

## 28. HÜLSENBERGER GESPRÄCHE

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### **Breeding for disease resistance and reduced disease transmission**

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There is compelling evidence for substantial natural genetic variation in animals' responses to infection for most farm animal species and pathogens. Based on this, "breeding for disease resistance" has been advocated as an effective long-term strategy to combat infectious disease in livestock. Theoretical predictions are backed up by empirical evidence for impactful genetic selection for increased disease resistance, including genetic selection of sheep for scrapie resistance or of Atlantic Salmon to Infectious Pancreatic Necrosis (IPN), both of which have greatly reduced disease-induced mortality rates in these species. Nevertheless, implementation of genetic disease control is still in its infancy in practice.

More recently, genomic selection and genome editing provide hitherto unforeseen opportunities for improving disease resistance in animals more effectively. However, surprisingly little is known how the genetics of individuals affects the transmission of infectious diseases in livestock populations, and thus whether genetic improvement of animals' disease resistance actually reduces disease prevalence in the population. This is because standard field and challenge test data and genetic models don't provide estimates for genetic effects associated with host traits controlling disease transmission (i.e. host susceptibility, infectivity and propensity to recover or survive infection).

This article gives a brief overview of alternative methods for genetic disease control using the porcine reproductive and respiratory syndrome (PRRS) in pigs as a case study. It then outlines key concepts and software tools for the design and analyses of field and challenge experiments to determine host genetic effects underlying disease transmission. Using results from a PRRS virus transmission experiment it is demonstrated that genetic selection for disease resistance may not necessarily reduce virus transmission. Lastly, it is shown how the findings from genetic studies together with genetic-epidemiological prediction models could be used to devise more effective disease control strategies. Although this article focuses on genetic disease control, it will be shown that many of the principles presented here also apply to vaccination, or to a combination of preventative measures to control infectious diseases in livestock.