

SFB 960-/BZR – Kolloquium

Donnerstag 28. November 2019, 14.00 Uhr
H 53



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“Co- and Post-transcriptional regulation of adaptive responses in microorganisms”

Work in my lab is focusing on understanding how microorganisms manage to rapidly adapt (and even thrive) to sudden changes in their environment. Many pathogenic species have developed very sophisticated mechanisms to efficiently scavenge essential nutrients from the host environment and even evade the immune system.

We hypothesize that this successful rapid adaptation program is underpinned by the ability of the microorganism to very rapidly remodel its gene expression profile. Obviously, transcription factors largely dictate which genes are switched on and off during adaptive responses. However, it is becoming increasingly clear that co- and post-transcriptional regulatory pathways also play a key role in this process by shaping gene expression profiles.

Small non-coding RNAs (sRNAs) and RNA-binding proteins (RBPs) are believed to play a crucial role in this type of regulation by modulating transcription, translation and stability of mRNA targets. However, for the vast majority their function is unknown, underscoring the need for a thorough analysis of these molecules.

Over the years my group and my collaborators have developed a number of powerful high-throughput methods that enable us to unravel these regulatory networks involving non-coding RNAs and RBPs. Our initial studies in yeast uncovered a novel role for RBPs in co-transcriptionally controlling the expression kinetics of stress-responsive genes as well as targets for thousands of bacterial sRNAs. We have also recently expanded our research into pathogenic bacteria. Collectively, our data provide intriguing insights into how non-coding RNAs and RBPs are employed to control gene expression in response to stress.

Results from these studies will be presented.

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