National Research Initiative (NRI)

New Bioinformatic Tools Accelerate Genome Assembly

by Stacy Kish, CSREES

Scientists have developed a new tool that will help them accelerate the assembly of the genome of any organism by identifying redundant and irrelevant segments of DNA. >>

Above: This research was featured on the cover of Plant Physiology Volume 146, Number 1.

Credit: American Society of Plant Biologists, reprinted with permission.

With funding from USDA's Cooperative State Research, Education, and Extension Service (CSREES) National Research Initiative (NRI), scientists in Iowa developed a computer software tool to identify the location and history of troublesome transposable elements in an organism's genome.

The genome of an organism contains all of the hereditary information encoded in the DNA. Unfortunately, this information may contain many repetitive sequences that are historical artifacts that either no longer function or could have been modified by evolution.

Transposable elements are mobile segments of DNA that produce the repetitive segments. These elements exist throughout the genome and can cause gene or chromosome mutations. These changes can provide the mechanism that allows gene functions to evolve.

Transposable elements vary between different organisms, but their occurrence is high in many flowering plants. For example, the human genome is composed of 45 percent repeat sequences, while the corn genome contains 67 percent repeat sequences. The segments are difficult for scientists to sort out, because they tend to hide within themselves like Russian nesting dolls. Little is known about the distribution and history of formation of transposable elements across the genome.

Brent Kronmiller and Roger Wise at Iowa State University developed a software tool called TEnest that allows scientists to identify all of the highly repetitive sequences in the genome. It also allows scientists to unravel the nested segments and reconstruct full-length repeats.

Transposable element populations replicate throughout the genome independently, propagating and evolving. With this new tool, the scientists can identify repeat insertions in the genome, calculate their age since integration into the DNA, and model their evolution.

TEnest is available for use both as a Web server on the Resource for Plant Comparative Genomics, www.PlantGDB.org, and as a stand alone downloadable version available from www.Wiselab.org.

To date, the tool has been applied to four agriculturally important grains—maize, barley, wheat, and rice—and an international effort to assemble the genome of each grain is underway. Oat, sorghum, and soybean sequencing groups have also expressed interest in developing organism specific databases.

"Bioinformatic tools such as TEnest increase the speed with which genomes are assembled and provide insight into the evolution of the plant," Wise said. "Understanding the genome of agricultural crops may allow scientists to develop crops capable of growing in arid conditions and resistant to pests."

CSREES funded this research project through the NRI Plant Genome and Plant Biology programs. The Plant Biological and Molecular Processes National Program of the USDA's Agricultural Research Service (ARS) also provided funds. Through federal funding and leadership for research, education and extension programs, CSREES and ARS focus on investing in science and solving critical issues affecting people's daily lives and the nation's future. For more information, visit www.csrees.usda.gov. and http://www.ars.usda.gov/Research/Research.htm. ∎

Above: The TEnest software has been applied to the genomes of maize, wheat, barley, or rice.

Credit: Julie Dickerson

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http://www.csrees.usda.gov/funding/nri/nri.html

References

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