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Researchers decipher the genome in chronic lymphocytic leukaemia

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A team of researchers from University of Barcelona (UB) and their collaborators report 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. 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, suggesting potential targets for the development and application of new therapies. The study was led by the UB lecturer Iñaki Martín-Subero, head of the Biomedical Epigenomics research group in IDIBAPS.

In recent years, leukaemia and cancer molecular studies have focused on molecular analysis with only one data layer, which 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.

The researchers previously published the sequencing of the genome and methylome in leukaemia. This new study is a complete molecular description of the disease. Using state-of-the-art sequencing techniques and advanced computational biology tools, this study provides a detailed map of the functioning of the leukaemia genome. Iñaki Martín-Subero notes that "knowing the genome sequencing is not enough to know how it works; in order to know its functions and its regulation, we need an analysis with multiple epigenetic layers."

One of the biggest challenges is the computational analysis of big data. With the collaboration of the Barcelona Supercomputing Center, researchers could achieve the high precision calculations needed to carry out this complex analysis. Renée Beekman says, "The most important challenge we had to face once the data was ready was to analyse and add so many data layers and to distill 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."

Researchers identified in detail those areas with specific functions, in particular, the dark areas of the genome, which were previously called junk DNA. They actually have many essential areas for the genome function. Martin-Subero says, "In a similar way to that of a geographical map, where there are urban areas, mountains, rivers, etc., we could completely map the functions of the genome in leukaemia, defining active genes, inactive genes, areas without genes but which control the expression, big inactive deserts in the genome, among others. We identified a total of 12 different functions in the map of the genome."

Apart from studying cells in leukaemia, researchers compared these to healthy cells. Renée Beekman says, "We could see how the leukaemia map changes compared to the healthy cell map, and how leukaemia are able to create an efficient molecular infrastructure to grow with no control. Metaphorically speaking, where there was a desert, there are now industrial areas created by cancer cells."

Iñaki Martín-Subero says, "We even found that only three protein families seem to be in charge of this change. In the lines of that metaphor, it's as if three companies were in charge of building and maintaining all industrial areas." This is an important aspect in the study, since the action of these three families of proteins can be inhibited by drugs which are still under development. In this sense, Elias Campo says, "This may be the most important translational aspect in the study, since

it offers a therapeutic perspective through which functional alterations in leukaemia can be reverted."

"This complete map allows us to understand leukaemia at a molecular level and it also offers a great source of information to other researchers, in order to translate findings into a better treatment and better life quality for the patients," concludes Iñaki Martín-Subero.

More information: Renée Beekman et al. The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia, *Nature Medicine* (2018). DOI: 10.1038/s41591-018-0028-4

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