

Assessment of Pathogen Prevalence Frequency Associated with Bovine Respiratory Disease (BRD) in Mexican Dairy Heifers Using the Technique of Polymerase Chain Reaction (PCR)

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INTRODUCTION

In Mexico, Bovine Respiratory Disease (BRD) is of significant economic importance at dairy farms. One of the main challenges in addressing this disease is to achieve a precise diagnosis of pathogens causing BRD. Advanced laboratory tests, such as Polymerase Chain Reaction (PCR), have emerged as highly sensitive and specific diagnostic tool. This test enables a rapid and effective identification of the pathogens associated with BRD.

OBJECTIVE

The objective of this study was to determine the prevalence of pathogens involved in BRD in dairy heifers using PCR testing.

MATERIALS AND METHODS

- ▶ A total of 114 nasopharyngeal swabs from Holstein heifers exhibiting clinical signs of pneumonia were collected from multiple dairy farms located in the center and western part of Mexico. The samples were collected prior to administration of any treatment and the swabs were shipped in a Stuart transport medium under refrigeration to perform pathogen identification using a PCR test.
- ▶ The PCR results were subjected to a Bayesian analysis to evaluate the probability of the frequency of each pathogen identified, without prior assumptions and considering a binomial distribution of 2x2.

Pasteurella multocida, *Mannheimia haemolytica*, *Mycoplasma bovis*, and bovine coronavirus are the main pathogens associated with Bovine Respiratory Disease (BRD) in this study. These findings justify the implementation of health preventive programs in Mexican dairy farms to reduce economic losses due to BRD.



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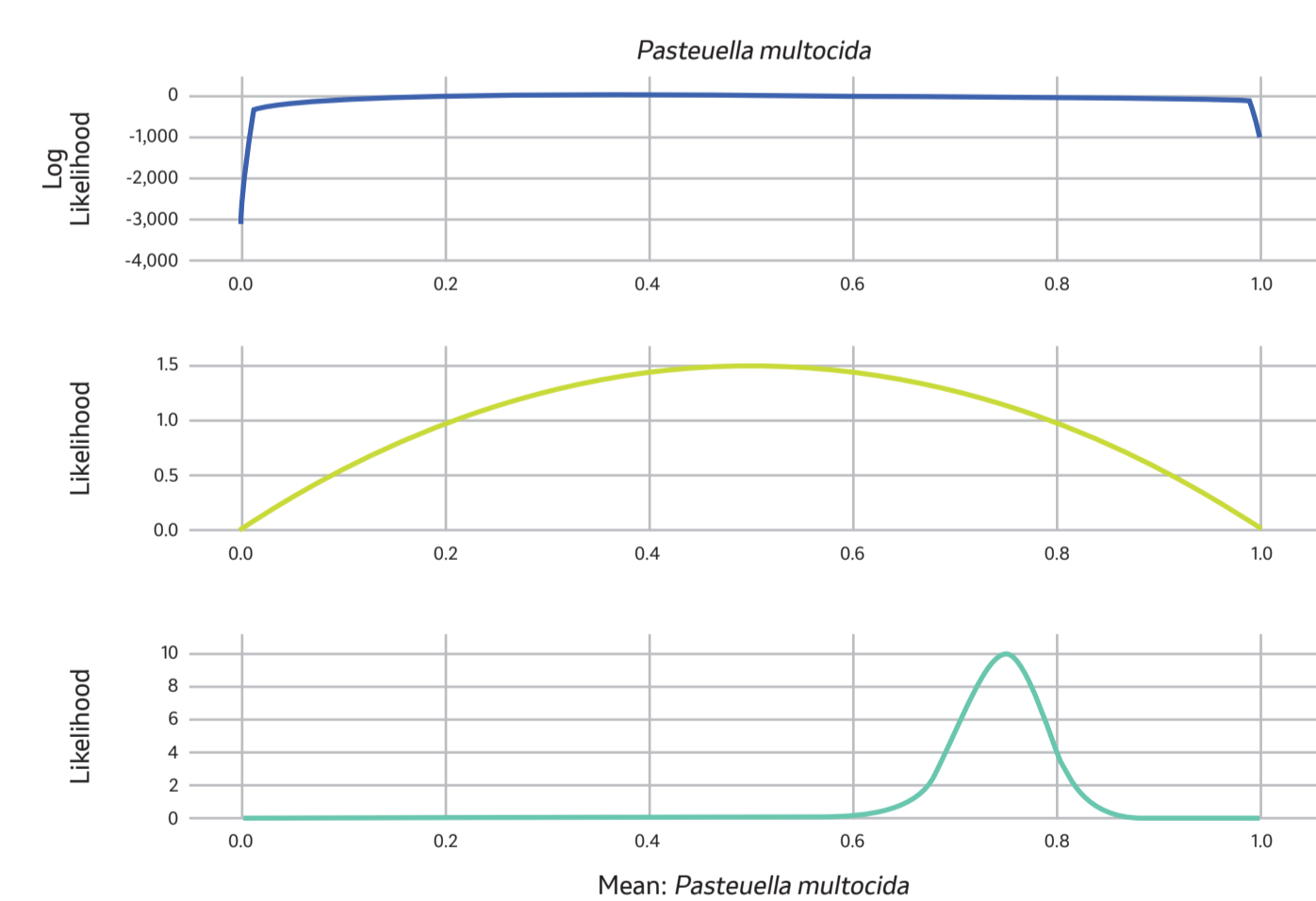
RESULTS

