

PRESS RELEASE

Barcelona, 1st December, 2015

CUT & PASTE IS NOW FOR DNA DARK MATTER TOO

Researchers from the Centre for Genomic Regulation have adapted the most revolutionary genome-editing technique to DNA dark matter, too.

For some time, scientists have been seeking a more efficient and reliable way to edit the genome and modify it to suit any need. A technique called CRISPR-Cas9 was recently launched as the solution to this problem, and has since taken a position as one of the most revolutionary techniques in molecular biology.

Although CRISPR-Cas9 is much more powerful than previous genome editing methods, it still has certain limitations. For example, it is very useful when dealing with genome fragments that code for proteins but, in reality, this covers just 1% of the genome. The remaining 99%, the "dark matter", or what was once known as "junk DNA" still could not benefit from the advantages offered by this revolutionary technique.

Now, researchers at the Centre for Genomic Regulation, led by Rory Johnson, are presenting a new method that makes it possible to use the CRISPR-Cas9 technique on DNA dark matter, too. The method has been presented in an article published in BMC Genomics and is available on an open-access basis for the entire scientific community.

"The method we're proposing expands the use of CRISPR to the DNA dark matter. Broadening the use to the whole genome takes this technique to a new level and allows us to simultaneously explore and edit certain genes that often have regulating functions, more efficiently and economically," say Rory Johnson and Estel Aparicio, the CRG researchers who authored the study. "This will be extremely useful in studies where the goal is to examine the functions of genes located in the dark area (called "long non-coding RNA's") and not only will we be able to "activate" or "deactivate" one gene at a time, we will also be able to manipulate thousands of different genes at the same time," state Johnson and Aparicio.

Much hope has been deposited in the CRISPR technique, and it is now being used in laboratories around the world. Although still being used at a very basic experimental level, it is thought that in the long term it will have major applications not only in the realm of biomedicine to design customized or new cells or treatments, but also for biofuels or agriculture. Thanks to the CRG researchers' proposal, this technique offers even greater possibilities. "We will finally have a method that allows us to easily cut, paste and edit the genome at every level," adds Roderic Guigó, coordinator of the CRG Bioinformatics and Genomics program. "Being able to perform broad-scale experiments and explore this 'dark' region will allow us to advance a great deal in the knowledge of gene expression regulation and therefore, delve further into how to manage the information that makes our cells, organs and tissues as they are and function correctly."

The new methodology will be the basis on which to explore all of the information now available thanks to the projects related with the human genome, and that make genomic data available to researchers. "The 'cut and paste technique will take us from simply reading the genome to understanding its functions and therefore, being able to have an impact on the disease," concludes Dr Johnson.



Reference work:

Estel Aparicio-Prat, Carme Arnan, Ilaria Sala, Núria Bosch, Roderic Guigó and Rory Johnson. "DECKO: Single-oligo, dual-CRISPR deletion of genomic elements including long non-coding RNAs" *BMC Genomics*. 2015 http://dx.doi.org/10.1186/s12864-015-2086-z

Funding:

This work has received the support of the European Union through the European Research Council (ERC) and the Spanish Ministry of Economy and Competitiveness.

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