

## 066 - ARB-RES-FOR-066

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Sequence data was provided for Seg-2 of BTV from two viraemic Latvian bovines (by Dr. Ieva Rodze, Head of Animal Disease Diagnostic Laboratory, Institute of Food Safety, Animal Health and Environment BIOR, Latvia by email on 29/11/12. These data showed 99.3 and 100% similarity respectively, to the vaccine / reference strains of BTV-14 over the region 545 to 839 (294bp).

These data collectively suggest the release of the BTV-14 reference or vaccine strain (which are identical in the regions analysed) into the field, possibly indicating the use of a live BTV-14 vaccine in the field. The similarities of these different samples (Russia 2011, Spain 2011, Poland 2012 and Latvia 2012 (data obtained in Latvia)) indicate that they are derived from a common source and suggest significant spread of the virus in the field.

Unfortunately we do not have full genome sequences for the South African vaccine strains, (including BTV-14) so it is difficult to confirm exactly how closely the Polish, Russian and Spanish strains of BTV-14 are related to the vaccine or reference strains in the rest of the genome.

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If further information is required concerning these results please contact the Non-vesicular Reference Laboratories, at The Pirbright Institute, UK.