The pathogens identified by the PCR technique were *Pasteurella multocida*, *Mannheimia haemolytica*, bovine coronavirus, *Mycoplasma bovis*, *Histophilus somni*, and bovine respiratory syncytial virus (Table 1).

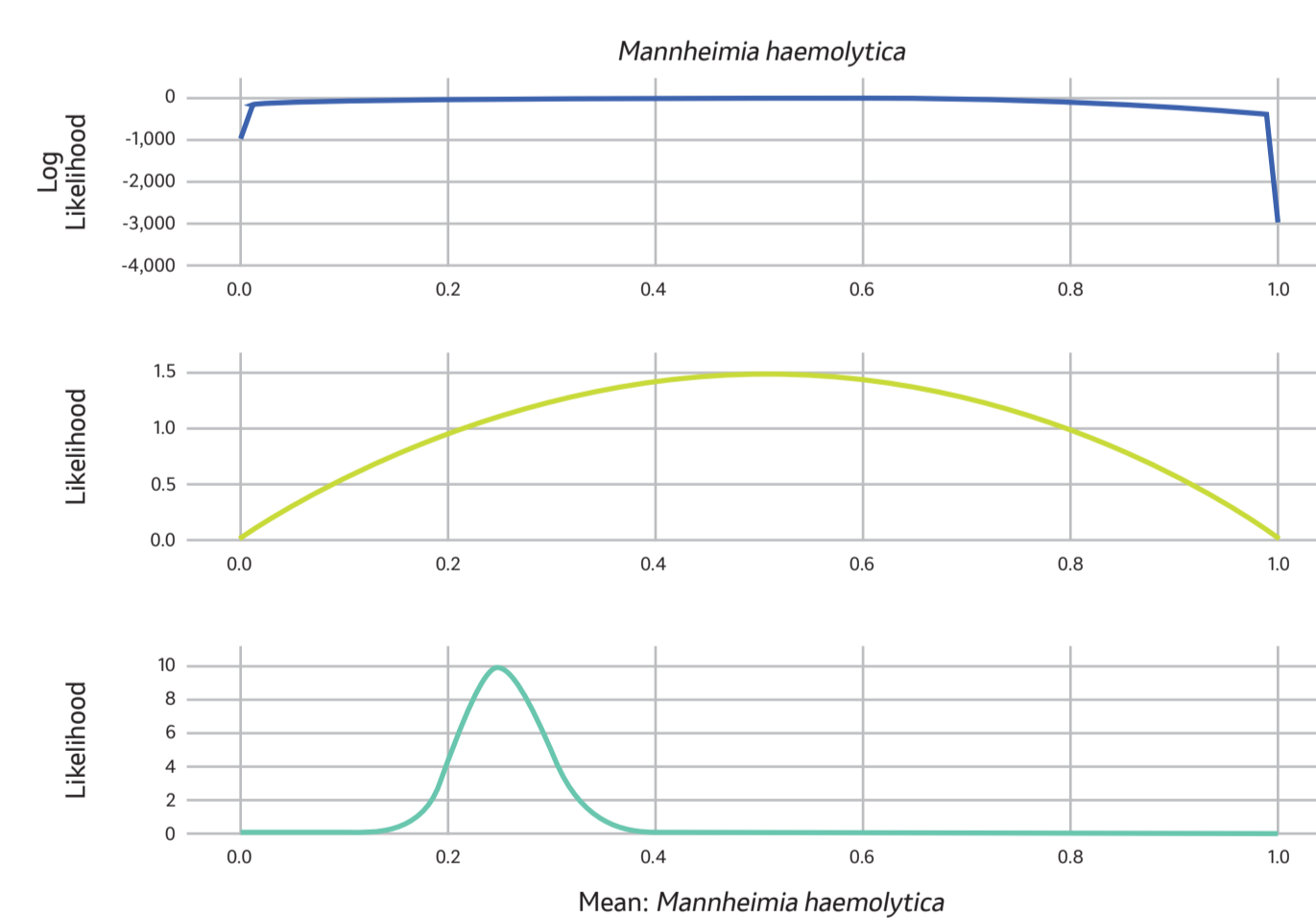
TABLE 1. PCR results by pathogen and frequency

