Website address:
https://www.gesundheitsindustrie-bw.de/en/article/press-release/higher-biological-age-higher-cancer-risk

Higher Biological Age - Higher Cancer Risk

Not only actual chronological age, but also individual aging at the molecular level is a key factor in the development of cancer. This was discovered by scientists at the German Cancer Research Center (DKFZ) and the Saarland Cancer Registry. If the so-called "epigenetic clocks" indicate accelerated biological aging, the likelihood of a cancer diagnosis increases. This finding could help identify at-risk groups and make early detection screenings more targeted

Cancer is considered a typical disease of old age. But which age matters—only the calendar age, or also the individual's biological age? Biological age describes the actual condition of the body at the molecular level and can differ significantly from calendar age. Epigenetic changes in the genome, particularly the attachment of methyl groups to specific DNA building blocks, are considered important markers of biological age. Some methylation patterns are associated with both aging and the development of cancer. Therefore, so-called "epigenetic clocks" based on DNA methylation can be helpful in assessing health risks.

Researchers led by Hermann Brenner at the DKFZ have now investigated how biological age and its changes over time are related to the occurrence of cancer. The goal was to determine what additional value epigenetic clocks can provide for cancer risk prediction.

The study is based on data from over 1,900 participants aged 50 to 75 years in the large population-based ESTHER* cohort. DNA methylation analyses were used to determine the participants' biological age at eight-year intervals and to correlate it with the occurrence of cancer over more than 20 years. The researchers evaluated five different epigenetic clocks, some of which take into account additional lifestyle-dependent parameters in addition to methylation patterns.

More Cancer Cases with Accelerated Biological Aging

At comparable chronological ages, a higher epigenetic age was consistently associated with an increased risk of developing cancer later in life. People who were significantly biologically aged had a more than 50 percent higher risk of cancer than those who remained comparatively young biologically, even at comparable chronological ages. This held true both for the measurement at the start of the study and for the second measurement after an eight-year follow-up period. A clear association was also found when the researchers considered not just a single point in time, but the progression of biological age over an eight-year period: Faster biological aging was associated with an additional increase in cancer risk. The various epigenetic clocks differed slightly in their predictive power.

Improved prediction of long-term cancer risks

The researchers also found that biological age is particularly relevant for improved prediction of long-term cancer risks. Over longer periods (more than eight years after the analysis of DNA methylation in the blood), an even more consistent and stronger association was observed between accelerated epigenetic aging and the incidence of cancer diagnoses.

Potential for personalized cancer prevention

Determining biological age could be used in the future to identify at-risk groups even more effectively and to target early detection screenings more precisely. "Our results show that biological aging processes play a central role in cancer development and can provide additional information about individual risk beyond chronological age," says study leader Hermann Brenner. "The use of epigenetic clocks for risk prediction and risk-adapted cancer screening must now be further investigated in clinical trials."

Publication:

Qiming Yin, Joshua Stevenson-Hoare, Bernd Holleczek, Ben Schöttker, and Hermann Brenner: Epigenetic aging and cancer incidence in a German cohort of older

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Further information

- German Cancer Research Center (DKFZ)