

“Genome Archaeology”: Evolutionary Changes of Genome Structures in Plants

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The “Plant Genome Research” group headed by Dr. Klaus Mayer studied effects and consequences of so-called polyploidization events. The fusion of two different genomes, so-called polyploidization, is very common in plants and occurs rather frequently in the course of evolution. The originally diploid set of chromosomes can be multiplied. Organisms with tetraploid, hexaploid or octaploid sets of chromosomes are known. During the course of evolution these are often reduced to a diploid set of chromosomes, a typical ploidy state for e.g. animals. As a consequence of iterative polyploidisation and subsequent reorganisation towards a diploid genome often duplicated regions with corresponding genetic information can be found in the respective genome. This also applies to maize, which emerged from an ancestor with a tetraploid set of chromosomes nearly five million years ago.

The GSF scientists compared corresponding, duplicated regions from two maize chromosomes. These regions were also compared against the corresponding region in the rice genome. They addressed questions about similarities and dissimilarities between the duplicated maize regions on one hand, and between the regions in maize and rice on the other. Unexpected and very dramatic changes in genome structure have been observed. In maize for parts of the investigated regions individual building blocks were lost, in other

regions building blocks were inserted or rearranged. As a consequence, the two corresponding regions are of strikingly different size. However, clear regularities for these changes cannot be determined yet.

Approx. ten per cent of the genes in the investigated maize regions do not have a corresponding gene in the rice genome and additional 20 per cent are found at different locations in the genome. The genes are surprisingly mobile within the maize genome: 20 to 25 per cent have been relocated to a different site. In the investigated regions two thirds of the original genes located on the tetraploid set of chromosomes disappeared.



Duplicated regions in the genome of maize are evolutionary remainders of ancient polyploidisation events. Comparisons of these regions with corresponding regions in rice give important clues towards genome dynamics and plasticity in evolution.



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Thus, due to the remarkable dynamics of polyploidisation and reduplication a high proportion of corresponding genes is located at non-corresponding locations in the genome. Modern plant breeding, which tries to specifically breed plants with certain properties, can make use of this insight. Understanding the sequence of the genetic building blocks and the dynamics and regularities that shape the maize genome will also be of highest importance to sequence and decode the genomes of important cereal plants such as wheat and barley.

Literature:

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