Spatial model of Bovine tuberculosis in two-host disease d ynamic system in the Republic of Ireland

*You chang[1], Mart de Jong[1]**

[1] Quantitative Veterinary Epidemiology Group, Wageningen University & Research, The Netherlands

* Corresponding author. E-mail: mart.dejong@wur.nl

Bovine tuberculosis, caused by *mycobacterium bovis*, is a zoonotic infectious disease mainly in domestic and wild animals. It is a chronic disease, which can cause chronic inflammation, coughing, weight loss and eventual death. It has a huge negative impact on the economic and animal welfare. The Republic of Ireland has been working on BTB eradication in cattle since 1954 and has spent an accumulative expenditure of over €5.5 billion. Although there is an ongoing decline, the herd prevalence of bovine tuberculosis has remained steady of around 5%. The previous control strategy test-and-removal on cattle was not sufficient to eradicate tuberculosis in the Republic of Ireland because badgers play a role in the transmission. This cross-species transmission has been proved by field trials which showed a link between badgers culling and reduction in cattle BTB incidence. Until very recently, badger vaccination was added to the control policy and is being rolled out across the country. However, researchers and policymakers are still unsure whether current control policy (test-and-removal plus badger vaccination) is sufficient to eradicate bovine tuberculosis in 2030.Therefore, this PhD project aims to understand better the spatial heterogeneity of BTB transmission in the Republic of Ireland by using mathematical and statistical models. In this study, we want to provide a model to generate risk maps and find the relative contribution of each transmission routes. To achieve the final goal step by step, we will develop several research objectives to have an advanced understanding of BTB transmission. Firstly, we will develop a new method to quantify indirect transmission without observing environmental data and evaluate this method by a simulation study. Then, we will develop a method to quantify transmission in a two-host system in the spatial context by combining transmission kernels with next generation matrix method. This method will be used to analyze field data and eventually generate a reproduction ratio map for the whole country. Lastly, a dynamical model will be developed to disentangle the relative importance of each transmission mechanism in BTB spread and estimate the cost-effectiveness of interventions on different transmission routes.