Changwon Kang, Professor Emeritus

Department of Biological Sciences, and KAIST Stem Cell Center, Korea Advanced Institute of Science and Technology (KAIST), Daejeon 34141, Republic of Korea

Fellow Emeritus, Korean Academy of Science and Technology

Tel: +82-10-5402-9718
Email: ckang@kaist.ac.kr

2022~present	Advisor, KAIST Stem Cell Center, KAIST
2017~present	Professor Emeritus, Department of Biological Sciences, KAIST
2014~2017	KT-Endowed Chaired Professor, KAIST
2010	President, Korean Society for Biochemistry and Molecular Biology
2008	President, Korea Genome Organization
2006~2008	President, Korea HapMap Consortium
2004~2006	Vice President of Academic Affairs, KAIST
2004	President, Life Chemistry Division of Korean Chemical Society
2002~2005	Editor-in-Chief, *Journal of Biochemistry and Molecular Biology*
1999~2006	Director, KAIST Bio21 Initiative, Brain Korea 21 Project
1999~2000	President, RNA Division of Korean Society for Molecular and Cellular Biology
1990~1992	Founding Executive Editor, *Molecules and Cells*
1986~2017	Assistant Professor, Associate Professor and Professor, Department of Biological Sciences, KAIST
1983~1986	Postdoctoral Research Associate, Department of Pharmacological Sciences, Stony Brook University School of Medicine, New York, USA
1983	Ph.D. of Chemistry, Columbia University, New York, USA
1974	B.S. of Chemistry, Seoul National University, Seoul, Korea

Research Interests:
Molecular biology, biochemistry and biophysics on the mechanisms of gene transcription; and human genetics and personal genomics of the common disease susceptibility variations

Selected Publications:

1. Kang W, Ha KS, ..., Hohng S, Kang C (2020) Transcription reinitiation by recycling RNA polymerase that diffuses on DNA after releasing terminated RNA. *Nat. Commun.* 11, 450
2. Song E, ..., Kang JY, Kang C, Hohng S (2022) Rho-dependent transcription termination proceeds via three routes. *Nat. Commun.* 13, 1663
3. Song E, ..., Hohng S, Kang C (2024) Compatibility of termination mechanisms in bacterial transcription with inference on eukaryotic models. *Biochem. Soc. Trans.* 52, 887-897
4. Song E, Han S, ..., Kang C, Hohng S (2024) Single-mode termination of phage transcriptions, disclosing bacterial adaptation for facilitated reinitiations. *Nucleic Acids Res.* 52, 9092-9102

Compatibility Paradigm of Transcription Termination

Changwon Kang

Department of Biological Sciences, and KAIST Stem Cell Center,

Korea Advanced Institute of Science and Technology, Republic of Korea

DNA-directed RNA polymerases (RNAPs) carry out transcription through diverse mechanisms of action. Textbooks depict its termination with one-step decomposition of transcription complexes into their RNA, DNA and RNAP components, permitting their three-dimensional diffusion for reinitiation to occur at any promoter in an unfacilitated fashion. Four years ago, we discovered that after RNA is released at termination, *Escherichia coli* RNAP often additionally remains bound to DNA for one-dimensional diffusion, expediting the recycling for reinitiation at the nearest promoter in a facilitated manner. The new mode is termed recycling termination in contrast with the textbook decomposing termination mode. These two modes are compatible at a single terminator with their ratio varying widely according to the terminators. Thus, post-termination RNAPs stay on or off DNA respectively for facilitated or unfacilitated reinitiation during the recycling stage, in which initiation factors are also regulated. This duality has been confirmed by other studies on *E. coli* and *Saccharomyces cerevisiae* RNAPs and our ongoing study on human RNAP III. On the other hand, we recently uncovered that bacteriophage T7, T3 and SP6 RNAPs perform at any terminator virtually only the decomposing termination, which appears homologous with the bacterial one. Thus, the recycling termination could be an adaptation conserved in bacteria, yeasts and humans. It facilitates the reinitiations to repeat at a promoter for accelerated expression and enables transcription coupling at adjoining promoters for coordinated regulation. Moreover, concomitant mechanisms operate at different speeds offering fail-safes and jointly achieve maximum possible efficiency. Thus, our compatibility paradigm of transcription termination could hold across all domains of life.