

Human Caliciviruses

a study of viral evolution, host genetics
and disease susceptibility

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This thesis describes the infectivity pattern of noroviruses and sapoviruses, both belonging to the family of human caliciviruses and known to cause acute gastroenteritis in humans. Gastroenteritis has emerged as a global health problem, and causes over five times more pediatric deaths compared to pediatric deaths caused by HIV/AIDS worldwide. Norovirus, the cause of the famous “winter vomiting disease”, is alone responsible for more than 200 000 deaths each year in children less than 5 years of age.

Unfortunately, the factors determining disease susceptibility, and in other words: “Who gets infected and why?” are still poorly known and understood. These factors are of great importance both for understanding disease mechanisms, as well as the design of prevention strategies and vaccines. This thesis aims to shed light on this question, and describes how the genes determining our blood groups may also determine our susceptibility to human calicivirus infection. This thesis also describes the ability of norovirus to evolve within an infected host, creating numerous novel virus variants and perhaps new epidemic subtypes.

To summarize, the results presented in this thesis show that the success of human calicivirus infection is probably determined by a delicate interplay between virus evolution and susceptibility of the host, both genetically and immunologically.



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