Evolution of epigenetic regulation in beetles (Coleoptera)

Prof. Joachim Kurtz (WWU Münster)

Prof. Sonja Prohaska (Leipzig University)

Beschreibung

Insects show a remarkable evolutionary flexibility concerning the means by which epigenetic regulation is achieved. Even within the group of beetles (Coleoptera), some species rely on CpG methylation, while other species do not seem to show any functionally relevant levels of CpG methylation. Accordingly, genes encoding DNA methyltransferases (Dnmt1 and 3 genes) have been partially (e.g., Tribolium castaneum) or completely (e.g., Dendroctonus ponderosae) lost in some beetle species. Surprisingly, knock-down of these Dnmt genes can have strong and even lethal effects, even in species lacking CpG methylation, suggesting additional functions of DNMTs. On the other hand, it is still unclear, which other epigenetic processes could have replaced CpG methylation in such species.

In vertebrates, histone modification plays a major role in gene regulation. Many core components of the histone modification system are even conserved from animals to plants. Both, histone modification and DNA methylation are global regulators that are mechanistically similar in the sense that they give rise to marks being set along the genome but distinct with respect to their material basis. However, the combined mode of control may range from the mere coexistence to indispensable and rich crosstalk.

Our project thus has the following three main aims: (1) Understanding the evolution of epigenetic regulation systems; (2) Elucidating alternative functions of DNA methyltransferases; (3) Assessing the mutual dependences between DNA methylation and histone modification. We will make use of the combined power of bioinformatics, sequencing technology to analyse epigenetic processes (Methyl-Seq, Cut&Tag, RNAseq) and functional validation (RNAi) in ten beetle species. Our project addressing the surprising evolutionary flexibility in something as crucial as epigenetic regulation will thus provide urgently needed basic knowledge of the evolution of epigenetic regulation systems even more generally, beyond insects.