

Indian scientists helped rewrite a 50-year-old biological rule

Posted On: 02 MAR 2026 3:38PM by PIB Delhi

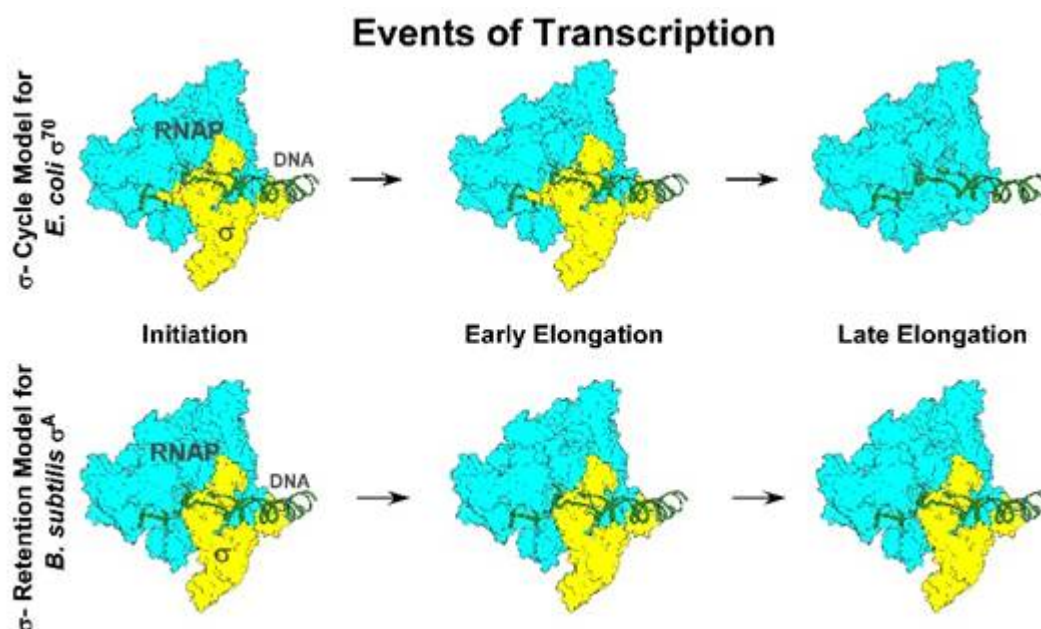
A new study overturns a central textbook model of bacterial gene regulation and unveils new paths for understanding bacterial gene regulation and its evolution.

This could help designing better antibiotics or regulatory inhibitors that block infection mechanism and design microorganisms that produce biofuels, biodegradable plastics, or therapeutic compounds efficiently.

For nearly 50 years, biology has related the story of how bacteria turn their genes on with the help of the so-called “ σ (sigma) cycle” – factors that bind RNA polymerase to initiate transcription and then dissociate to allow elongation. This concept was built largely on observations of bacterial strain *E. coli* $\sigma 70$.

However, Researchers from the Bose Institute, an autonomous institute of the Department of Science and Technology (DST) and Rutgers University reveal that the cycle is not a universal phenomenon.

In a study published in the *Proceedings of the National Academy of Sciences* (PNAS) they have reported that, contrary to decades of scientific belief, the principal transcription initiation factor in *Bacillus subtilis* — σA —and a modified version of the *Escherichia coli* $\sigma 70$ factor remain bound to RNA polymerase throughout transcription, rather than being released after initiation.



“Our work shows that in *Bacillus subtilis*, the σA factor stays attached to RNA polymerase all the way through the transcription process,” said Dr. Jayanta Mukhopadhyay, corresponding author from the Bose Institute. “This fundamentally changes how we think about bacterial transcription and gene regulation.”

Using a combination of modern techniques like biochemical assays, chromatin immunoprecipitation, and fluorescence-based imaging — the researchers watched the sigma factor’s behaviour in real time. They found that *Bacillus subtilis* σA and an *E. coli* $\sigma 70$ variant lacking a part called 1.1 remain stably associated with transcription complexes. This is in stark contrast to full-length *E. coli* $\sigma 70$, which is released stochastically during elongation.

“These findings provide compelling evidence that the long-accepted σ cycle does not apply to all bacteria,” added co-author Aniruddha Tewari of Bose Institute. “It opens new avenues for understanding bacterial gene regulation and its evolution.”

The discovery has broad implications for microbiology, potentially influencing how researchers approach bacterial physiology, stress response, and the development of antibiotics targeting transcription.

The study, was authored by Aniruddha Tewary, Shreya Sengupta, Soumya Mukherjee, Nilanjana Hazra, from Bose Institute and YWE and RHE and Yon W. Ebright, Richard H. Ebright, and Jayanta Mukhopadhyay from Rutgers University, USA

Publication link: [doi:10.1073/pnas.2503801122](https://doi.org/10.1073/pnas.2503801122)

NKR/FK

(Release ID: 2234503) Visitor Counter : 384

Read this release in: Urdu , বাংলা , Tamil