



BioMed Research International

Special Issue on  
**Innovative “Omics” Tools for Detecting and Studying Livestock Bacteria**

# CALL FOR PAPERS

Good health is in the interest of livestock and contributes to sustainable farming. Next generation sequencing (NGS) of pathogens whole genomes is revolutionizing the science behind clinical diagnostics, epidemiology, and the field of microbiology in general. Never before have scientists had access to and been able to analyze and compare thousands of complete genomic sequences of bacteria. This vast amount of genomic data permits a better understanding of virulence traits and transmission to farm animals, along with a host of other valuable pieces of information. The proposal will also provide a critical look at the relevant “omics” techniques and their current limitations and advantages with respect to classical risk assessment methods.

Potential topics include, but are not limited to:

- ▶ **Epidemiology:** new methods (genome sequencing, RNA-seq, and proteome approaches) to study population dynamics of infectious diseases in animal populations and to analyze the evolutionary changes in historic and recently emergent hypervirulent strains
- ▶ **Metagenomics:** identification and exploitation of microbial communities for developing more effective and comprehensive methods for early detection of threats to animal health (monitoring and early detection of dangerous microbial contaminants) and the development of management practices that maximize the beneficial attributes of microbial communities in and around farm animals
- ▶ **Functional genomics** approaches to study the pathogenesis of infection
- ▶ **Proteomics** of bacteria infecting and colonizing livestock; proteomics and pathway analyses to understand bacterial infections and the interactions between microorganisms and their hosts; proteomics of microbial communities for understanding their metabolism and their interactions with the host and the environment
- ▶ **Metabolomics:** the impact of the bacterial infections on the metabolism of the affected hosts; the interaction of bacterial pathogens with mammalian hosts leads to a variety of physiological responses of the interacting partners aimed at an adaptation to the new situation; these responses include multiple metabolic changes in the affected host cells which are most obvious when the pathogen replicates within host cells as in case of intracellular bacterial pathogens; metabolomic studies of microbial communities in the context of the colonized organisms or environments will also be covered
- ▶ **Fluxomics:** connecting “omics” analysis and phenotypes (the availability of modern sequencing techniques has led to a rapid increase in the amount of reconstructed metabolic networks. Using these models as a platform for the analysis of high throughput transcriptomic, proteomic, and metabolomic data can provide valuable insight into conditional changes in the metabolic activity of an organism. While transcriptomics and proteomics provide important insights into the hierarchical regulation of metabolic flux, metabolomics shed light on the actual enzyme activity through metabolic regulation and mass action effects)

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