

# Letters

## NOTIFIABLE DISEASES

### Foot-and-mouth disease in Bulgaria

FURTHER to the letter from Nigel Gibbens, the UK Chief Veterinary Officer (VR, February 5, 2011, vol 168, pp 136-137), we would like to provide additional information about the recent appearance of foot-and-mouth disease (FMD) in south-eastern Bulgaria.

Since the end of December 2010, three outbreaks of FMD have been reported in Burgas region, close to the border with Turkish Thrace, which is a FMD-free zone (with vaccination). Samples collected from the first recognised case, in wild boar shot near to Kosti village, Tsarevo Municipality, were tested locally at the National Reference Laboratory for FMD, Sofia, and at the EU Community Reference Laboratory for FMD at the Institute for Animal Health (IAH) – Pirbright. Although it was not possible to isolate FMD virus (FMDV), viral antigen was detected by ELISA and a lateral-flow device, and viral RNA was detected by a real-time RT-PCR.

Subsequent molecular analysis of the sequence encoding the viral VP1 capsid protein revealed a close genetic relationship between the Bulgarian virus and contemporary serotype O FMD viruses from Turkey and Iran characterised within the ME-SA topotype (PanAsia-2

strain, ANT-10 sublineage) (Fig 1). The closest of these isolates represented field strains collected during 2010 from seven different provinces in Turkey where FMD is endemic (Fig 1). These Turkish sequences differed by only a single nucleotide from each other and from the Bulgarian FMDV sequence. Although this is critical information, there are limitations to using VP1 analysis (<8 per cent of the complete genome) for discrimination between closely related viruses, in order to determine the most likely origin of disease incursions.

Complete genome sequences of the Bulgarian and one of the closely related Turkish viruses (O/TUR/18/2010 from Gümüşhane Province) have now been determined (B. Valdazo-González and others, unpublished data). Genome sequence data were used previously during the 2001 and 2007 outbreaks in the UK to reconstruct virus transmission events occurring at the farm-to-farm level (Cottam and others 2006, 2008). Pairwise comparisons revealed 46 nucleotide changes between these two genome sequences (divergence rate 0.26 nucleotide substitutions/day), findings that were consistent with the rate observed during the UK 2001 epidemic (0.24 nucleotide substitutions/day) resulting from continuous replication of FMDV within susceptible hosts.

Further work is ongoing to determine the full genome sequences of the remaining closely related viruses from Turkey, as well as additional samples from Bulgaria (Rezovo, Kosti and Gramatikovo regions

to determine the most likely molecular epidemiological links between these outbreaks.

Begoña Valdazo-González,  
Nick J. Knowles, Jemma Wadsworth,  
Donald P. King, Jef M. Hammond,  
EU Community Reference Laboratory for FMD, IAH, Ash Road, Pirbright, Surrey GU24 0NF  
e-mail: donald.king@bbsrc.ac.uk  
Fuat Özyörük, Müge Fırat-Saraç, Ünal Parlak, Foot-and-Mouth Disease Institute, PO Box 714, 06044, Ulus, Ankara, Turkey  
Lilyana Polyhronova, Georgi Kirilov Georgiev, National Diagnostic and Research Veterinary Medical Institute, 1606 Sofia, Bulgaria

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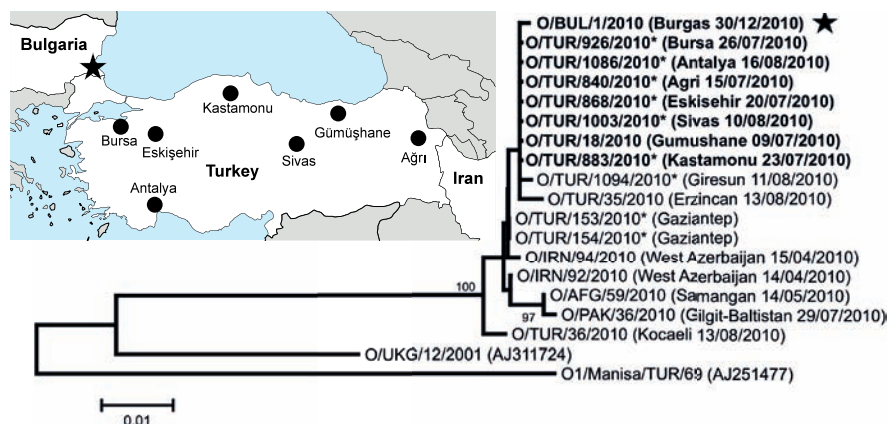


FIG 1: Midpoint rooted neighbour-joining tree (MEGA 4.0) showing the relationships between the VP1 nucleotide sequences of foot-and-mouth disease (FMD) type O viruses from Bulgaria, Turkey, Iran, Afghanistan and Pakistan (with sample locations and collection dates). The vaccine strain (Manisa) and UK 2001 outbreak strain (PanAsia) are included for reference. The locations of the Bulgarian outbreak (star) and the seven most closely related Turkish viruses collected from Anatolia (circles) are shown on the map insert. \* Not World Reference Laboratory for FMD reference numbers



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Begoña Valdazo-González, Nick J. Knowles, Jemma Wadsworth, et al.

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