

## **Linking Biological and Modeling Elements of Research with Rift Valley Fever**

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Rift Valley fever (RVF) is a mosquito-borne viral disease that causes explosive epidemics in sub-Saharan Africa and has been exported to nearby areas with disastrous results. Major prospects for control should it be introduced into this country would involve classical measures plus application of a live-attenuated vaccine. A human vaccine candidate attenuated by point mutations has been shown to be protective in domestic livestock with onset of virus-neutralizing antibody between days 7-14 in >95% of cattle. Other potential RVF vaccines are being developed at FAZD based on deletions or vectored RVF genes that could provide additional genetic stability and that could have DIVA capability.

These vaccines can be compared as to their ability to induce neutralizing antibodies (a known surrogate for protection against this virus). It will not be possible to compare the ability of these vaccines in the field to stop RVF spread, nor do we even have a detailed quantitative description of epidemics in Africa (much less an introduction into this country). Therefore, we need modeling of the African situation to allow us to describe the epidemic potential in this country, as well as to help discriminate the most favorable vaccine characteristics (time to onset of immunity, fraction of non-responders, duration of antibody, etc) in dealing with an introduction.

A multicompartiment SEIR model has been developed taking into account the complex transmission among mosquitoes (conventional horizontal spread as well as vertical transovarial transmission) and livestock and the differential equations carefully examined [Holly D. Gaff, David M. Hartley, Nicole P. Leahy, An Epidemiological Model Of Rift Valley Fever, *Electronic Journal of Differential Equations*, (2007)]. The epidemic potential,  $R_0$ , can be calculated from the model and is dependent on the environmental temperature. We have also developed the methodology to do spatiotemporal analysis of virus transmission and found it to be highly dependent on  $R_0$  and rainfall. This model has been validated through application to recent epidemics in Kenya and Sudan.

Next steps will be to apply to interventions such as vaccine characteristics, vaccination strategies, control of mosquito adults and larvae. In addition we will be able to study interactions with transport, calculate more complex numbers for  $R_0$ , and analyze the economic impact of virus and alternative control methods.