

Measuring between-farm variation in *Culicoides* (Diptera: Ceratopogonidae) density, the vectors of bluetongue virus

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ABSTRACT: *Culicoides* midges are ubiquitous on farms in the UK, but little research has explored their abundance, an important determinant of disease risk. Models to explain and predict variation in their abundance are needed for effective targeting of control methods against bluetongue (BT) and other *Culicoides*-borne diseases. Midge abundances were estimated using light traps on 35 farms in north Wales. *Culicoides* catches were combined with remotely-sensed ecological correlates, and on-farm host and environmental data, within a general linear model. Local-scale variation in abundance exhibited an almost 500-fold difference between farms in maximum Obsoletus Group catches. The variance explained was consistently high for the BT vector species (81% for Obsoletus Group; 80% for Pulicaris Group, 73% for *C. pulicaris*, 74% for *C. punctatus*). The abundance of all vector species increased with the number of sheep on farms, but this relationship was missing from any of the non-vector models. At a large spatial scale, there is significant variation in *Culicoides* Obsoletus Group abundance, which undermines attempts to record their nationwide distribution in larger scale models. A prior survey should be undertaken for farms with high *Culicoides* catches within a sampling area and stability in catch size should be checked between seasons and years.

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