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Evolutionary Dynamics of Bluetongue virus Strains Circulating in Italy, 2024-2025

Inhalt

In 2024, Italy experienced a major resurgence of Bluetongue (BT), a viral disease of ruminants caused by Bluetongue virus (BTV), an RNA virus circulating in multiple serotypes transmitted by Culicoides midges. By April 2025, over 7,000 confirmed cases had been reported, mainly involving serotypes BTV-3, BTV-4, and BTV-8. We performed whole-genome sequencing (WGS) and phylogenetic analyses on BTV strains collected across multiple Italian regions in 2024. Among the BTV-3 strains, we identified at least three distinct genomic constellations: two resulting from multiple reassortment events with other European strains, and one closely related to Northern European BTV-3. BTV-4 strains also displayed diverse genomic profiles, with individual gene segments of varied origin. BTV-8 showed up to 100% nucleotide identity in segment 2 with strains from France, suggesting likely spread via trade of viremic animals. Moreover, BTV-8 genome segments were found within both BTV-3 and BTV-4 strains, highlighting the role of reassortment in shapingBTV evolution. These findings reveal the complex genomic landscape of BTV in Italy and emphasize the value of WGS for monitoring viral dynamics.

Keywords

Bluetongue, genome sequencing, genetic identity, viral evolution

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

Track Klassifizierung: Genomics & Proteomics

Typ des Beitrags: Both options possible