

## Host responses to influenza virus infection in the peripheral blood are similar in mice and men

### Inhalt

Influenza virus (IV) infections represent a very serious public health problem. At present, no established biomarkers exist to support diagnosis for respiratory viral infections. Mouse human cross-species comparisons are often compromised by the fact that animal studies concentrate on the infected lungs whereas in humans almost all studies use peripheral blood from patients. In addition, human studies do not consider genetic background as variable although human populations are genetically very diverse. Therefore, we performed a cross-species gene expression study of the peripheral blood from human patients and from the Collaborative Cross (CC) mouse population after IV infection. The recently established CC is a mouse genetic reference population derived from eight genetically different founder strains including classical lab strains as well as mouse models for human diseases like diabetes and obesity. In addition, three wild-derived strains strongly enhance the genetic diversity. Inbreeding for more than 20 generations has led to the CC strains whereby their genetic diversity is similar to that of the human population. We demonstrate that changes of gene expression after influenza infection in individual genes are highly similar in mice and humans. The top-regulated genes in humans are also differentially regulated in mice. We conclude that the mouse is a highly valuable *in vivo* model system to validate and to discover candidate genes, which can be used as biomarkers in humans. Furthermore, mouse studies allow confirmation of findings in humans in a well-controlled experimental system to understand the function of human candidate genes.

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