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Eight challenges in modelling infectious livestock diseases

E. Brooks-Pollock[a,*], M.C.M. de Jong[b], M.J. Keeling[c], D. Klinkenberg[d], J.L.N. Wood[a]

[a] Disease Dynamics Unit, Department of Veterinary Medicine, University of Cambridge, Cambridge CB3 0ES, UK
[b] Department of Quantitative Veterinary Epidemiology, Wageningen University, P.O. Box 338, 6700 AH Wageningen, Netherlands
[c] Mathematics Institute, University of Warwick, Coventry CV4 7AL, UK
[d] Faculty of Veterinary Medicine, Utrecht University, 3584 CL Utrecht, Netherlands

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ABSTRACT

The transmission of infectious diseases of livestock does not differ in principle from disease transmission in any other animals, apart from that the aim of control is ultimately economic, with the influence of social, political and welfare constraints often poorly defined. Modelling of livestock diseases suffers simultaneously from a wealth and a lack of data. On the one hand, the ability to conduct transmission experiments, detailed within-host studies and track individual animals between geocoded locations make livestock diseases a particularly rich potential source of realistic data for illuminating biological mechanisms of transmission and conducting explicit analyses of contact networks. On the other hand, scarcity of funding, as compared to human diseases, often results in incomplete and partial data for many livestock diseases and regions of the world. In this overview of challenges in livestock disease modelling, we highlight eight areas unique to livestock that, if addressed, would mark major progress in the area.

Introduction

The global livestock population is growing rapidly in order to meet the increasing demand for meat and dairy products from the expanding human population. The Food and Agricultural Organization (FAO) estimate that there are currently upwards of 1.5 billion cattle, 1.1 billion sheep, 0.97 billion pigs and goats and 60 million horses in an industry that employs at least 1.3 billion people. Infectious diseases pose a persistent challenge for the livestock industry. The World Organisation for Animal Health's list of notifiable diseases includes 65 diseases that affect livestock and 12 diseases of poultry and fowl, including well-known infections such as Foot-and-Mouth Disease (FMD), Classical Swine Fever (CSF) and Highly Pathogenic Avian Influenza (HPAI). A major motivation for countries reporting and controlling infectious threats is international trade as losing a "disease-free" status can have major economic consequences.

In this paper we define eight challenges related to modelling diseases of livestock. They are broadly ordered by scale: challenges 1 and 2 deal with transmission within farms and herds; challenges 3 and 4 deal with the need for data and methodological challenges involved in repurposing veterinary databases; challenges 5, 6 and 7 place livestock modelling within a wider context with the need for improved spatial models, unifying multiple scales of transmission and links with other species. Finally, challenge 8 deals with the politics and economics of modelling livestock diseases.

1. Linking models to transmission experiments

To draw reliable conclusions from data analyses, it is essential that there is a clear relationship between models and data, whether obtained by experiments or field observations. Much attention is given to host and microbe heterogeneity (see challenges 2 and 6), but a third issue is at least as relevant: the type and frequency of transmissive contacts between infected and recipient hosts, and how this depends on circumstances. Density of the host is often used as a proxy to scale contact rates, but this is dependent on knowledge of transmission pathways. Observational data on endemic diseases could be used to address such questions in the field (Carslake et al., 2011). Transmission experiments are also valid tools to address these questions; for instance, it has been shown experimentally that, for some diseases at least, if the relevant density is constant, contact rates should not scale with population size (De Jong et al., 1995).

Recent experimental results have shown that simple extrapolations are not valid if transmission is indirect, via the environment.

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* Corresponding author at: Disease Dynamics Unit, Department of Veterinary Medicine, University of Cambridge, Madingley Road, Cambridge CB3 0ES, UK.
Tel.: +44 01223 764 957; fax: +44 01223 764667.
E-mail address: ebp20@cam.ac.uk (E. Brooks-Pollock).

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In the case of faecal-oral transmission, when starting with a few infected individuals in a clean environment, the transmission rate will initially increase, then reach a plateau (Velkers et al., 2012), and continue but decrease after the last infected individual has been removed. If indirect transmission occurs when individuals are spatially separated, when starting with a clean environment, the transmission rate remains zero for some time, and then gradually increases (Dekker et al., 2013; Van Bunnik et al., 2014). These results show that a proper way to scale indirect transmission with population size and density is needed: an important new challenge to be addressed by transmission experiments and, wherever possible, field observations to ground experimental data.

Experiments are also very useful to make the link between epidemiology and within-host dynamics, as they allow intensive testing during the course of an infection. This allows quantification of heterogeneity between animals based on underlying (immunological) processes and thus helps to explain and predict infectivity (Chase-Topping et al., 2013).

