

Press release**Max-Planck-Institut für Evolutionsbiologie****Michael Hesse**

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<http://idw-online.de/en/news848961>Research results, Transfer of Science or Research
Biology
transregional, national**Extreme Mutation Hotspot in Bacteria Discovered: Study Links High Mutation Rates to Transcriptional Activation**

Max Planck researchers discovered a 5,000-fold increase in the mutation rate in the genome of *Pseudomonas fluorescens*. The mutation regularly occurred in the promoter region of the *rpoS* gene and was promoted by its activity. Suppressing the *rpoS* promoter reduced the mutation rate by a factor of 60. This suggests that similar mutation hotspots could exist in other genes and bacterial species.

A new study published in PLOS Genetics has identified an extreme mutational hotspot within the genome of *Pseudomonas fluorescens*, providing unprecedented insight into the relationship between gene regulation and mutation rates. The findings could have broad implications for understanding bacterial evolution, adaptation, and antibiotic resistance.

The research, conducted by Andrew D. Farr, Christina Vasileiou, Peter A. Lind, and Paul B. Rainey, reveals that mutations in the promoter region of the *rpoS* gene occur at an astonishing rate—approximately 5,000 times higher than expected. The mutation was observed across multiple independent bacterial populations, occurring predictably in 137 out of 153 replicate cultures.

This mutation is directly linked to transcriptional activity: the more a promoter is active, the more frequently mutations appear in this promoter. In experiments where transcriptional activation was blocked, the mutation rate dropped nearly 60-fold, demonstrating a clear causal relationship between gene expression and mutagenesis.

“Our findings highlight an unexpected link between gene regulation and mutation rate, suggesting that certain genomic regions may be more prone to mutational change,” said Andrew Farr, lead author of the study. “This could have important implications for understanding bacterial adaptation and antibiotic resistance evolution. We are currently investigating the precise molecular interactions that cause these high mutation rates and are now building principles to predict where these mutational hotspots may occur.”

Implications for Evolution and Antibiotic Resistance

Mutations are fundamental to evolutionary change, driving the emergence of new traits, species, and, in some cases, resistance to antibiotics. This study provides strong evidence that transcriptional activation can locally increase mutation rates, potentially influencing bacterial genome evolution and the development of antibiotic resistance.

By uncovering a mechanism by which gene activity itself influences mutation rates, this research challenges traditional views on mutagenesis and opens new avenues for studying genome evolution in bacteria and beyond. Understanding the molecular basis of these hotspots could help predict where and how mutations might occur in other microbial species, offering new strategies to mitigate bacterial adaptation to environmental pressures, including antibiotics.

contact for scientific information:

Andrew Farr
Research Group Leader
Microbial Genetics
Max Planck Institute for Evolutionary Biology

Original publication:

Andrew D. Farr , Christina Vasileiou, Peter A. Lind, Paul B. Rainey (2025)
An extreme mutational hotspot in nlpD depends on transcriptional induction of rpoS
<https://doi.org/10.1371/journal.pgen.1011572>