Bovine tuberculosis (TB) and paratuberculosis (Johne's disease) Symposium: What we know and what we need to know

254 A three-year study of bovine tuberculosis in an enzootic area, the Nile Delta. Adel M. Talaat*[1], Hazem A. Abdelaal[1], and Essam A. Nasr[2], [1]*University of Wisconsin-Madison, Madison, WI,* [2]*Veterinary Serum and Vaccine Research Institute, Cairo, Egypt.*

Bovine tuberculosis (BTB) is a chronic infectious disease characterized by the formation of granulomatous lesions in organs, mainly lungs and lymph nodes. BTB is caused by slowly growing bacilli, mainly *M. bovis*. In developed countries, BTB in animals is significantly in decline with rates that reached down to <0.001% in cattle herds in the United States. In developing countries, BTB represent a major problem with a prevalence that could reach up to 10 to 15% of cattle herds in some parts of Africa. In Egypt, BTB transmission among animals and from animals to humans represents a major problem because of the complexity of animal husbandry and animal trade. In this study, our teams in both the United States and Egypt used the single intradermal comparative skin test (SICST) to examine the herd level prevalence of BTB in 5 different regions within the Nile Delta of Egypt. During the years of 2012–2015, several farms were visited where SICST was conducted on all animals in the herd alongside collecting all of the historical background of disease prevalence in these farms. As expected, farms with a known history of risky management behavior (e.g., introduction of new animals without testing, or not testing at all for BTB) were associated with high level of BTB prevalence that reached up to 45% in some herds. Interestingly, clinical health condition of animals and milk yield were not associated with the BTB herd-level prevalence. However, where BTB was enzootic, the highest percentage of SICST-positive animals (average 14%) were among the 6–12 mo of age while newly testing farms identified the highest percentage of SICST positive (60%) in animals above 24 mo of age. This result highlights the importance of periodical testing and intervention to control BTB in dairy herds. Overall, the prevalence of BTB among total number of 2799 examined animals was 7.3% during the 3 years screening project. Recommendation to reduce the BTB in these herds included the frequent testing of animals using SICST, especially before restocking of a dairy herd.

Key Words: bovine tuberculosis, prevalence, enzoology

255 Host genomics—What have we learned? Holly L. Neibergs*, *Washington State University, Pullman, WA.*

The study of the genomic variation in cattle has been undertaken to identify loci that allow the prediction of cattle susceptible to *Mycobacterium avium* ssp. *paratuberculosis* (MAP) infection. The application of this information is to assist in disease prevention through selective breeding of cattle that are less likely to become infected should MAP exposure occur. A genetic predisposition to MAP infection in cattle was established through differences in prevalence of MAP infection found across breeds and across sires. Heritability estimates for susceptibility to MAP infection have been computed from family and genomic studies and typically range from 0.01 to 0.18, although higher estimates have been reported. Candidate gene and genome wide association studies have both been used to identify the loci associated with MAP infection. Phenotypes of susceptible and non-susceptible cattle have been based on serum ELISA, milk ELISA, fecal culture, tissue culture, PCR of tissue or feces or a combination of these diagnostic methods. The disparity in the sensitivity of the diagnostic methods affects the reliability of the controls, and the stage of MAP infection at which the animal is diagnosed. These differences make comparisons across studies difficult, as genomic studies are sensitive to phenotypic differences. Consequently, few studies have identified the same susceptibility loci in independent cattle populations. This lack of agreement across studies is most likely due to small sample sizes (most studies have less than 500 cases and 500 controls), the lack of consistency in the definition of phenotypes, and the polygenic nature of the disease which could result in different genes having a different level of effect within and across breeds. Identifying loci associated with MAP infection offers a permanent preventative strategy to lower the prevalence of bovine paratuberculosis and to have a better understanding of the disease etiology. To obtain concordant results, larger studies with a consistent phenotype are needed and must be followed with independent validation and functional studies. This will allow genomic prediction to deliver its translational promise to assist in preventing MAP infection in cattle.

Key Words: host genomics, bovine paratuberculosis

256 Johne's disease and bovine tuberculosis: Updates on control and prevention. Scott J. Wells*[1], Kimberley L. VanderWaal[1], Catalina Picasso[1], Eva A. Enns[1], Meggan Craft[1], Federico Fernandez[2], Andres Gil[3], Julio Alvarez[1], Lucas Dominguez[1], and Andres Perez[1], [1]*University of Minnesota, St Paul, MN,* [2]*Ministerio de Ganadería, Agricultura y Pesca, Montevideo, Uruguay,* [3]*Facultad de Veterinaria, Universidad de la República, Montevideo, Uruguay.*

