisionPLUS™ 2x qPCR MasterMix	10 µl
T.equigenitalis primer/probe mix (BROWN)	1 µl
Internal extraction control primer/probe mix (BROWN)	1 µl
RNAse/DNAse free water (WHITE)	3 µl
Final Volume	**15 µl**

2. **For each DNA sample prepare an endogenous control reaction according to the table below (Optional):**
   This control reaction will provide crucial information regarding the quality of the biological sample.

Component	Volume
oasig™ or PrecisionPLUS™ 2x qPCR MasterMix	10 µl
Endogenous control primer/probe mix (BROWN)	1 µl
RNAse/DNAse free water (WHITE)	4 µl
Final Volume	**15 µl**

3. **Pipette 15µl of each mix into individual wells according to your real-time PCR experimental plate set up.**

4. **Prepare sample DNA templates for each of your samples.**

5. **Pipette 5µl of DNA template into each well, according to your experimental plate set up.**
   For negative control wells use 5µl of RNAse/DNAse free water. The final volume in each well is 20µl.

6. **If a standard curve is included for quantitative analysis prepare a reaction mix according to the table below:**

Component	Volume
oasig™ or PrecisionPLUS™ 2x qPCR MasterMix	10 µl
T.equigenitalis primer/probe mix (BROWN)	1 µl
RNAse/DNAse free water (WHITE)	4 µl
Final Volume	**15 µl**

7. Preparation of standard curve dilution series.

n.b. A new standard curve should be prepared from the positive control template on each occasion rather than freeze/thawing.

1) Pipette 900µl of RNAse/DNAse free water into 5 tubes and label 2-6
2) Pipette 100µl of Positive Control Template (RED) into tube 2
3) Vortex thoroughly
4) Change pipette tip and pipette 100µl from tube 2 into tube 3
5) Vortex thoroughly

Repeat steps 4 and 5 to complete the dilution series

Standard Curve	Copy Number
Tube 1 Positive control (RED)	2 x 10^5 per µl
Tube 2	2 x 10^4 per µl
Tube 3	2 x 10^3 per µl
Tube 4	2 x 10^2 per µl
Tube 5	20 per µl
Tube 6	2 per µl

8. Pipette 5µl of standard template into each well for the standard curve according to your experimental plate set up.

The final volume in each well is 20µl.

Amplification Protocol

Amplification conditions using oasig™ or PrecisionPLUS™ 2x qPCR MasterMix.

	Step	Time	Temp
50 Cycles	UNG treatment (if required) **	15 mins	37 °C
	Enzyme activation	2 mins	95 °C
	Denaturation	10s	95 °C
	DATA COLLECTION *	60s	60 °C

* Fluorogenic data for the control DNA should be collected during this step through the FAM and VIC channels
** Required if your Mastermix includes UNG to prevent PCR carryover contamination

Interpretation of Results

Target	Internal control	Negative control	Positive control	Interpretation
+ive	+ive	-ive	+ive	+ive
+ive	-ive	-ive	+ive	+ive
+ive	+ive	+ive	+ive	*
+ive	-ive	+ive	+ive	*
-ive	+ive	-ive or +ive	+ive	-ive
-ive	-ive	-ive or +ive	-ive	Experiment fail
-ive	+ive	-ive or +ive	-ive	Experiment fail

* Where the test sample is positive and the negative control is also positive the interpretation of the result depends on the relative signal strength of the two results. This is calculated using the delta CT method by subtracting the target CT value from the negative control CT value (NC CT value – sample CT value). Where the test sample is positive and the NC is detected much later (delta CT ≥ 5) then the positive test result is reliable. Where the NC detection is at a similar level to the test sample (delta CT<5) then the positive test result is invalidated and a negative call is the correct result.

Internal PCR control

The CT value obtained with the internal control will vary significantly depending on the extraction efficiency, the quantity of DNA added to the PCR reaction and the individual machine settings. CT values of 28±3 are within the normal range. When amplifying a T. equigenitalis sample with a high genome copy number, the internal extraction control may not produce an amplification plot. This does not invalidate the test and should be interpreted as a positive experimental result.

Endogenous control

The signal obtained from the endogenous control primer and probe set will vary according to the amount of biological material present in a given sample. An early signal indicates the presence of a good yield of biological material. A late signal suggests that little biological material is present in the sample.