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Tracing the Introduction and Rise of a Single *Leptospira Pomona* Clone in Animals in Israel

Content

Leptospirosis is a globally important animal infection and zoonosis caused by pathogenic *Leptospira* species. In Israel, *Leptospira* serovar *Pomona* emerged over the past two decades from undetected to endemic status, becoming the dominant cause of bovine leptospirosis. Incidence in cattle culminated in large-scale outbreaks in 2018, coinciding with an exceptional human outbreak. These events prompted enhanced wildlife surveillance. From 2015–2024, >3,400 wildlife sera and ~400 kidney samples were tested by MAT and PCR. PCR-positive samples underwent 7-locus MLST, serovar-specific PCR, and high-resolution AmpSeq (42 genes, ~10,000 bp); isolates from cattle and wild boars were whole-genome sequenced. The highest seroprevalence was found in wild boars (20–43%), with high titers and PCR confirming actual infection with *L. interrogans* serovar *Pomona*. MLST identified ST52 in all typed samples from cattle and wildlife. AmpSeq and WGS confirmed complete identity of ST52 profiles across samples from 2011 to 2024. Notably, archival DNA from a 2011 outbreak related to imported cattle—among the first *Pomona* cases in Israel—matched all later samples, providing genomic evidence of a single introduction event. These findings identify wild boars as key reservoirs and demonstrate the establishment of a single *Leptospira Pomona* clone in Israel following introduction. Continued surveillance and coordinated response across the wildlife–livestock–human interface are essential.

Keywords

Leptospira, molecular epidemiology, bovine leptospirosis, wildlife, emergence

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Professional Status of the submitter, who is also the speaker

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Comments:

Genomics track could be a secondary option.