

## Short Communication of Molecular Genetics of Plant Genomes

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### Short Communication

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Plant genomes are described in terms of genome size, gene content, extent of repetitive sequences and duplication events. The plants also possess mitochondrial and chloroplast genomes. Their nuclear genome is that the largest and most complex. Nevertheless, the estimations suggest that ancestral angiosperms had no quite 12,000-14,000 genes. Plant nuclear genomes. Most of the bacteria have a genome that consists of one DNA molecule. So, that the bacteria are ready to grow and divide much faster than eukaryotic cells can. With relevance the genome, viruses are broadly divided into DNA viruses and RNA viruses. The study of the way genes and genetic information are organized within the genome, the methods of collecting and analyzing this information, and the way this organization determines their biological functionality is mentioned as genomics. Plant genomes contain various repetitive sequences and retrovirus-like retro transposons containing long terminal repeats and other retro elements, like long interspersed nuclear elements and short-interspersed nuclear elements. It is widely accepted that 70-80% of flowering plants are the merchandise of a minimum of one polyploidization event. <sup>[1]</sup>

Many economically important plant species, like corn, wheat, potato, and oat are either ancient or newer polyploids, comprising quite one, and in cases like wheat, three different homologous genomes within one species. Duplicated segments also account for a major fraction of the rice genome. The event of molecular markers has allowed for constructing complete genetic maps for many economically important plant species. The genetic variation directly at the DNA level. An arrangement represents the ordering of molecular markers along chromosomes still because the genetic distances, generally expressed as centi morgans, existing between adjacent molecular markers.

The build up of EPRVs in plant genomes and ERVs in animal genomes requires that viral infection and integration occur in cells that contribute to the germ line. The problematic for plants because known DNA viruses are generally excluded from apical meristems, the tissue which supplies rise to germ cells. The para retrovirus giving rise to TEPRVs must be an exception, although it's out of the question to demonstrate this directly because the free virus has never been observed or isolated. This can be problematic for plants because known DNA viruses are generally excluded from apical meristems, the tissue which supplies rise to germ cells. The lifetime of such viruses may be brief on an evolutionary continuance if their tendency to integrate into host chromosomes in germ line cells leads ultimately to host immunity. <sup>[2]</sup>

In plants, there are two interesting samples of EPRVs causing disease. One concerns banana streak virus (BSV), which-together with TEPRVs-provided one in all the primary instances of EPRVs. The strain of tissue culture apparently stimulated recombination. Productive infections probably ensued because the endogenous BSV sequences are present at a coffee copy number within the banana genome and that they aren't significantly mutated. Apparently, the sequences were activated only upon formation of the hybrid genome, perhaps thanks to epigenetic changes, like loss of methylation, within the new genomic background. Endogenous viruses by demethylation in novel environments may well be relevant for xenotransplantation of organs from pigs to humans. <sup>[3]</sup>

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