Fundamentals of epigenetic regulatory processes and their potential applications in plant protection and plant breeding

Prof. Dr. Gabi Krczal

RLP AgroScience, Neustadt

The most common form of epigenetic regulation is DNA methylation, which suppresses gene expression at the transcriptional level, and modifications of histone proteins, which also influence gene activity. DNA methylation is sequence-specific and controlled by RNA molecules, which is why it is referred to as RNA-directed DNA methylation (RdDM). At the post-transcriptional level, gene activity can be 'switched off' by means of RNA interference (RNAi), usually triggered by double-stranded (ds) RNA molecules. Both the RdDM and RNAi pathways produce small (s)RNAs and involve conserved Argonaute and Dicer proteins and RNA-dependent RNA polymerases. RdDM is associated with the response to abiotic stress and the regulation of important developmental transitions, while RNAi is associated with the defence against foreign RNA, e.g. from viruses.

The natural adaptation of plants – including woody plants – to abiotic stress is often correlated with altered methylation patterns, but there are few examples to date of induced, sequence-specific methylation for stress adaptation as a tool for plant breeding.

'RNAi sprays' have great potential in plant protection: they are applied to plants like a pesticide. The dsRNA molecules they contain are taken up by the targeted pests and then block the respective target gene without altering the genome of the plant or pest.

Research results from both areas will be presented.

Dept Life Science Systems

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Prof. J. Kollmann (Tel. 08161-714144, johannes.kollmann@tum.de)