SNPs in C-reactive protein are not associated with increased risk of cancer

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Gene variants associated with increased circulating levels of C-reactive protein, a marker of inflammation, are not associated with an increased risk of cancer, according to a new brief communication published online January 7 in the *Journal of the National Cancer Institute*.

Stig E. Bojesen, M.D., Ph.D., of the Department of Clinical Biochemistry, Herlev Hospital, and Copenhagen University Hospital in Denmark, and colleagues used a Mendelian randomization design to test whether C-reactive protein (CRP) polymorphisms were associated with increased circulating plasma CRP levels and to determine whether this increase was associated with cancer. The study population included about 10,000 participants in a prospective study and about 36,000 in a cross-sectional study of the adult general population of Denmark, all of whom where genotyped for CRP single-nucleotide polymorphisms (SNPs).

The researchers found that variants in the CRP gene were associated with altered plasma levels of CRP but did not find an association between these gene variants and an increased risk of cancer. The authors write that "…although we may be able to exclude CRP per se as a cause of cancer, we cannot exclude the possibility that inflammation could lead to cancer. Also, our results do not invalidate the potential clinical use of slightly increased plasma CRP levels to predict the risk of certain cancer subtypes."

In an accompanying editorial, Paolo Boffetta, M.D., of the International Prevention Research Institute, in Lyon, France, notes: "The study is an elegant example of how genetic variants that have a functional impact can be used to explore associations between environmental factors and disease, and specifically to identify and control for confounding factors, based on the approach that has become known as Mendelian randomization…"

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