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IISc explores ways to control tumour progression

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Glitch in protein synthesis could affect tumour growth, a new study reveals



In a new study published in the Journal of Cell Science, researchers at the Indian Institute of Science (IISC), Bengaluru have zeroed in on a gene that codes for a protein called FEM1B. They show how FEM1B mRNA readthrough plays a key role in the cell cycle, with implications for cancer cell proliferation and tumour growth.

The FEM1B protein is part of a complex that marks other proteins for degradation. Its job is to make sure that the right proteins are marked. The complex targets key proteins involved in many cellular processes – one of them being the cell cycle, to keep a check on how much cells proliferate.

In the study, the researchers found that stop codon readthrough causes the translation machinery to make a longer and more unstable version of FEM1B. Ironically, this marks FEM1B itself for degradation, leading to reduced levels of the protein. The team found that a specific nucleotide sequence at the tail end of the FEM1B gene directs this readthrough.

The researchers further deployed the CRISPR-Cas9 system, commonly used “molecular scissors”, to snip off the sequence driving the readthrough from the FEM1B gene. Preventing readthrough led to increased levels of the FEM1B protein, and therefore increased degradation of target proteins, and a delayed cell cycle. This caused the cancer cells to proliferate less.

Researchers are now keen on nailing down the molecular machinery involved, which will help make any therapeutic approach more specific. “If we know the mechanism, we can target and regulate the readthrough process, which in turn might help in controlling the tumour progression”, said Sandeep Eswarappa, Associate Professor at the Department of Biochemistry, Indian Institute of Science (IISc).