

THESIS SUMMARY

Viruses are the most numerous and genetically diverse biological entities in the biosphere. Yet, despite the demonstrated ubiquity of viruses, there remain substantial gaps in our understanding of their ecological roles, taxonomic diversity and distribution. In the oceans, where most research has been conducted on the subject, viruses have been demonstrated to perform key functions in global nutrient cycling and microbial diversification. However, it is still a matter of debate whether the same ecological importance holds true for viruses within terrestrial ecosystems. Thus, this study aimed to explore the taxonomic diversity and function of viruses in a major terrestrial biome: the desert ecosystem. Two hyperarid, thermally-contrasted desert biomes were studied: the Dry Valleys of Antarctica and the Namib Desert in Namibia. Prior to this research project, only very limited data were available on the presence and the genomes of viruses in these ecosystems.

In the Antarctic desert, virus diversity was compared between surface soil and rock-associated microbial communities (i.e., hypoliths). In the Namib Desert, the effects of a water availability gradient on virus diversity and distribution were assessed. Viruses were extracted from surface soils (Antarctic and Namib Desert samples) and rock-associated microbial communities (Antarctica only). Analysis of virus communities was conducted by the purification of viral metagenomic DNA, amplification by PCR and sequenced through NGS. Sequence data were used to determine the taxonomic composition of virus communities using homology-based searches against reference virus genomes in public sequence databases. For the Namib Desert study, the effects of soil microbial activity and physicochemical properties on the biogeography of soil viruses were determined. Bivariate correlation analyses were conducted to establish any putative links between virus distribution and edaphic factors.

Metagenomic analysis of soil virus communities in both desert biomes have shown that the virus composition is largely unknown (60-80%). Of the identified viruses, the dominant (90%) group were tailed, bacterial viruses (Order: *Caudovirales*). The remaining fraction was composed of eukaryotic viruses of algae, amoeba and insects. No archaeal viruses were found in this study. Furthermore, the taxonomic composition of viruses in all desert samples was strongly habitat- and sample- specific, with minimal overlap of virus species distribution. In the Namib Desert, significant correlations between virus abundance and microbial activity and several soil chemical constituents were found. It is suggested that virus communities in this hot hyperarid desert are not directly influenced by environmental conditions. Rather, the biogeographical patterns of the extracellular virus fraction are primarily determined by host distribution. In addition, a positive correlation between viral abundance and microbial activity is the first indirect indication of active viral propagation, and the possibility that soil viruses may contribute to nutrient cycling in a hot hyperarid desert soil environment. Collectively, the results in this thesis provide the first in-depth characterisation of a novel pool of viruses in hyperarid soils.