New research shows how mobile DNA survives -- and thrives -- in plants, animals

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(PhysOrg.com) -- Bits of movable DNA called transposable elements or TEs fill up the genomes of plants and animals, but it has remained unclear how a genome can survive a rapid burst of hundreds, even thousands of new TE insertions.

Now, for the first time, research led by plant biologists at the University of Georgia have documented the impact of such a burst in a rice strain that is accumulating more than 40 new TE insertions per plant per generation of an element called mPing.

The big surprise of their study is that the impact on the host seems to be modest. Not only that, the research shows that the genetic diversity created by massive and rapid TE insertions can actually benefit the plant in entirely unexpected ways.

"What we discovered was brand new and really stunning," said Susan Wessler, UGA Foundation Chair in the Biological Sciences and leader of the research. "We found that the TE we studied avoids insertion sites in exons [sequences of DNA that code information for protein synthesis that is transcribed to messenger RNA]. But even more important may be that this shows that for rice and other `selfing' plants [ones that essentially pollinate themselves], TE bursts may be one of the critical solutions to rapidly generate genetic diversity in the face of an ever-changing environment."

The research was published today online in the journal *Nature*. Other authors of the paper include Ken Naito, Feng Zhang, Nathan Hancock and Aaron Richardson of Wessler's lab at UGA, and Takuji Tsukiyama, Hiroki Saito, Yukata Okumoto and Takatoshi Taniska of Kyoto University. Wessler and her lab are part of the department of plant biology, which is in the Franklin College of Arts and Sciences at UGA.

Transposable elements have been known to science for more than six decades. Despite making up half of the human genome and more than 90 percent of some plant genomes, the reasons for their success has remained elusive. Several things came together, however, to make the new research possible.

First, the complete rice genome sequence is now available including the location of most of its roughly 30,000 genes. Using this resource, Wessler and co-workers were able to decipher the precise sites for almost 2,000 new mPing insertions using a new high-throughput DNA sequencing method.

Next, they used DNA chip technology to determine the effect of most of these insertions on rice gene expression. And third but not least, the team demonstrated that a large subset of new alleles (different forms of a gene) that contain mPing "may actually benefit the host by creating potentially useful . . . and novel, stress-induced regulatory networks." The stresses tested that demonstrate this were drought and salt-tolerance.

"One thing to remember is that for virtually all plants and animals characterized to date, most of their TEs were inserted hundreds of thousands to millions of years ago," said Wessler, "so being able to observe the effects of their rapid increase in a well-characterized genome like rice gives us tremendous insights into these critical early events and permits us to glimpse how they alter the host organism."

Demonstration that a rapid burst of TE insertions generate new regulatory networks is consistent with the ideas of Barbara McClintock, the scientist who discovered transposable elements and who was the first to propose that they were tools of evolutionary change.

It appears, the team said, that the ability of mPing to target its insertion sites helps to mitigate the effects of sudden rapid bursts of large-scale TE insertions—something one might think could be detrimental to the health of the host.

"Catching" a TE in the act of actual amplification, as the team did, brings important new insights into insertions that happened in the distant past and may finally help unravel why these ubiquitous bits of DNA comprise the majority of the genomes of plants and animals.

Source: University of Georgia (news : web)

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