Bioprospecting and Functional Analysis of Neglected Environments

Advances in Next Generation Sequencing technologies made it possible to sequence DNA extracted from environments and organisms at a reasonable cost allowing research fields such as metagenomics and whole transcriptome sequencing (RNA-seq) to be established. These techniques allow the study of functional relationships in single organisms and environments. The sequencing data can also be mined for novel compounds and enzymes. The process of exploiting biological resources for commercial use is known as bioprospecting.

This PhD thesis describes the concept of bioprospecting in the post genomic era (Chapter 1) and introduces the research fields of metagenomics and RNA-seq (Chapter 2) as concepts to access and analyze biological resources. When attempting to discover and commercialize such biological resources, legal obligations have to be met, which is generally governed by the Convention on Biological Diversity (explained in Chapter 3). Proteolytic enzymes – described in Chapter 4 – are the target for bioprospecting due to their high market value. Section II describes methods used for the analysis of metagenomic and RNA-seq datasets, including Manuscript I, which includes the taxonomic annotation of a late Pleistocene horse metagenome and the functional annotation of the donkey genome. The functional analysis and the identification of novel proteolytic enzymes in the polar marine environment and the full transcriptome analysis of the carnivorous plant Dionaea muscipula is also presented.

The polar seas are unique, extreme habitat with constant low temperatures and no light penetration in the deep. Water samples at varying depth (40 m – 4,300 m) were collected during the Galathea III and LOMROG II polar expeditions. The sample DNA was extracted and sequenced. Comparative functional analysis of arctic marine metagenomes reveals bacterial strategies for deep sea persistence (Manuscript II). Furthermore, this extreme environment is a fertile ground to mine for novel proteolytic enzymes. Manuscript III presents a bioinformatics approach to identify sequences for potential commercialization.

Carnivory is a rare trait in the plant kingdom, and only few species are able to trap and digest prey. The sequencing, assembly and functional annotation of a normalized transcriptome of the most famous carnivorous plant, the Venus flytrap (Dionaea muscipula), is presented in Manuscript IV.

Chapter 12 summarizes the thesis and includes final remarks on the future perspectives on the presented research. In summary, this thesis demonstrates how biological resources can be exploited for commercial use. Furthermore, the findings give a better understanding of the microbial community’s persistence in the deep sea. Lastly, the transcriptome data of the Venus flytrap provide a public resource for unveiling features of the carnivorous syndrome such as digestion.

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