While improved understanding of within-herd transmission of *Mycobacterium avium* ssp. *paratuberculosis* through conduct of longitudinal herd control studies has led to identification of effective long-term herd control measures, between-herd transmission continues unabated in many cattle herds through movements. Cattle movements serve as one important contributor to transmission of *Mycobacterium bovis* between herds, pointing to the need to better understand the role of cattle movements in disease transmission. Although complete cattle movement and traceability information is not available in the United States, the origin and destination farms for cattle movements in some countries, such as Uruguay and Spain, are captured in official cattle traceability systems. This information can be critical to understanding the risk of disease spread in the endemic cattle populations, which could be adapted to improve understanding of transmission in US cattle. In Uruguay, while the prevalence of *M. bovis* in cattle has been low since implementation of an active surveillance program, multiple outbreaks were reported during 2011–2013. In our study, Uruguayan cattle movements were evaluated using network analysis to understand cattle flows and identify high-risk farms for surveillance and control. Farms represented nodes in the network, which were linked based on the frequency and number of cattle moved. The distribution of in-movements and out-movements from farms was severely right-skewed, and the 10% most highly connected farms accounted for 72–83% of cattle moved each year. In comparison, during the time when bovine tuberculosis was identified in Minnesota (2008 to 2011), 20% of farms performed 90% of the movements. This heterogeneity in movement patterns indicates that some farms are likely critical for disease spread. In Uruguay, farms that experienced outbreaks of *M. bovis* during this period engaged in substantially more movements than the population average. Results from these studies highlight the importance of collecting livestock movement data, and of integrating and coordinating actions for infectious diseases to understand the vulnerability of livestock trade networks to infectious diseases.

Key Words: bovine tuberculosis, cattle, movement

257 MDA outreach: Communicating for a change. Julia M. Smith*, *University of Vermont, Burlington, VT.*

If a veterinary practitioner has tried to persuade a client to take action and nothing happens, is the problem that the client did not listen well or that the practitioner did not communicate well? An understanding of a few communication and behavior change models can enhance one's ability to make change a reality. Key principles of risk communication and social marketing of behavior will be discussed in the context of controlling mycobacterial diseases of animals (MDA). Risk communication can be understood as the process of sharing information and opinion about something hazardous, where uncertainty is a characteristic feature of the risk. When addressing Johne's disease or bovine tuberculosis, the disease is the hazard and uncertainty is associated with disease progression, detection, and success of control strategies. An approach known as message mapping can be a useful tool when developing risk communication messages. According to Prochaska's stages of change model, the process of converting a decision-maker into a change-maker takes time and involves distinct changes in attitude toward doing something new or different. To have the most effective conversations, it is important to identify at what stage of change the decision maker is and to tailor one's key points accordingly. Selling someone on behavior change to prevent or control a disease is a lot like selling someone on buying the latest gadget. The Academy for Educational Development has developed a process for marketing behavior change using the BEHAVE framework. This framework involves asking a few more questions before developing a strategy designed to achieve a behavior change. The strategy guides the development of a marketing plan. An essential element of a BEHAVE-based marketing plan is prototyping and pre-testing messages and aspects of the plan. When practicing risk communication and social marketing of behavior, it is essential to actively listen to the client or potential change-maker. Converting a decision-maker into a change-maker makes all the difference in controlling diseases such as *Mycobacterium avium* ssp. *paratuberculosis* and *Mycobacterium bovis*.

Key Words: risk communication, stages of change, social marketing of behavior

258 Zoonotic potential of bTB and MAP—Nothing to worry about…right? Tim Bull*, *Institute of Infection and Immunity, St George's University of London, London, UK.*

The threat of mycobacterial zoonotic transmission (particularly bTB) has driven expensive eradication efforts and large culling projects. In the absence of reliable vaccines however, the cost and complexity of programs needed to secure eradication from domestic herds and wildlife maintenance reservoirs has had limited progress. Few have succeeded in eradication and some arguably increased transmission rates. As a result bTB and MAP remain prevalent in domestic animals and wildlife reservoirs. Given the opportunity and a favorable host susceptibility these mycobacteria can cause disease in humans. Acute bTB infection is a potentially life threatening disease clinically indistinguishable from tuberculosis. Pasteurization remains an effective defense reflected by the fact that most human bTB cases are either a result of direct animal contact or re-activation from an older latent infection. For MAP, the issue is less clear cut. Despite significant indications that MAP invades, is present and persistent in many humans and has the capacity in susceptible individuals to trigger inflammatory bowel conditions such as Crohn's disease, the role of MAP as a direct human pathogen is still not widely accepted. Worryingly MAP survives pasteurization and prevalence is such that viable MAP is now significantly present in retail and dried infant formula milk. If MAP is truly a human pathogen, current ineffectual MAP control methods are permitting an extensive, unchecked, worldwide, chronic exposure to humans, some of whom are susceptible to developing disease. Latency and persistence are important characteristics of mycobacterial disease evoking long term immunological influences promoting disease. These states have been difficult to quantitate due to dormant unculturable phenotypes. Better tests are needed but the likelihood is that the extent of bTB and MAP disease burden in humans is not yet fully evident. The threat from bTB and MAP to human health thus remains tangible. Only vigilance currently prevents many potential animal reservoirs becoming re-seeded. Failure to improve screening and eradication tools will continue to allow global spread, increase the risk of human exposure and ensure more trouble is in store.

Key Words: bovine tuberculosis, paratuberculosis, zoonotic potential