Healthy blood stem cells have as many DNA mutations as leukemic cells

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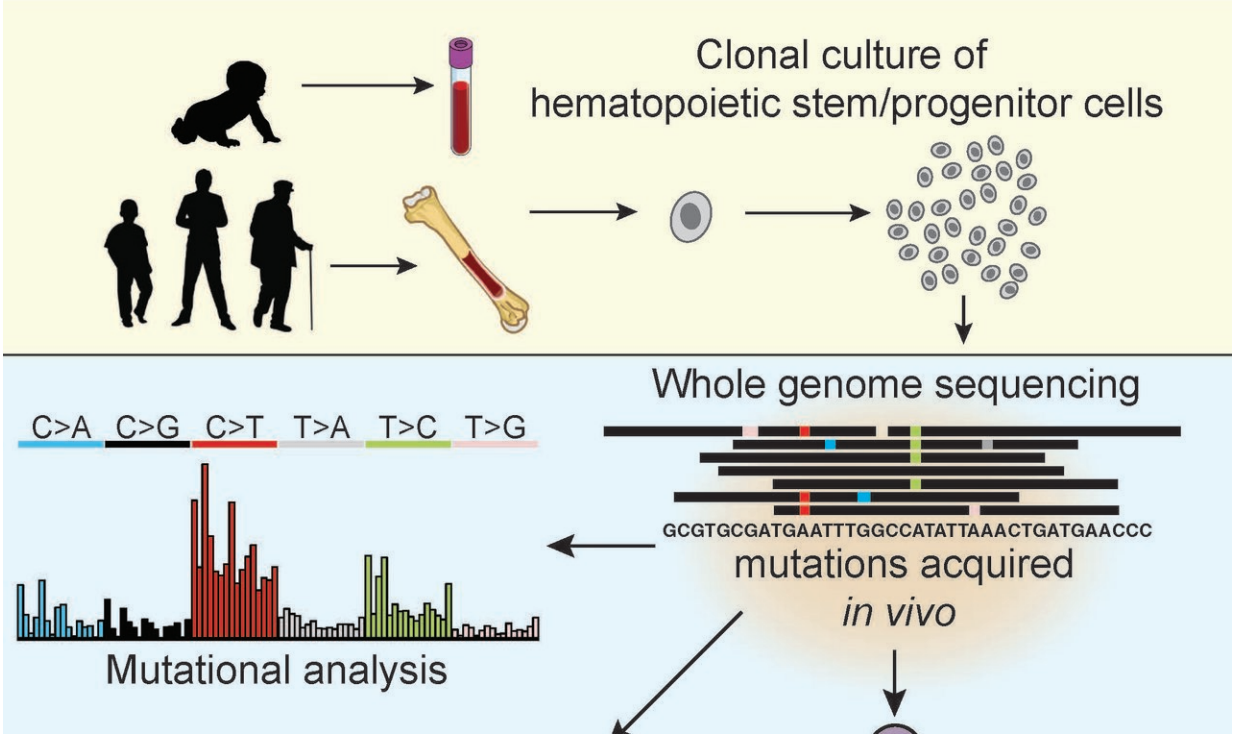

Osorio et al. report lifelong mutationaccumulation in human hematopoieticstem and progenitor cells, which isexplained by three distinct mutationalsignatures. Shared somatic mutationsbetween cells of the same donor enablethe construction of a developmentallineage tree and quantification of eachbranch to mature blood cell populations. Credit: Osorio et al., *Cell Reports*, 2018

Researchers from the Princess Máxima Center for Pediatric Oncology

have shown that the number of mutations in healthy and leukemic blood stem cells does not differ. Rather, the location of DNA mutations is relevant. Using the mutation patterns in hematopoietic stem and progenitor cells (HSPCs), the team was able to trace the developmental lineage tree of the cells.

Van Boxtel, together with his team, studied healthy blood stem cells from seven people of different ages. "Blood stem cells divide about once every 40 weeks," says Van Boxtel, "and we saw that eleven mutations occur during one division." The older the test subject, the more mutations the researchers found, because the mutations accumulate over the years. Yet, these people were healthy.

Nevertheless, mutations in blood stem cells may also lead to leukemia. "We thought that people with leukemia would have more mutations than healthy people," says Van Boxtel, "but this is not the case." The HSPCs of patients with acute myeloid leukemia (AML) contain as many mutations as those from healthy people. The researchers published their results in the open access journal *Cell Reports*.

Developmental lineage tree

The researchers were also able to trace the developmental lineage tree of hematopoiesis using the mutation pattern of HSPCs. "If you study the pattern of mutations of a cancer cell, you can figure out which cell it comes from," explains Van Boxtel. "We have shown this for HSPCs now, but especially for solid tumors, the origin of the cancer cell is relevant for selecting the most effective treatment strategy."

The technique has a lot of potential, according to the authors. The next step for Van Boxtel and his team will be to study the origin of causative mutations in second cancers in survivors of pediatric cancer.

"So far, we assumed that new mutations occur as a result of intensive treatment during childhood and cause second cancers later in life. We can now test whether these mutations are indeed new or already existed and contributed to both incidences of cancer. This is relevant knowledge when making a treatment plan for children with cancer."

More information: Fernando G. Osorio et al, Somatic Mutations Reveal Lineage Relationships and Age-Related Mutagenesis in Human Hematopoiesis, *Cell Reports* (2018). DOI: 10.1016/j.celrep.2018.11.014

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