Pathogens	Samples	Total positive	Total negative	Frecuencies of positive
<i>Pasteurella multocida</i>	114	86	28	0.754
<i>Mannheimia haemolytica</i>	114	28	86	0.246
<i>Bovine coronavirus</i>	114	20	94	0.175
<i>Mycoplasma bovis</i>	114	22	92	0.193
<i>Histophilus somni</i>	114	16	98	0.140
Bovine respiratory syncytial virus	114	6	108	0.053
Bovine parainfluenza 3 virus	114	0	114	0.000

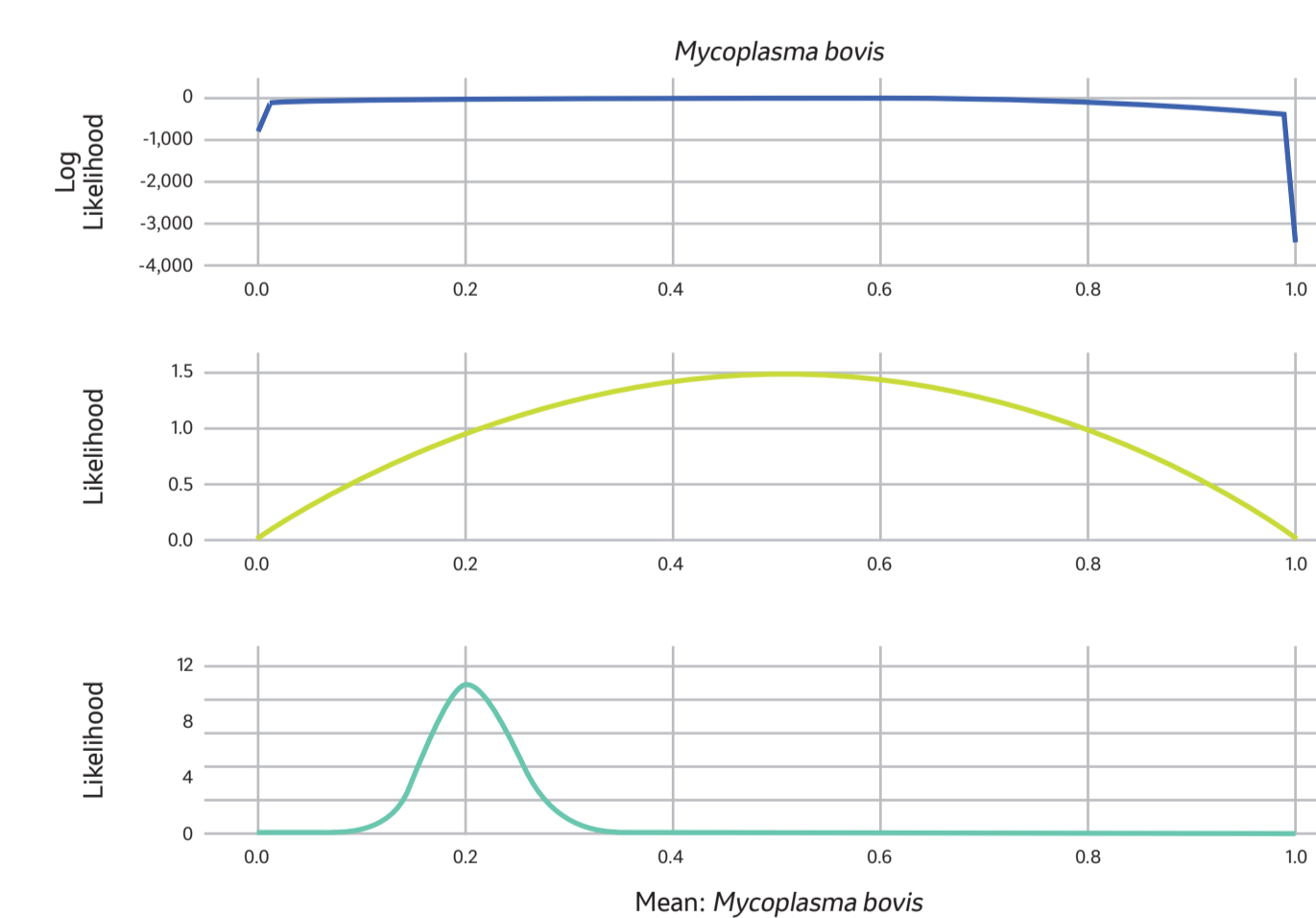
Pasteurella multocida resulted in the highest probability at 75%, CI-95 [6-82]



