

How cells pass on regulatory information

A project funded by the Baden-Württemberg Stiftung at the Max Planck Institute of Immunobiology and Epigenetics in Freiburg is investigating the interplay between RNA modifications and epigenetic mechanisms during cell division – and its potential significance for treatment resistance in cancer.

The Baden-Württemberg Stiftung is investing in an exciting research question: How is the regulatory information that allows a cell to maintain its identity passed on during cell division? And could a disruption of this process explain why leukemia cells respond differently to therapies?

The new research project in Valentin Flury's laboratory at the Max Planck Institute of Immunobiology and Epigenetics is funded as part of the foundation's "Epitranscriptomics" program. The goal is to further develop existing analytical to study the role of RNA modifications and epigenetic processes for gene regulation during the cell cycle. Previous studies have often relied on large, mixed cell populations. Differences between individual cells and between different phases of the cell cycle can thus remain undetected.

Two layers of gene regulation

When a cell divides, it does not only pass on a copy of its genetic material to the two daughter cells. These cells must also know which regions of the DNA to should use. Only in this way can they preserve their identity and function. However, it is not yet fully understood how this regulatory information is preserved across cell division.

In the cell nucleus, DNA is packaged together with proteins to form what is known as chromatin. Epigenetic regulation influences the structure of chromatin via chemical marks and thus helps determine which sections of DNA are accessible to the cell and to what extent the genes located there are expressed.

When a gene is transcribed, RNA molecules are produced. They transmit and process genetic information, but can also perform regulatory functions themselves. For example, chemical marks on RNA molecules influence their processing, stability, and activity. Research into this additional level of regulation is referred to as epitranscriptomics.

What happens during cell division?

"Chromatin regulation and RNA regulation are not separate systems. Epigenetic and epitranscriptomic mechanisms are closely intertwined. We want to understand how this interaction works and how it changes over the course of the cell cycle," explains Max Planck Group Leader Valentin Flury.

Conventional methods for analyzing gene regulation typically analyze many cells simultaneously, which masks subtle differences between individual cells. "A single sample contains cells in every possible phase of the cell cycle at the same time. If an effect actually occurs only within a short time window, it is simply averaged out when considering all cells," says Valentin Flury.

The team want to develop methods that are sensitive and selective enough even with a very small subset of this cell population to measure and understand how the finely balanced system of epigenetics and epitranscriptomics interacts before, during, and after cell division.

A possible source of leukemia cell diversity

The project also has a medical perspective. In leukemia, epigenetic processes are often disrupted in addition to genetic changes. Research findings suggest that changes in RNA regulation, including epitranscriptomic processes, can contribute to the development of certain leukemias. Even leukemia cells with similar genetic profiles can differ significantly in their growth, degree of maturation, and sensitivity to therapies. This diversity within the disease is considered a possible cause of treatment

resistance.

The research team is investigating the hypothesis that an imbalance between epigenetic and epitranscriptomic regulation could contribute to this diversity. If regulatory states are not reliably maintained during cell division, the resulting daughter cells could respond differently to therapy and survive treatment.

“We want to find out whether disruptions in non-genetic information transmission are a previously underestimated source of variation among leukemia cells. You can think of the epitranscriptome as a highly complex, information-rich system. For each cell, it provides deeper insights into specific cellular and disease states that go beyond the DNA sequence alone. We want to tap into this information,” says Boyang Gao, who will be conducting the project in Valentin Flury’s lab.

Valentin Flury expresses gratitude for the generous support of the Baden-Württemberg Stiftung: “We now have the chance to combine Boyang’s unique expertise in epitranscriptomics, cancer resistance, and low-input methods with the lab’s focus on epigenetics and cell-cycle regulation. Thanks to this synergy, we can now ask important questions about the crosstalk between epigenetics and epitranscriptomics across the cell cycle.

About Boyang Gao

Boyang Gao completed her bachelor’s degree at Tsinghua University in China. She then earned her Ph.D. in the laboratory of Professor Chuan He at the University of Chicago in the United States. There, she investigated how RNA modifications influence epigenetic regulation in leukemia cells. After completing her Ph.D. in 2025, she joined Valentin Flury’s research group as a postdoctoral fellow at the Max Planck Institute of Immunobiology and Epigenetics in Freiburg.

About the Baden-Württemberg Stiftung

The Baden-Württemberg Stiftung was established in 2000 and is one of the largest foundations in Germany. As an independent and nonpartisan state foundation, it is particularly committed to the people of Baden-Württemberg. With a clear mission and a clear stance, it shapes change—in society and culture, in education, and in cutting-edge research. For a shared future built not on “I,” but on “we.” The Baden-Württemberg Stiftung is committed to a vibrant civil society and promotes social and cultural participation. Through ideas and investments in education, science, and culture, it works to ensure a sustainable and livable Baden-Württemberg.

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