New advances in the chronic lymphocytic leukaemia genome

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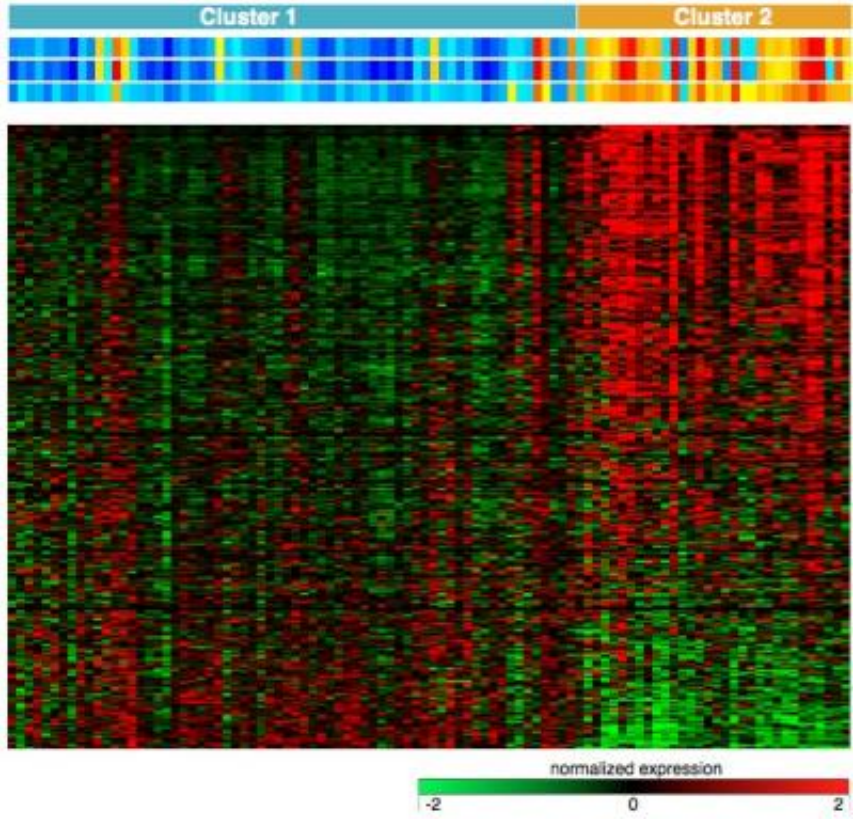

Compared expression of some DE genes and pathways between C1/C2 is shown. Credit: (photo by Núria Lopez)

A study led by Dr. Roderic Guigó from the Centre for Genomic Regulation in Barcelona, as part of the Chronic Lymphatic Leukaemia Genome Consortium, has made new advances in the study of this

disease. The work, which was published (in print version) last week in the journal *Genome Research*, scrutinised the functional profile of the genes and mutations associated with leukaemia.

The Spanish Chronic Lymphatic Leukaemia Genome Consortium had previously identified the principal mutations involved in the development of the disease. However, its functional profile, the activity of these mutated genes, had not been studied. Now, the researchers have sequenced the functional part of the genome of the leukaemia cells, the RNA, and several populations of healthy B lymphocytes from 98 patients.

The scientists found that there are thousands of genes that are expressed in a distinct way in leukaemia cells in comparison to the healthy B lymphocytes, and that their functions are also very different. In particular, in the leukaemia cells many genes are expressed relating to certain metabolic pathways that make them more active.

By observing these differences, the researchers have also clearly identified two subgroups of patients with different disease behaviour, making up one group of patients that do not need treatment for a long time, while others need it more quickly. In addition, they observed that the origin of these two subgroups could be found in the activating signals received by the leukaemia cells in the lymph nodes. "Thanks to the functional study of the genome we have been able to identify two clear subgroups amongst patients and we have confirmed that the aggressiveness of the disease is different in the two groups. Understanding the molecular basis of these two subgroups will enable specific treatments to be established for each of them", says Dr. Guigó.

Provided by Center for Genomic Regulation