Reply to “Intercontinental Movement of Bluetongue Virus and Potential Consequences to Trade”

We recently published the complete genome sequences from six bluetongue virus (BTV) isolates from India (belonging to serotypes 1, 2, 3, 10, and 23) (8–13). We have also carried out similar analyses for the BTV reference strains and multiple additional BTV isolates from other geographic regions of the world. The data generated indicate the circulation of BTV genes derived from both eastern and western geographic groups (topotypes), as well as from live attenuated vaccine strains, in the subcontinent.

Rao et al. (20) commented on these data and conclusions in a letter to the editor in this journal (20). We would like to respond to some of the points made. They indicate that Seg-2 of a BTV-3 strain from India was derived from a western topotype. While this may certainly be true (e.g., for isolate IND2003/08 of BTV-3 [8] as well as isolate IND1982/01 of BTV-2 [10]), the paper cited appears to provide sequences for an isolate of BTV-9 (21). They also suggest that Seg-2 of an Indian BTV-16 strain may have a western origin, since it is similar to Seg-2 from the reference strain of this serotype. However, the widely accepted BTV-16 reference strain (ReoID database, http://www.reoviridae.org/dsRNA_virus_proteins/ReoID/btv-16.htm#RSArrr/16) was originally isolated in Pakistan and therefore belongs to an eastern lineage (1). This may have led to some quite understandable confusion.

The sequences of five complete genome segments (VP2, VP6, VP7, NS1, and NS2) were reported for an Indian isolate of BTV-10 by Gollapalli et al. (5). Together with our full genome sequence data for isolate IND2004/01 of BTV-10, these show the highest (>99%) sequence identity in genome segment 2 to the U.S. BTV-10 vaccine strain. Full genome sequence data are not currently available (as far as we are aware) for the American BTV-10 vaccine strain. We therefore wish to correct the implication that this level of similarity had been confirmed in all genome segments of IND2004/01 (13). However, in all other segments, >99% identity to the prototype U.S. strain (CA-8) of BTV-10 (which represents the original source of the U.S. vaccine) was detected (4, 15, 16, 19).

We agree with Rao et al. (20) that these data suggest that both live attenuated vaccine viruses and the international trade in livestock may play important roles in the geographical (intercontinental) movement of BTV genome segments and in the arrival of western BTV strains or genome segments in India. Indeed, the report of Rao et al. (20) states that cattle were imported into India during 2002 to 2005 from Belgium, France, Germany, Nepal, Russia, South Africa, Thailand, the United Kingdom, and the United States (FAOSTAT, Food and Agriculture Organization of the United Nations [http://faostat.fao.org/DesktoModules/Faostat/WATFDetail/2/wat.aspx?PageID=536, accessed 5 April 2012]). The Central Sheep Breeding Farm (CSBF), Hisar, Haryana, India, also imported Corriedale, Merino, and Dorset sheep from Australia and Rambouillet sheep from America during the late 1970s and 1980s (2, 7, 18). As Rao et al. (20) point out, some of these countries used live attenuated vaccines during this period. It is therefore possible that introduction of BTV western and/or vaccine strain genome segments into India could potentially be linked to animal movements.

However, we cannot yet rule out other routes of virus movement. The possibility of undetected or unauthorized movement of vaccine viruses between continents, despite trade restrictions, is of real concern. Live attenuated BTV vaccines can cause significant levels of viremia postvaccination, which can lead to infection of adult Callicoides midges during blood feeding and subsequent virus transmission. Indeed the circulation of unauthorized vaccine strains of BTV-6 and BTV-11 was detected in northern Europe during 2008 (3, 14). Fully infected midges transmit BTV with very high efficiency. It is therefore possible that the movement of even very small numbers of infected midges provide an alternative mechanism for the movement of BTV (and possibly other viruses) over very large distances. This route has been suggested for the introduction of BTV-8 and Schmallenberg virus into northern Europe during 2006 and 2011, respectively (e.g., in flowers or other produce) (6, 17, 22).

We agree with the comment that full genome sequences of additional BTV isolates (e.g., for all live attenuated vaccine and reference strains, as well as additional field isolates from Asia and South America) are needed to fill gaps in our current epidemiological knowledge concerning strain distribution. These additional data would support further development of diagnostic agents/assays, help in the identification of appropriate vaccine strains, support molecular-epidemiological studies to clarify virus movements, and inform decisions concerning appropriate control strategies. We have already generated full genome sequence data for attenuated monotypic vaccine strains of BTV serotypes (BTV-1, -2, -4, -9, and -16) from the orbivirus reference collection at the IAH, Pirbright, United Kingdom. We now have sequence data for full genomes of the reference strains of all 26 BTV serotypes, many of which were used to generate the South African live attenuated vaccine viruses between continents, despite trade restrictions, is of real concern. Live attenuated BTV vaccines can cause significant levels of viremia postvaccination, which can lead to infection of adult Callicoides midges during blood feeding and subsequent virus transmission. Indeed the circulation of unauthorized vaccine strains of BTV-6 and BTV-11 was detected in northern Europe during 2008 (3, 14). Fully infected midges transmit BTV with very high efficiency. It is therefore possible that the movement of even very small numbers of infected midges provide an alternative mechanism for the movement of BTV (and possibly other viruses) over very large distances. This route has been suggested for the introduction of BTV-8 and Schmallenberg virus into northern Europe during 2006 and 2011, respectively (e.g., in flowers or other produce) (6, 17, 22).

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REFERENCES


4. Fukusho A, Yu Y, Yamaguchi S, Roy P. 1989. Completion of the sequence of bluetongue virus serotype 10 by the characterization of a struc-


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