2. Disease control by selective breeding

The increasing use of genetic data on infectious diseases is one of the current major developments in infectious disease modelling. By far most of this work is related to genetics of the pathogen, either to reconstruct transmission pathways or to study the evolutionary process itself, for example with respect to escape from vaccine control or virulence (Hoa et al., 2011). In veterinary applications, the genetics of the host is relevant as well, not only to identify carriers of genes or SNPs related to increased susceptibility, but also in breeding programmes.

Breeding for production traits and health characteristics is generally done by use of quantitative genetic methods. Breeding for infectious disease resistance is generally not very successful for several reasons. Firstly, heritability estimates from observational data on disease development are generally low (Bishop and Woolliams, 2010). Secondly, selection of animals is ineffective because it takes time until symptoms of disease develop and development of disease depends on the level of exposure. Thirdly, by selecting animals that do not develop the disease, one might select for lower susceptibility or higher tolerance, but not necessarily for reduced infectivity. For control of infectious diseases, the latter is as least as relevant to reduce transmission and thus incidence in the population (Lipschutz-Powell et al., 2012). Moreover, modern transgenic techniques may allow introduction and rapid selection through breeding pyramids of animals with substantial resistance to infection and less infectivity (Lyall et al., 2011).

With the advancement of sequencing techniques, selective breeding may become more relevant as a method for disease control in the future as selection can be based on genetic information instead of phenotype. A first challenge in this respect is the further development of statistical techniques to relate measured (genetic) variation to observable traits in animals related to infectious diseases, and to predict the effectiveness of selection. Breeding for infectious disease resistance is still relatively new, as heritability of resistance measured by classic methods has been low and breeding ineffective (Van Hulzen et al., 2014). When favourable genetic traits are identified, a second challenge is the incorporation of infectivity measures in breeding programmes. Quantification of variation in infectivity, in relation to more easily observable traits for selection, can only be done indirectly and may be done experimentally or by use of transmission models with observational data.

3. Applying models to data/resource-poor settings

The global burden of livestock diseases disproportionately affects the world's poorest countries, however many of the state-of-the-art livestock models are heavily based on large-scale databases which are not available in resource-poor settings. Epidemic data are often patchy or not available for less-common endemic diseases. There are multiple challenges involved in data collection, including maintaining anonymity and controlling access to sensitive information, consistent recording and database maintenance, and sharing of (raw) data when publishing analyses of these data. Our challenge here is to model diseases in a global context, share expertise and data, develop methods for repurposing existing models for limited data and to develop efficient and targeted data capture systems.

Only a small proportion of diseases that affect livestock have compulsory reporting and are of high political priority, therefore often little is known about their epidemiology (Carslake et al., 2011). Furthermore, modelling livestock epidemics at a national level often involves spatial models that can capture local heterogeneity and predict the impact of localised control measures (Keeling et al., 2001). Essential information for developing spatial models includes locations, sizes and types of farms and livestock holdings. Livestock tracing systems have been used to refine spatial models (see challenge 4) and the FAO help implement national agricultural censuses. However, as of 2014, nearly 50% of countries, mainly in Africa, South-East Asia and Latin America, had yet to conduct a census. This is reflected further in the use of models for contingency planning: only 28% of countries in Africa and the Middle East use models due to either a lack of data, expertise, resources or perceived need (Dube et al., 2007).

Developing models for livestock epidemics in the absence of population or epidemic data is challenging and relies on many inbuilt assumptions. Even when data are available, adapting existing models to new countries can be problematic and at least require a re-estimation of parameters (Tildesley and Keeling, 2008). Some novel methods for overcoming a lack of spatial population data include using land-use cover to infer farm locations (Tildesley and Ryan, 2012), predicting disease spread based on environmental data (Purse et al., 2007) and reconstructing transmission trees based on spatial case data alone (Metras et al., 2013). International collaborations are key, and in data-poor settings there are opportunities for developing model-guided surveillance methods.

4. How best to exploit rich livestock data?

In contrast to the previous challenge, there is a need to develop models and techniques for capturing the rich detail of livestock data. Livestock are closely managed populations that can yield both targeted data on infection and transmission in small groups of animals and detailed population-wide statistics, that would be regarded as impractical or invasive in other species. The many dimensions of livestock data can be collapsed in a multitude of ways to address a wide variety of different problems. This particularly rich potential source of realistic data provides crucial information for modelling disease transmission and can be used to investigate the role of population structure in models of other species and systems.

Over the past 20 years, individual animal tracing has become a routine component of livestock management in many industrialised countries and is being implemented in new regions and for new species. The United States of America is a notable exception, where the implementation of a national system has been limited by privacy concerns. Birth, death and movement records provide a daily census of the current population that can be used to estimate seasonal forcing and timing of epidemics (Kao et al., 2006), the impact of diseases in subpopulations (Brooks-Pollock et al., 2013) and the role of farm management in disease risk (Gates et al., 2013), to name just a few applications. An approach