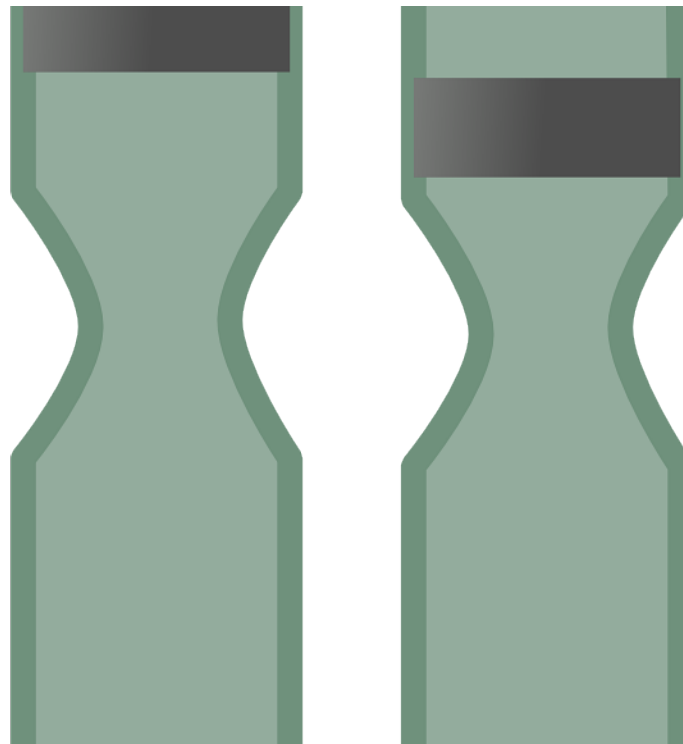


Mobile genetic elements that alter the function of nearby genes

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Raúl Castanera-Andrés, an engineer in the Agri-Food Engineering and Rural Environment Department of the NUP/UPNA-Public University of Navarre, has worked on detecting mobile genetic elements (transposons) in basidiomycete fungi, a type of well-known fungi because they produce edible mushrooms and are active degraders of lignocellulosic

waste.

Transposons are DNA fragments capable of "jumping" from one chromosomal region to another and bringing about permanent changes in the [genome](#). In his study, the researcher has shown that besides causing mutations and reordering in the genome, some transposons can switch off the functioning of the genes in their vicinity, thus silencing the expression of the gene in question and preventing the protein encoded for it from being synthesised.

The famous Central Dogma of Molecular Biology, stated by Francis Crick, establishes that the genetic information stored in the genes is transferred from the DNA to the RNA (a molecule very similar to DNA), which is used as a mould to produce the proteins. "We have seen that when a [transposon](#) is inserted into the vicinity of a gene, the production of its RNA may be altered, and therefore the protein encoded for it may be reduced or even totally eliminated," explained Raúl Castanera. What is more, through a comparative analysis of transcriptomes (the global collection of transcripts of the genes present in the genome of an organism), this mechanism has been seen to be present only in species that have active cytokine methylation machinery.

Impact of transposons on the genome

For many years the importance of transposons has been underestimated due to the fact that they are not part of the genome's encoding region. Yet these elements are highly plentiful in eukaryotic genomes, since they make up about 50% of the [human genome](#) and about 85% of the genome of certain plants, such as maize.

What is more, their mobile nature means that they are essential elements in the evolution of eukaryotic organisms. Although on occasions they may constitute an adaptive advantage, the mutations that these elements

cause on the whole lead to negative consequences for the organism. "In the case of [fungi](#) that produce mushrooms, the multiplication of these elements leads to the degeneration of the variety, which translates into a lack of stability of the cultivated strains, alterations in their growth and decreases in production. On the other hand, basidiomycete fungi produce a huge range of proteins of industrial interest and transposon activity could block the production of these proteins," he pointed out.

Bioinformatic tools

After studying the genome of numerous species, Raúl Castanera developed bioinformatics tools enabling him to identify thousands of transposon insertions and obtain detailed maps of the presence of these elements in over 70 basidiomycete fungi, many of which are of great importance in the biotechnological and agri-food industry.

The information emerging from these maps could be used, among other things, for the molecular typing of fungi or for developing biotechnological tools that allow the function of unknown [genes](#) to be identified.

Finally, during his research he made the annotation of the genome of the lignin-degrading fungus *Coniophora olivacea* and of the genome of the pathogenic grape fungus *Elsinoë ampelina*, the sequencing of which was coordinated by the NUP/UPNA's Genetics and Microbiology Group as part of the international "1000 Fungal Genomes Project."

Provided by Public University of Navarre

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