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Bacterial Methylomes

Leopoldina Lecture by
Nobel Laureate Sir Richard J. Roberts

Monday, 26 May 2014 | 6:30 p.m. – 8:00 p.m.

German National Academy of Sciences Leopoldina
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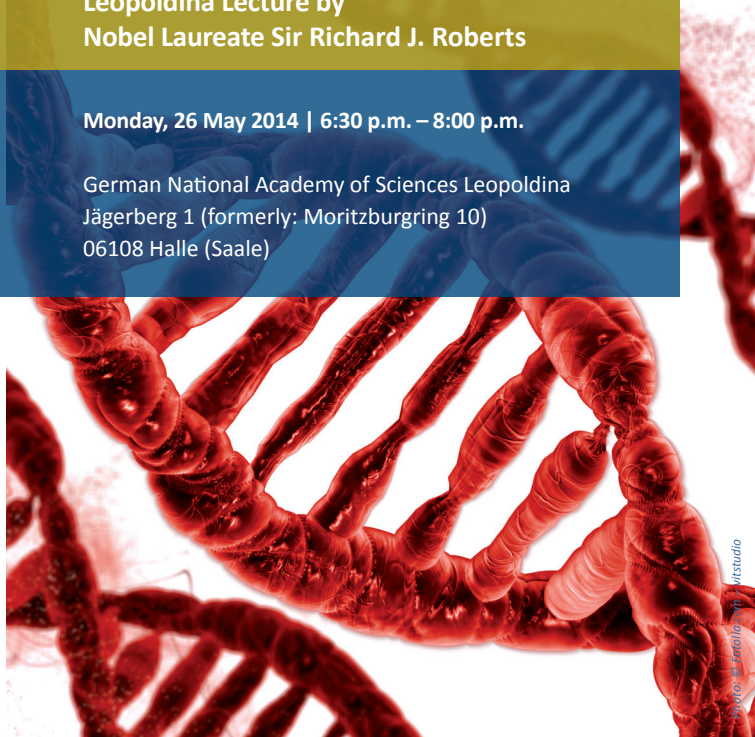

Sir Richard J. Roberts

is the Chief Scientific Officer at New England Biolabs, Beverly, Massachusetts. He was awarded the 1993 Nobel Prize in Physiology or Medicine with Phillip Allen Sharp for the discovery of introns in eukaryotic DNA and the mechanism of gene-splicing.

After an education in England and postdoctoral work at Harvard, Sir Richard Roberts worked at Cold Spring Harbor Laboratory from 1972 to 1992. Here he focussed on the newly discovered Type II restriction enzymes and his laboratory was able to clone the genes for several restriction enzymes and their cognate methylases.

Sir Richard Roberts has also been involved in studies of transcription of Adenovirus-2 that led to the discovery of split genes and mRNA splicing in 1977. His laboratory pioneered the application of computers in this area and continues to develop computer methods of protein and nucleic acid sequence analysis.

In the field of DNA methyltransferases an important discovery of structural changes induced by the *Hha*I methyltransferase has been made in collaboration with Dr. Xiaodong Cheng, Cold Spring Harbor Laboratory.

Sir Richard Robert's present research interest embraces the semi-automatic identification of restriction enzyme and methylase genes within the GenBank database and the development of rapid methods to assay function. Most recently, Sir Richard Roberts is one of the leaders of the COMBREX project that is concerned with the functional annotation of prokaryotic genomes.

Bacterial Methylomes

Bacterial DNA methyltransferases (MTases) are enzymes which methylate DNA, causing a recognizable epigenetic change to the DNA. They are important components of restriction-modification (RM) systems, which allow bacteria to detect and destroy foreign DNA, for example from viruses.

Until recently, rigorously determining the specificity of MTases has been a tedious process. With the advent of SMRT sequencing from Pacific Biosciences this situation has changed dramatically. Now it has become very simple to determine MTase recognition sequences both for individual MTases cloned in plasmids and also for whole bacterial genomes.

This offers new insights into the functioning of bacteria and has led to the discovery of many novel MTases with unexpected properties. A new door on bacterial life has been opened and raises many questions.

Programme

6:30 p.m. Welcome

Prof. Dr. Jörg Hacker ML, President of the Leopoldina

Lecture

Bacterial Methylomes
Sir Richard J. Roberts

Discussion

Moderation
Prof. Dr. Jörg Hacker ML

ML – Member of the Leopoldina