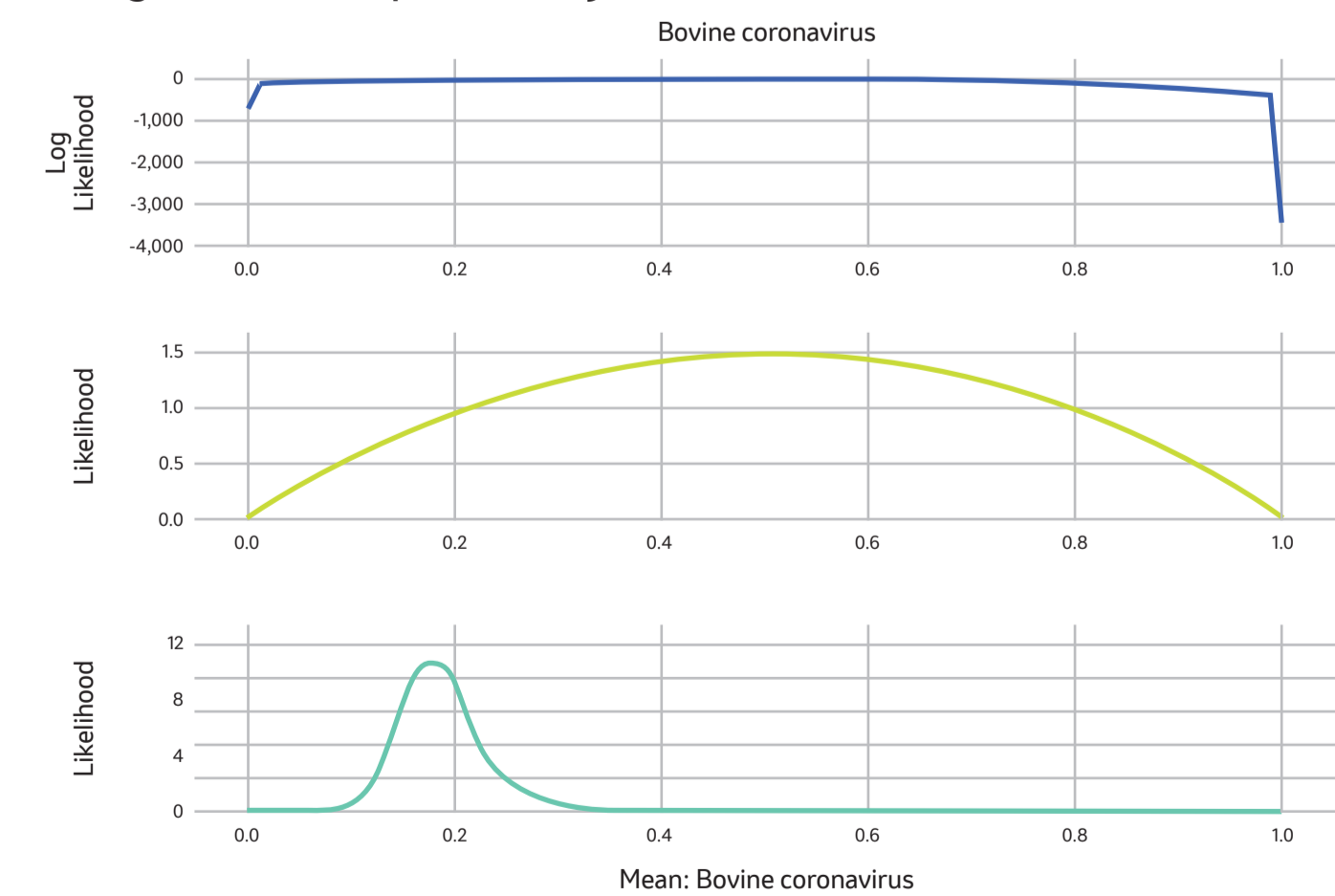
Mannheimia haemolytica showed a probability of 25%, CI-95 [19-34]



