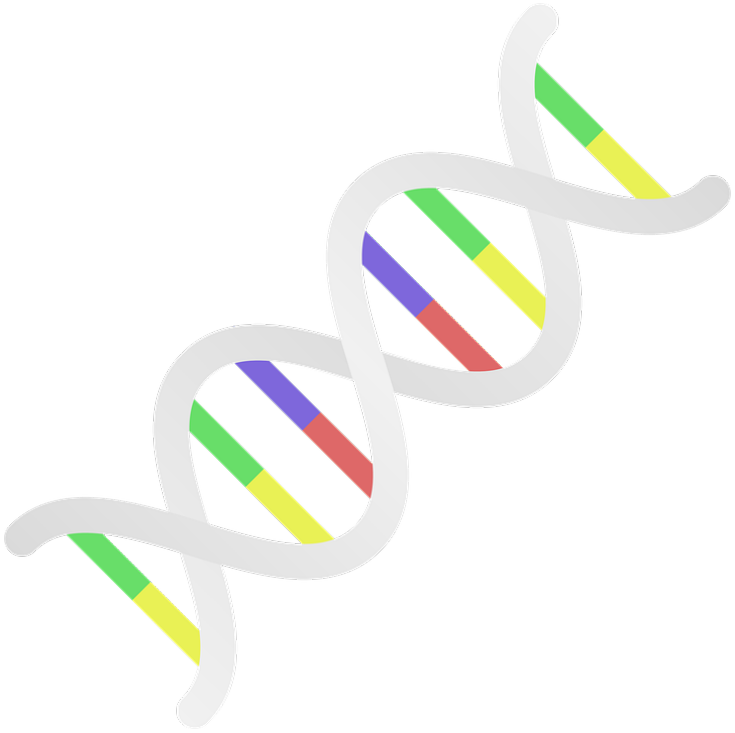
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Research from XJTLU advances RNA modification mapping

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Led by Dr Jia Meng from the Department of Biological Sciences, the research was recently published in Nucleic Acids Research.



Researchers from Xi'an Jiaotong-Liverpool University have completed a high-resolution prediction of the whole-transcriptome m6A RNA modification, successfully creating the world's most accurate map of the m6A epitranscriptome.

Led by Dr Jia Meng from the Department of Biological Sciences, the research was recently published in *Nucleic Acids Research*.

Dr Meng says the results may have promising implications for a range of diseases.

"It's hard to predict which diseases will benefit from the research into m6A RNA methylation but studies indicate the enzymes of m6A RNA methylation play a key role in leukemia, lung cancer and breast cancer," he says.

"As a fundamental layer of gene regulation, I wouldn't be surprised to see epitranscriptome regulation through reversible m6A RNA methylation playing an important role in many diseases.

"Cancer is proving to be a promising direction to explore further."

Dr Meng says RNA stands for ribonucleic acid – known as the 'cousin' of DNA – and that m6A RNA modification is a type of biochemical modification of RNA molecules, which can alter their biological properties and regulate gene expression without

changing its sequences.

"Previously the accuracy of m6A RNA modification site prediction could only reach approximately 80 percent using conventional sequence information," he says.

"What we found is that by adding 35 additional genomic features, we can increase the accuracy to 90 per cent, which is a big step forward."

Dr Meng says it's a hot topic in biological science today, as there are more than 100 different types of RNA modifications, and their functions are largely unknown.

According to Dr Meng, the m6A is the most abundant and is likely to be the most valuable to study.

The research team used a machine-learning approach when drafting the map of the m6A epitranscriptome, establishing a prediction model based on the conventional sequence features and new genomic features to predict the precise locations on genes that might be related to RNA modifications.

PhD student Kunqi Chen says more accurate predictions and a better understanding of the site of the RNA modifications allow scientists to more easily identify which enzymes are involved in the process.

"Our work contributes to the study of genetic functions and traits, and the relationship between genes and some human diseases," he says.