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In Vitro Reassortment Between Eastern BTV-16 and Western BTV-1 Reveals Unique Genome Constellations

Monday, October 13, 2025 3:00 PM (15 minutes)

Bluetongue virus (BTV), an arbovirus transmitted by Culicoides biting midges and circulating as multiple serotypes, possesses a genome composed of 10 segments of double-stranded RNA. BTV evolution is strongly driven by genetic reassortment, which occurs during the co-infection of host cells by two or more BTV strains and may result in novel genotypes with unpredictable phenotypic traits. Therefore, the frequent co-circulation of multiple serotypes in the field increases the probability of such events. In this study, we investigated in vitro the reassortment potential between two genetically distant BTV strains: eastern BTV-16 (BTV-16e) and western BTV-1 (BTV-1w). Using co-infection in cell culture followed by plaque purification, we isolated 157 viral plaques. Among these, 111 were Seg-2 monotypic and included in downstream genomic analyses. Of these, 91 retained the complete genome constellation of either BTV-1w or BTV-16e, while 20 were reassortants, each displaying a unique genomic profile. Segment analysis revealed that BTV-1w predominantly contributed Seg-2 and Seg-7, whereas Seg-3 mostly originated from BTV-16e. Notably, 4 out of 20 reassortants harbored Seg-2 and Seg-6 from different parental strains, while the remaining 16 inherited both segments from the same parent. Ongoing studies are focused on evaluating the virulence and antigenic properties of these reassortant viruses to better understand their potential impact in natural settings and in serological diagnosis.

Keywords

Bluetongue virus; BTV serotype 1; BTV serotype 16; Reassortment; topotypes.

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Professional Status of the Speaker

Senior Scientist

Junior Scientist Status

No, I am not a Junior Scientist.

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