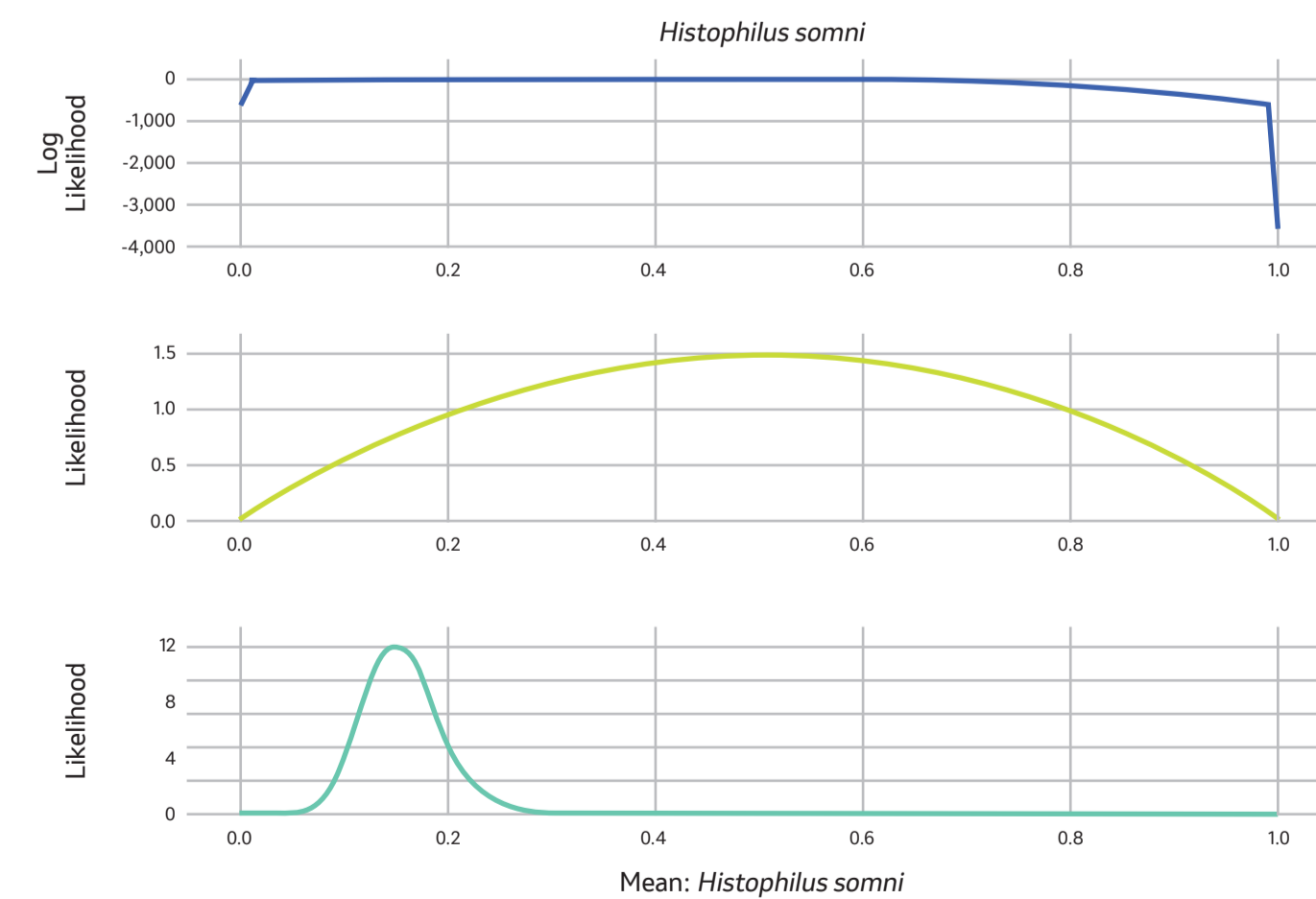
Mycoplasma bovis resulted in a probability of infection of 19.8%, CI-95 [9-22]



