

The influence of virus variant selection on *Culicoides* vector competence for bluetongue virus

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Bluetongue is an infectious, non-contagious viral disease of domestic and wild ruminants, caused by bluetongue virus (BTV), (Orbivirus: Reoviridae); a double stranded, segmented RNA virus transmitted by biting midges (*Culicoides* spp.).

BTV can infect all ruminants but causes severe disease mostly in sheep, resulting in significant economic losses to the agriculture sector of many countries. Currently, there are 27 known serotypes of BTV and numerous virus strains per serotype, all of which differ in key characteristics such as virulence and replication ability in the insect vector. Most importantly BTV can exchange genome segments when two BTV strains infect the same cell and such gene reassortment complemented by genomic mutations leads to the constant formation of new variants. Studies using conventional molecular methods have already shown that individual blood-feeding *Culicoides* select different BTV variants from the virus pool present in a viraemic blood-meal. However, the impact of virus variant selection on vector competence is currently unknown.

Therefore, the aim of this project is to determine BTV variant selection in a *Culicoides sonorensis* laboratory model (originally supplied by the Pirbright Institute) from a viral variant pool with next generation sequencing techniques.

For this, laboratory reared *C. sonorensis* will be fed via artificial membrane systems on blood-virus mixtures containing virus variant pools of a highly competent BTV-4 strain and virus variants present within the blood meal will be compared to those selected by fully disseminated insects. Initial experiments will be followed by assessing the impact of viral dosage limits and different vector incubation temperatures on virus variant selection.

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