Reviewing Vector Competence Studies in Europe: What Do We Know and What Do We Need to Know?

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The correct identification of all potential vectors of bluetongue virus (BTV) is crucial for the implementation of integrated control measures, disease risk analysis and management of this disease. The collection of *Culicoides* midges and virus isolation from the captured midges will give an indication of what *Culicoides* species may be involved in the transmission of the virus. The number of midges collected with light traps will give an indication of the risk of the virus spreading in the area.

Reliable detection of BTV from field-collected vectors is difficult due to several constraints related to the vector itself and to laboratory procedures. A clear recommendation will be to maximise insect collections after viraemias are detected in mammals. Where possible, captured individuals should be identified to species level and populations' age graded. Virus detection in the collected midges is conducted by using molecular techniques [e.g. polymerase chain reaction (PCR)], and virus isolation is performed using either embryonated chicken eggs or cell cultures. Positive results from either pools or individuals have different meanings in terms of vector competence and need to be evaluated with care. Individually analysed parous midges from which virus could be isolated indicate that the insect has fed on a viraemic host. It does, however, not show that the virus has replicated in the vector and that transmission could be related to that species.

Current laboratory techniques for measuring vector competence have several drawbacks, e.g. low blood feeding rates (especially so for European *Culicoides* species), the small size of *Culicoides* species involved, and the limited availability of laboratory colonies of European *Culicoides* species. Some techniques, as for example multiplex PCR, have increased the number of samples which can be processed in one day (up to 800 insects). A recent trial, with field-collected *Culicoides* fed and incubated in the laboratory, showed transmissible infection levels in *C. scoticus* for BTV-9 and 8 similar to that reported from the field. Future needs in this field are the evaluation of cell types, e.g. *Culicoides* cell lines for virus isolation, detection of the virus in the saliva of *Culicoides*, the development of a reference colony (i.e. *C. sonorensis*), the sequencing of its genome, as well as the standardisation of experimental procedures run across wide geographic areas.

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