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Lost gene from maize's wild ancestor could rewrite future of animal feed

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A team of Chinese scientists has identified a rare gene from teosinte, the wild ancestor of modern maize, that significantly boosts protein content in corn without compromising grain yields, offering a potentially transformative tool for crop breeders seeking to improve the nutritional value of one of the world's most important staple crops.

The breakthrough, published in the journal Nature , was achieved by researchers from the Center for Excellence in Molecular Plant Sciences of the Chinese Academy of Sciences, Shanghai Normal University, and Sichuan Agricultural University.

The discovery addresses a long-standing challenge in maize breeding. Although maize has undergone nearly 9,000 years of domestication and genetic improvement, breeding efforts historically focused on yield, adaptability and agronomic performance rather than nutritional quality. As a result, many naturally occurring genetic variants associated with higher protein accumulation gradually disappeared from cultivated maize populations.

Today, modern maize varieties generally contain relatively low protein levels, contributing to the livestock industry's dependence on imported protein sources such as soybean meal.

The newly identified gene, known as Teosinte High Protein 3 (THP3-T), appears to reverse part of that historical trade-off.

Researchers found that THP3-T encodes glutamate-oxaloacetate transaminase 1 (GOT1), a critical enzyme involved in nitrogen metabolism. The team discovered that unique natural variations within the gene increase both its expression and biological activity, enabling maize plants to convert nitrogen into protein more efficiently.

According to the researchers, these beneficial variants became progressively less common during maize domestication and modern breeding. While relatively widespread in wild teosinte populations, the superior form of THP3-T is now present in only a small fraction of modern maize germplasm.

The study further revealed that the gene's impact becomes even more pronounced when paired with another previously identified high-protein gene, THP9-T, which regulates nitrogen utilization through a different biochemical pathway.

To test the practical value of the discovery, scientists introduced both favorable gene variants into Zhengdan 958, one of China's most widely cultivated commercial maize hybrids.

The results were striking.

Seed protein content increased from approximately 8.5 per cent to between 12 per cent and 13 per cent, while whole-plant protein content rose from roughly 7 per cent to more than 9 per cent. Importantly, these nutritional gains were achieved without reducing grain yieldâ??an outcome long regarded as one of the most difficult objectives in crop improvement.

The findings shed new light on how centuries of domestication inadvertently reduced the nutritional quality of maize while selecting for other desirable traits. More importantly, they demonstrate how beneficial genetic diversity preserved in wild crop relatives can be reintroduced into modern breeding programs to address contemporary food and feed challenges.

Researchers say the work provides a valuable new genetic resource for developing maize varieties with enhanced protein content, particularly at a time when rising global demand for livestock feed is placing increasing pressure on agricultural supply chains.

The discovery also highlights a broader trend in crop science: the growing effort to unlock useful traits hidden within the wild ancestors of modern crops. By recovering genetic variations that were lost during domestication, scientists hope to improve nutritional quality, resource-use efficiency and resilience without sacrificing productivity.

With maize remaining a cornerstone of global food, feed and industrial supply chains, the identification of THP3-T represents a significant advance in efforts to produce more nutritious crops while maintaining the yields needed to support a growing global population.

The study marks the latest milestone in China's expanding agricultural genomics research program and builds upon earlier work that first identified THP9-T, another key gene linked to elevated protein accumulation in maize. Together, the two discoveries offer breeders a powerful new toolkit for developing the next generation of high-protein corn varieties.