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

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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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