

# Genome archaeology illuminates the genetic engineering debate

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Genome Research's cover story for Oct. 2 tells a tale of "genome archaeology" by genetic researchers who dug deeply into the long history of maize and rice. Their resulting insights into plant genomic evolution may well fuel the fires of the genetically modified organism (GMO) controversy.

"Our findings elucidate an active evolutionary process in which nature inserts genes much like modern biotechnologists do. Now we must reassess the allegations that biotechnologists perform 'unnatural acts,' thereby creating 'Frankenfoods,'" said Professor Joachim Messing, project leader and director of the Waksman Institute of Microbiology at Rutgers, The State University of New Jersey.

By comparing corresponding segments of two maize (corn) chromosomes with each other, and then to a corresponding segment of rice, project scientists reconstructed a genetic history replete with "reconfiguration and reshuffling, reminiscent of working with Lego blocks," Messing said.

Public awareness groups have argued that genetic engineering of crops deviates from "natural processes" when biotechnologists insert genes at seemingly random places, altering the normal order of genes in the genome. The view of genes being fixed in their position in the genome is largely based on studies in animal genomes. In contrast to those studies, however, the authors show that plant genomes evolved from a far more dynamic structure than previously believed.

Maize dominates domestic agriculture, where approximately 9 billion bushels are produced annually at a value of \$30 billion. Corn is an important dietary staple in much of the third world and a bio-fuel source; rice is the primary dietary staple for more than half the world's population.

Scientists have long known that the number of chromosomes among some plant species has changed over time, with some evolutionary phases showing four, six, eight or more sets. "Maize, for example, began with four sets of chromosomes about five million years ago and eventually trimmed down to the set of two that we see today," Messing said.

With these duplications and reductions, genes in chromosome segments can be lost, replicated or shifted over to other chromosomes, Messing explained. As a consequence, plant genomes today contain rearranged segments and many duplicated regions with corresponding sets of genes. In the maize genome, genes were apparently lost in some parts and new "stuffer" pieces (intervals between genes) inserted so that the corresponding segments became different in size.

The researchers found that about 10 percent of the genes in the maize segments were missing completely in rice, and about 20 percent were in new positions. Within the maize segments, genes appear to be very mobile: 20 to 25 percent have "jumped" to other locations in the genome during the course of evolution. Two-thirds of the original genes from the ancestral four sets of chromosomes have disappeared completely. Corresponding genes wound up in completely different locations within the genome and have likely undergone changes in how they affect biological operations.

"The research, conducted by an international collaboration of scientists, will help scientists and farmers improve these significant crops and gain

new and important insights in the evolution of the grass species in general," Messing said.

"The vast pool of genetic material in plants can be an important resource from which biotechnology can draw genes for insertion into an array of plants, generating unique genomes not achievable by conventional breeding," Messing said. "We could engineer plants to provide a more sustainable, healthy and productive source of food, while reducing the environmental impacts of their cultivation."

Source: Rutgers, the State University of New Jersey

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