Infectious disease caused by influenza A virus (IAV) is a very serious health problem worldwide. In the US, annual IAV epidemics cause more than 30,000 deaths. We are using the mouse model system to study in detail the function of innate immune genes and the influence of genetic background for susceptibility and resistance to IAV infections. In addition, we have analyzed changes in gene expression of IAV-infected human patients to identify markers for severe respiratory IAV disease.