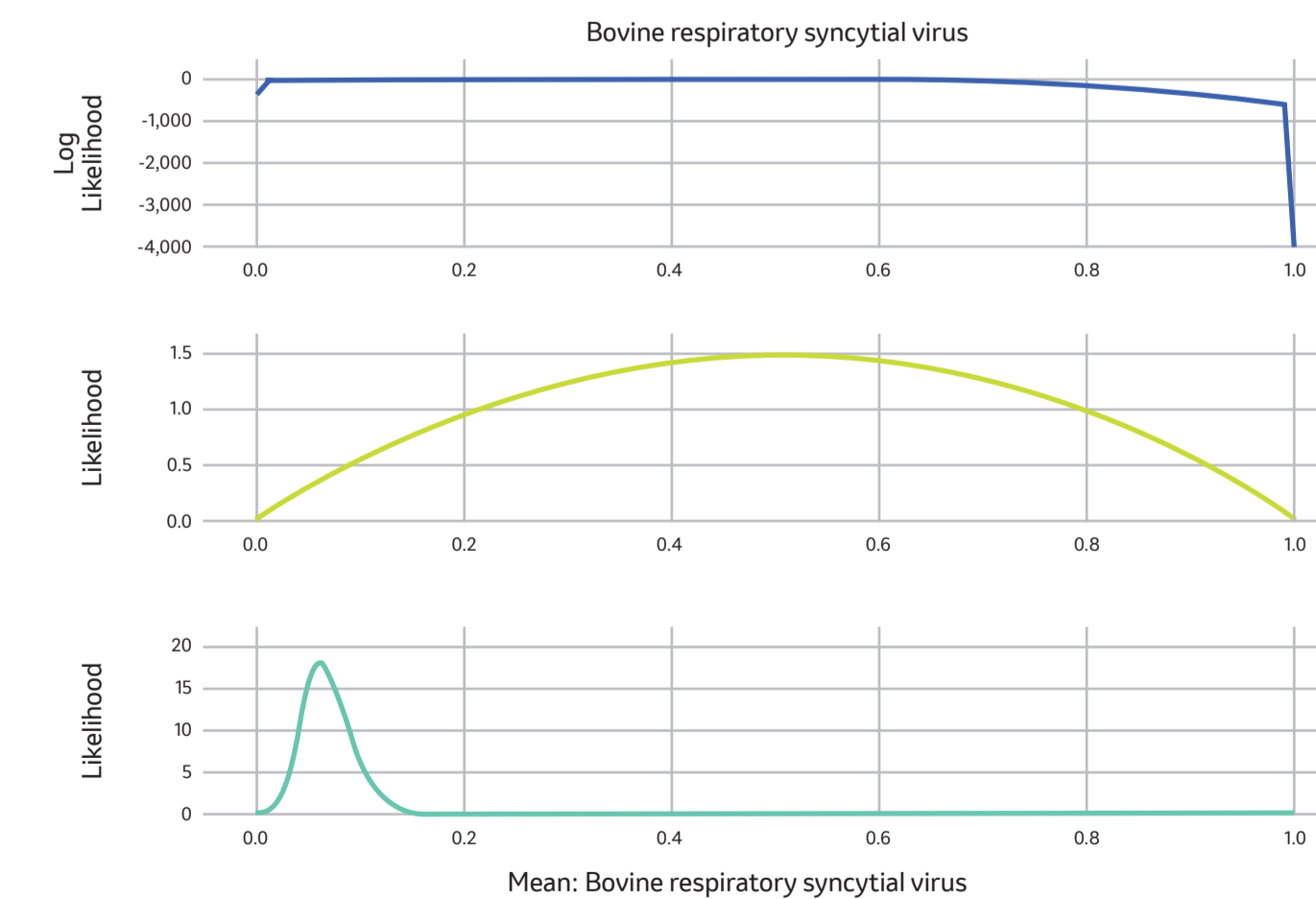
Amongst the virus identified, the infection probability for bovine coronavirus was the highest with a probability of 18%, CI-95 [12-26]



Histophilus somni had a probability of infection of 15%, CI-95 [9-22]



Bovine respiratory syncytial virus had a probability of 6%, CI-95 [3-12]



— Log Likelihood Function — Prior Distribution — Posterior Distribution

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