



PLANT BIOLOGY AND BIOTECHNOLOGY INTERNATIONAL CONFERENCE

Best Western Plus Atakent Park Hotel
May 28-30, 2014, Almaty, Kazakhstan

МАТЕРИАЛДАР PROCEEDINGS МАТЕРИАЛЫ

ӨСІМДІКТЕР БИОЛОГИЯСЫ ЖӘНЕ БИОТЕХНОЛОГИЯСЫ БОЙЫНША ХАЛЫҚАРАЛЫҚ ҒЫЛЫМИ КОНФЕРЕНЦИЯ

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МЕЖДУНАРОДНАЯ НАУЧНАЯ КОНФЕРЕНЦИЯ ПО БИОЛОГИИ И БИОТЕХНОЛОГИИ РАСТЕНИЙ

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В сборнике представлены материалы «Международной конференции по биологии и биотехнологии растений», проведенной в г. Алматы 28-30 мая 2014 г. В публикации изложены результаты оригинальных исследований в области изучения, сохранения и использования генетических ресурсов, генетики и селекции, физиологии и биохимии клеточной и генетической инженерии растений.

Сборник рассчитан на биологов, селекционеров, экологов, специалистов занимающихся генетическими ресурсами растений, фермеров, и студентов биологического и сельско-хозяйственного профиля.

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GENETIC MODELS OF RNA SILENCING AND ITS SUPPRESSION BY PLANT VIRUSES

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RNA interference (RNAi) in animals; initially introduced as post-transcriptional gene silencing (PTGS) in plants, commonly represents an evolutionary conserved pathway that operates as a regulatory developmental mechanism to down-regulate gene expression. RNAi in higher plants probably also evolved as a natural host-defense response for selective recognition and subsequent degradation of invading viruses. The initial and triggering event in RNAi is the generation/synthesis of double-stranded (ds) RNA. The next functional step of RNAi involves the action of Dicer like enzymes (DCL) (members of the RNase III family) that catalyze the generation of short (21-30 nucleotide (nt)) interfering RNAs (siRNAs) with signature 2-nt overhangs at the 3' ends containing 5' monophosphate and 3'-OH groups.

Recent studies in plants indicate that methylation of siRNAs also seems to play an important functional role by protecting these molecules from oligouridylation and subsequent degradation. The methylation of siRNAs occurs on the 2'-OH at their 3'-terminus, and this enzymatic modification is catalyzed by HUA ENHANCER1 (HEN1) methyltransferase.

In a subsequent step of RNAi, siRNA duplexes contribute one of the strands to the effector unit referred to as the RNA-induced silencing complex (RISC). While incorporated into RISC, the siRNAs function as guiding "search-primers" to direct nucleotide sequence-specific recognition of the targeted transcripts and their subsequent enzymatic hydrolysis or translational repression. The base pairing between siRNA and target RNA ensures effective and sequence-specific recognition of the target. Evidence suggests that siRNAs and Argonaute family (AGO) proteins represent the universal components of RISC. Conserved signature motifs of AGO proteins are referred to as PAZ and PIWI, and structural studies of the PAZ domain revealed that AGO directly interacts with the small RNA in RISC. To enable this, the PAZ interacts with the 3' ends of siRNAs, and this occurs for AGO, as well as for DCL that also contains this domain. The PIWI domain of AGOs represents the key catalytic entity of RNAi because it has the capacity to cleave the targeted

In response to host-defensive RNAi, viruses developed specific strategies to combat this effective surveillance system. It is now known that as a most effective countermeasure against RNAi, many viruses encode proteins (viral suppressors of RNA silencing (VSRs)) that interfere with the host-mediated defense system in order to block (or to a certain degree compromise) silencing-mediated degradation of cognate RNA. The expression of VSRs by viruses to combat this sophisticated host-surveillance system in plants is used to argue that RNAi may have originally evolved as a molecular defense mechanism against viral pathogens.

Many viral proteins currently known as VSRs were initially identified as pathogenicity or virulence factors, since their expression modulates symptom severity in viral infections. For the most part, they are not mandatory for replication but required for successful virus accumulation and spread during infection. Although a wide array of viral proteins exhibit VSR activity, the precise modes of their biochemical activities have only recently begun to unravel. For instance, latest molecular, biochemical and structural studies of diverse VSRs provided valuable insight into detailed mechanisms of silencing suppression. It turns out that these proteins interfere with various steps of the RNAi pathway and represent examples of a complex and intense "evolutionary battle" between viruses and plants. The co-evolution between virus-encoded VSRs and the host RNAi machinery also illustrates the adaptive nature of pathogen adaptation to the host-defense system.

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