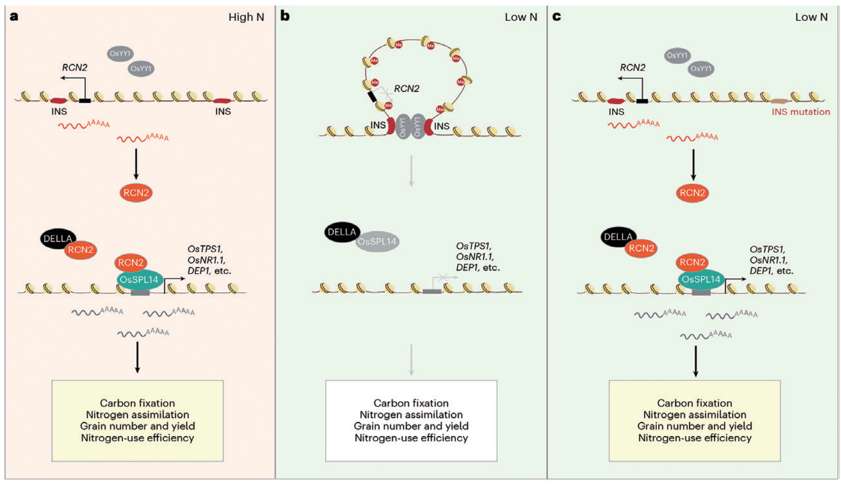
Life Science

More Grain, Less Fertilizer: The Hidden DNA Loop Powering a New Green Revolution



Enhanced sustainable Green Revolution yield via chromatin loop extrusion-driven transcriptional regulation of *RCN2*. (Image by IGDB)

A team from the Institute of Genetics and Developmental Biology (IGDB) of the Chinese Academy of Sciences has discovered a hidden 3D DNA structure in rice that enables higher grain yields with less nitrogen fertilizer, with findings published in *Nature Genetics* (doi: 10.1038/s41588-025-02376-y). A looping section of DNA called a "chromatin loop" controls the gene *RCN2*, which governs how rice forms its grain-bearing branches. Adjusting this loop simultaneously boosted yield and nitrogen use efficiency (NUE)—two traits that typically conflict. Lead researcher Prof. FU Xiangdong explains that maximizing yield requires strengthening both the plant's "source" (leaves that produce sugars through photosynthesis) and "sink" (grains and other growing parts that store and consume those sugars), and this discovery advances both goals at once.

To uncover how this coordination occurs, the researchers identified a major genetic region, or quantitative trait locus, called qINCA2. This locus influences photosynthesis, nitrogen assimilation, and grain number—three core traits for productivity. Within this region, the researchers pinpointed a single nucleotide polymorphism (SNP) located 8,765 base pairs upstream of a gene known as *RCN2*, which plays a key role in how rice forms its grain-bearing branches, or inflorescences.

That tiny DNA change dramatically increased *RCN2* activity. The *RCN2* protein then altered how two other molecules—OsSPL14 and DELLA—interact. By loosening their bond, *RCN2* effectively freed the OsSPL14 transcription factor to switch on genes responsible for carbon–nitrogen metabolism and panicle development. This chain reaction allowed rice plants to produce more grains and use nitrogen more efficiently—two goals that typically trade off against each other.

The team then turned to a deeper question: How does the SNP trigger such a strong effect on gene expression? Their investigation revealed that the region containing the SNP also carries a series of tandem DNA repeats—CCCTC motifs—known in animals to anchor 3D loops in chromatin, the tightly packed form of DNA. In mammals, such loops are controlled by a protein called CTCF, but no plant equivalent had ever been confirmed.

FU's group identified OsYY1 as the first plant protein to act in this way. OsYY1 binds to the CCCTC-rich DNA sequences near *RCN2* and promotes the extrusion of chromatin loops, reshaping the three-dimensional architecture of the genome. This looping mechanism determines whether *RCN2* is turned on or off by bringing distant control elements into contact with its promoter region.

By precisely editing these regulatory DNA sequences, the researchers were able to fine-tune chromatin looping at the *RCN2* site. The result was enhanced flow of carbon compounds from source tissues to developing grains—the sink—leading to higher harvest index (HI), greater yield, and stronger NUE, even under low-nitrogen conditions.

This discovery introduces chromatin loop extrusion as a new mechanism for crop improvement. Beyond its immediate implications for rice, it opens the door to next-generation breeding strategies that could help feed a growing global population with fewer environmental costs.

(Source: IGDB)