

# Delineation of Clinical Disease Profiles Associated with Infectious Diseases and Application to the “One Health” Initiative

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Infectious diseases have the potential to cause definite signs of disease in humans and various animal models that can be correlated to a specific clinical disease profile, or disease signature. And like the signature of a person, each clinical disease profile or disease signature may be specific to the causative agent. A disease signature can be associated with physical signs of disease or with specific biomarkers related to the respective pathogen and the host. Establishing the clinical profile or disease signature associated with the pathogen may add to improved diagnostics and may be necessary to establish correlates of protection in both humans and animals. For example, previous published work has suggested that virulence factors and mortality associated with various influenza viruses may correlate with several host and viral factors including the presence of influenza receptors on cells; temperature changes; induction of cellular necrosis; viremia and viral titers in host tissues; and the induction of a severe immune response, and is specific to the individual Influenza virus strain [1-3]. Additionally, clinical disease profiles associated with animals infected with infectious diseases may be similar to those observed in humans, and these disease profiles may be applied to the “One Health Initiative.” The One Health Initiative can be defined as a strategy that involves improving and expanding communications and research in all aspects of human and animal health care with respect to the environment. Animal health and human health within a particular ecosystem are interconnected and understanding this relationship will aid in understanding the epidemiology of a disease outbreak; delineating the relationship of the pathogen and the host; and defining any mutations that may influence virulence that are associated with emerging and reemerging zoonotic diseases. Thus, understanding the clinical disease profile resulting from a pathogen infection in both animals and humans may result in quicker more accurate diagnostics, which in turn can lead to earlier treatment, and perhaps better control of the outbreak. Establishing the clinical profile or disease signature in both humans and animals has been historically difficult, but modern technology is rendering more methods to determine the various parameters, or biomarkers, associated with specific signs of disease. Delineation of the disease signature would lead to a better understanding of the disease progression, improve diagnostics, improve the time required for diagnosis, and aid with determining the efficacy of vaccine, therapeutic, and prophylaxis treatments.

Because ferrets are susceptible to infection with human influenza A and B viruses, share similar lung physiology to humans, and the disease state resembles that of human influenza, these animals have been widely used as a model to study influenza virus pathogenesis and assess vaccine, therapeutic, and prophylaxis efficacy [4-6]. A statistical analysis comparing the changes of various biological parameters that can be used to define clinical profiles and predictors of survival and mortality as a result of Influenza virus infection was performed in our laboratory and may provide a case study using statistical analyses to determine a disease profile and establish correlates of protection [7]. In all, the data suggested that the severity and duration of febrile temperatures, overall lymphocyte and platelet numbers, changes in MCV, and overall body weight associated with the host animal after influenza infection may have a role in the pathogenesis and disease state

associated with Influenza virus infection, and may serve as correlates of clinical disease in ferrets. The statistical methods used to establish the disease profile and potential correlates of protection in ferrets may be extrapolated to humans, a “One Health Initiative” concept.

To be successful, the One Health Initiative involves education of future graduate, medical, veterinary, and public health students to lead to more collaboration in different aspects of human and animal health and medicine. Better cross-communication is required from scientists and animal and human health care professionals to better understand various aspects of zoonotic diseases. Research and data involving zoonotic diseases in humans and animals should be shared and communicated in public conferences to inform scientists, human health care professionals, and animal health professionals of groundbreaking pathogen research as it applies to human and animal health. This may allow for collaborative efforts to develop and test the efficacy of different vaccines, therapeutics, and prophylaxis, evaluate novel diagnostic and research tools, and improve surveillance efforts and the dissemination of information and data. The amalgamation of human and veterinary medicine for the One Health Initiative and the identification of clinical disease profiles in humans and animals research could lead to an improvement in biosafety in areas endemic to specific zoonotic diseases. Taken as a “proof of principal,” the ferret study, previously described, used statistics to define the clinical disease profile and correlates of protection associated with different Influenza viruses and this method can be applied to other aspects of infectious disease models and general research. Not only can the process distinguish among various infectious diseases, but the process may be used to distinguish various among different pathogen strains. Once the clinical disease profile, associated with a specific pathogen, is defined in animal models, the data may be extrapolated to define the disease profile in humans and other animals, or define parameters to determine product efficacy.

Altogether, utilizing the “One Health Concept” can allow for data obtained from infectious disease research and animal modeling to be employed to define a clinical disease profile and correlates of protection and extrapolated to human health; which, in turn, can improve the overall biosafety associated with infectious disease research, and lead to advances in epidemiology, diagnostics, and understanding pathogen mutation as it relates to the host and dissemination from the host.

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