세미나 초록

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발표 주제	대장암의 전이과정에서 원형 RNA (circular RNA)의 역할
발표 내용	**Circular RNA as a key player in colon cancer metastasis** **Hyeon Ho Kim** Samsung Advanced Institutes for Health Sciences and Technology, Sungkyunkwan University & Institute for Future Medicine, Samsung Medical Center Circular RNAs (circRNAs) are a novel type of endogenous long non-coding RNA. They are previously considered as a byproduct of splicing error, but recent researches have revealed that circRNAs influence the overall regulatory processes of gene expression, such as transcription, splicing, and translation. Unlike linear RNAs, circRNAs are characterized by covalently closed loop structure with no 5' end cap structure and 3' end poly A tail. In eukaryotic cells, pre-mRNA is transcribed by RNA polymerase and simultaneously spliced by spliceosome to remove introns and connect exons. While exons are constitutively spliced together, sometimes several exons are selectively included or excluded. This process is called as alternative splicing, allowing to generate multiple mRNAs from a single gene. CircRNA is synthesized by a unique back-splicing process which ligates the ends of linear RNA to form a single-strand covalently closed loop. Based on their biogenesis features, circRNAs are divided into three categories: exonic circRNAs (ecircRNAs), intronic RNAs (ciRNAs), and exon-intron circRNAs (eiciRNAs). Despite the detailed mechanism for circRNA biogenesis has not been fully elucidated, two main models are proposed: lariat-driven circularization and intron-pairing-driven circularization. CircRNA is characterized by several properties as follows: evolutionary conservation, tissue-specific expression, and higher stability than linear mRNA. The closed structure of circRNAs renders them resistant to exonuclease-mediated degradation. Due to their remarkable stability, circRNAs are considered as a powerful tool in the diagnosis and treatment of cancer. CircRNAs are reported to participate in the regulation of gene expression at both transcriptional and post-transcriptional level through functioning as a competitive endogenous RNA (ceRNA) of microRNA (miRNA) and RNA-binding protein (RBP). CircRNAs contain one or more miRNA recognition elements (MREs), which enable them to interact with mRNAs. As a ceRNA, circRNA competes with target mRNA in binding to miRNAs, which mitigates their inhibitory effects. For example, tumor-suppressive circRNAs, like other tumor suppressors, are downregulated in cancer, suggesting that it is closely associated with the upregulation of oncogenic miRNAs and suppression of tumor-suppressing targets. Conversely, the oncogenic circRNA sequesters tumor-suppressing miRNA from its oncogenic target genes. In addition to miRNA sponge, circRNAs are also able to interact with RBP, indicating that their sequestration of RBPs influences the function of RBPs and regulates the expression of their downstream target genes.