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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
2004~2006	Vice President of Academic Affairs, KAIST
1999~2006	Director, KAIST Bio21 Initiative, Brain Korea 21 Project
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
1975~1983	MA, MPhil and PhD of Chemistry, Columbia University, New York, USA
1970~1974	BS 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. Kang W, ..., Kang C, Hohng S (2021) Hopping and flipping of RNA polymerase on DNA during recycling for reinitiation after intrinsic termination in bacterial transcription. *Int. J. Mol. Sci.* 22, 2398
3. Song E, ..., Kang JY, Kang C, Hohng S (2022) Rho-dependent transcription termination proceeds via three routes. *Nat. Commun.* 13, 1663
4. Song E, ..., Kang JY, Kang C, Hohng S (2023) Transcriptional pause extension benefits the stand-by rather than catch-up Rho-dependent terminations. *Nucleic Acids Res.* 51, 2778-2789
5. 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
6. 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

Transcription Termination Mechanism Compatibility

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Abstract

Transcription for RNA synthesis is carried out by DNA-directed RNA polymerases (RNAPs) through diverse mechanisms of action. Textbooks illustrate its termination with one-step decomposition of transcription complexes into their RNA, DNA and RNAP components, permitting three-dimensional diffusion for reinitiation to occur at any promoter in an unfacilitated fashion. A few years ago, we discovered that after RNA is released at termination, *Escherichia coli* RNAP often 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 comparison with the textbook mode called decomposing termination. These two mechanisms are compatible at any single terminator. 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. Our paradigm of transcription termination mechanism compatibility has been reinforced in subsequent studies on *E. coli* and *Saccharomyces cerevisiae* RNAPs by other groups. In addition, a few months ago, we uncovered that bacteriophage T7, T3 and SP6 RNAPs perform virtually only the decomposing termination at any terminator. This decomposing termination appears homologous between phages and bacteria. Then, the recycling termination could be bacterial adaptation conserved in the budding yeast and possibly other organisms. It facilitates reinitiations to repeat at a promoter for accelerated expression and enables transcription coupling at adjoining promoters for coordinated regulation. Moreover, the compatible mechanisms of termination operate at different speeds providing fail-safes and jointly achieve maximum possible efficiency.