Regional and spatial analysis of Bluetongue in Switzerland in 2009 and 2010

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Aim of the study
The aim of the project is to investigate regional and spatial heterogeneity in BT prevalence and surveillance intensity. Furthermore, the influence of the regional vaccination coverage on the prevalence in autumn 2008 and 2009 should be quantified. Using CAR models, estimates for regional and global components of spatial heterogeneity in prevalence with and without consideration of the vaccination coverage as independent variable will be calculated and analyzed. Estimates for the influence of the variation of vaccination coverage between cantons on the probability of BT persistence will be calculated.

Material and methods
The population of interest were all cattle farms and cattle registered on the 1st of May in 2008 and 2009 (Tier-verkehrsdatenbank TVD; 2008: n=1,628,435 animals/44,559 farms; 2009: n=1,642,613 animals/44,202 farms. Firstly, animal and farm data were considered at a regional level, allowing inclusion of data without spatial point coordinates. Secondly, point-referenced data of each farm were analysed with explanatory variables specific to the location of the farm. For the regional analysis, the geographical coordinates of each farm were spatially joined to a shapefile of the 17 BT-regions in order to estimate the population at risk per BT-region. Data from three simultaneous but independent surveillance programmes were included in the analysis: reported cases of clinical suspicion, official targeted surveillance where 10 cattle from 20 randomly selected farms of each BT-region were sampled per year (BVET, 2009), and pre-movement testing. An animal was considered vaccinated against BTV-8 following two vaccine doses administrated within an interval of 21 to 63 days. A farm was re-garded vaccinated if at least one animal at that farm had been vaccinated. Vaccine efficacy was assumed to be 100%. The relative risk of one unit being infected at the regional level was analyzed in a Bayesian hierarchical framework. For the analysis of point-referenced farm data, a Bayesian geoadditive model (Kneib and Fahrmeir, 2006) was adapted.

Results and significance
A substantial change in the underlying risk for BTV-8 infection between 2008 and 2009 was detected. However, the increase in vaccination coverage from 2008 to 2009 was not sufficient to explain the temporal change in relative risk of a unit being infected. The models explain most spatial variation in relative disease risk at farm level after adjusting for regional vaccination and surveillance intensity. Although the results of the study point in this direction, a significant effect of vaccination coverage on disease occurrence was not demonstrated on the regional level. By obtaining reliable estimates of relative disease risk, efforts to control disease can be targeted in higher risk areas. The method could be adapted to evaluate and compare the effect of alternative control measures and serve as a basis in policy development.

Publications, posters and presentations
Willgert, K.J.E.; Schroedle, B.; Schwermer, H.; Spatial analysis of bluetongue cases and vaccination of Swiss cattle in 2008 and 2009. Geospatial Health, 5, 2, May 2011, 227-237

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