Neuroblastoma: thus genome editing becomes a weapon against cancer

Neuroblastoma: regions that activate the genes responsible for severe disease discovered in "non-coding" DNA

Another milestone towards understanding neuroblastoma was reached at Ceinge-Advanced Biotechnologies of Naples. Thanks to state-of-the-art genetic engineering, sequencing and bioinformatics techniques, the institute's researchers have identified the regulatory regions that target genes whose impaired functionality is responsible for the greater aggressiveness of one of the children's nervous system tumors. Scholars, led by Mario Capasso and Achille Iolasconprofessors of Medical Genetics of the Department of Molecular Medicine and Medical Biotechnology at Federico II and principal investigator of Ceinge, this time focused on the so-called "non-coding" DNA, in the past erroneously indicated with the contemptuous nickname of "Junk DNA": it is a huge portion of the genome (about 99% of the total) containing particular sequences whose role in determining diseases remains to be discovered.

"We have discovered the regulatory regions of the genome of this pediatric tumor"

"We have studied in particular the regions of the DNA that regulate the transcription of genes, in jargon called" intensifiers "or" enhancers "- explains Capasso – which can be imagined as the volume knob of a radio with which we can increase or decrease the intensity of production of specific genes. We analyzed 25 neuroblastoma cell lines using the ChiP-seq sequencing technique and found the regulatory regions of the genome of this pediatric cancer which for many children remains incurable. Once identified and localized, we went to see if mutations were present in them, this time analyzing over 200 samples, an important number since it is a rare disease. And we actually found it, in a higher quantity than the remaining part of the DNA ».

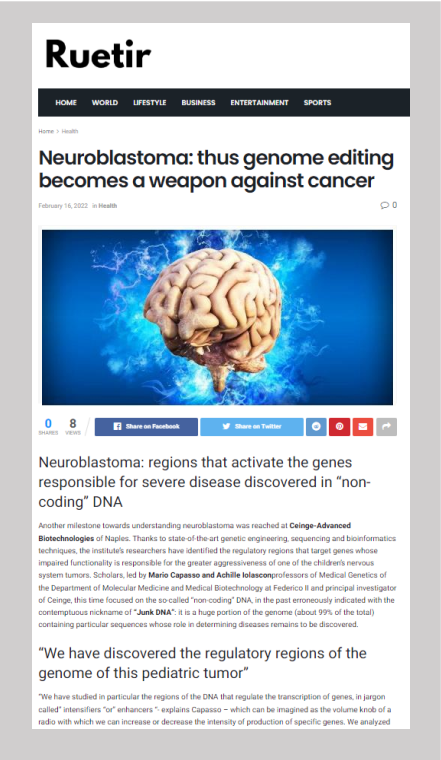
Genome editing and disease prognosis

Researchers have also shown that all of these neuroblastoma genome enhancers, when mutated, are among the causes of a poor prognosis for young patients. The journey through the Non-coding DNA it didn't end here. Using an additional sequencing technique integrated with advanced bioinformatics analysis (HiC data analysis), performed by Dr. Alessandro Vito Lasorsa (bioinformatic expert from Ceinge), the researchers evaluated all the possible interactions of the regulatory regions identified with all the genes known to date and discovered that they interact with just three genes known to play a key role in the development of tumors. And they demonstrated it with in-vitro studies, creating an engineered cell line in the laboratory: «Thanks to a technique of genome editing of the latest generation called CRISPR-Cas9 – clarifies Achille Iolascon– we have confirmed that the mutations affecting the intensifying regions identified regulate precisely the three genes which, together with others, are

involved in embryonic development and in the response of the immune system. Many of these genes are also classified as either therapeutic targets for cancer or as markers of a disastrous prognosis of the disease.

The research was funded by the Airc Foundation for Cancer Research, Open Onlus, the Italian Foundation for the Fight against Neuroblastoma and was published in the high-impact international journal Cancer Research.

Neuroblastoma: thus genome editing becomes a weapon against cancer - Ruetir



Ruetir

HOME WORLD LIFESTYLE BUSINESS ENTERTAINMENT SPORTS

Neuroblastoma: thus genome editing becomes a weapon against cancer

Neuroblastoma: regions that activate the genes responsible for severe disease discovered in "non-coding" DNA

Another milestone towards understanding neuroblastoma was reached at **Ceinge-Advanced Biotechnologies** of Naples. Thanks to state-of-the-art genetic engineering, sequencing and bioinformatics techniques, the institute's researchers have identified the regulatory regions that target genes whose impaired functionality is responsible for the greater aggressiveness of one of the children's nervous system tumors. Scholars, led by **Mario Capasso and Achille Iolascon**professors of Medical Genetics of the Department of Molecular Medicine and Medical Biotechnology at Federico II and principal investigator of Ceinge, this time focused on the so-called "non-coding" DNA, in the past erroneously indicated with the contemptuous nickname of "**Junk DNA**". It is a huge portion of the genome (about 99% of the total) containing particular sequences whose role in determining diseases remains to be discovered.

"We have discovered the regulatory regions of the genome of this pediatric tumor"

"We have studied in particular the regions of the DNA that regulate the transcription of genes, in jargon called" intensifiers "or" enhancers ": explains Capasso – which can be imagined as the volume knob of a radio with which we can increase or decrease the intensity of production of specific genes. We analyzed