BSC participates in the research to decipher how leukaemia's genome works

The IDIBAPS study has been published in the *Nature Medicine* magazine and steps forward into cancer molecular research.

A team of researchers from IDIBAPS show for the first time the complete epigenome of chronic lymphocytic leukaemia, the most common type of leukaemia. The study, published in *Nature Medicine*, provides a high-resolution map of the functions of the genome, which steps forward into cancer molecular research. The comparison of the map for this type of leukaemia with the map of healthy cells shows hundreds of regions that change their functionality in leukaemia which help to understand the illness better and represent potential targets for the development and application of new therapies.

The study has been led by Inaki Martín-Subero, head of the Biomedical Epigenomics research group in IDIBAPS and UB lecturer, also member of the team led by Elias Campo, director of IDIBAPS, research director in Hospital Clínic and professor at the UB. The first signer of the article is Renée Beekman, researcher in the same group.

Over the last years, leukaemia molecular studies-and in other types of cancer- have focused on the molecular analysis with only one data layer, which provided a partial vision and did not allow researchers to create a precise map on the functions of the genome. “This study has no precedents in cancer genomic research and it emphasises the importance of bringing different molecular data layers for a better understanding of the illness”, says Elias Campo.
One of the biggest challenges is the computational analysis of big data. With the collaboration of the Barcelona Supercomputing Center (BSC), researchers could access the necessary high precision calculations to carry out this complex analysis. David Torrents, BSC Computational Genomics group manager and co-author of the paper, explains that BSC contribution has consisted in the genomic analysis, search of mutations and computational resources management.

Renée Beekman says that “the most important challenge we had to face once the data was ready was to analyse and add so many data layers and to distil information that can help us to understand leukaemia better. It’s been three intense years of computer analysis to finally complete the functional map of leukaemia”.

The study was carried out within the context of the European Commission Blueprint for the study of the epigenome and the Spanish Chronic Lymphocytic Leukaemia Genome Consortium, in which a total of 51 researchers from twenty-three different institutions of six different countries have taken part.

Article reference:

The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia.

Further information here.

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Barcelona Supercomputing Center - Centro Nacional de Supercomputación