

The Aging Cancer Survivor Population

Bluethmann *et al.* _____ Page 1029

Cancer incidence and survival data from the Surveillance, Epidemiology, and End Results (SEER) Program were used by Bluethmann and colleagues to estimate current cancer prevalence. The authors also report cancer projections using U.S. Census Bureau data and the Prevalence Incidence Approach Model. In 2016, there were 15.5 million cancer survivors living in the U.S. and the prevalent population is projected to reach 26.1 million by 2040, with 73% of survivors being 65 years and older. Older adults now constitute the majority of cancer survivors and will continue to dominate the survivor population over the next 24 years.

Circulating Cancer-Associated Macrophages as Biomarkers

Adams *et al.* _____ Page 1037

Circulating cancer-associated macrophage-like cells (CAML) are associated with the presence of solid malignancies. Adams and colleagues measured CAMLs prospectively to ascertain their prevalence, specificity, and sensitivity to breast disease status at clinical presentation. CAMLs were found in 93% of known malignant patients, but none were detected in the healthy controls. In subjects undergoing core biopsy for initial diagnosis, CAMLs were found in 88% of subjects with invasive carcinoma. These preliminary studies suggest that the presence of CAMLs may differentiate patients with malignant disease, benign breast conditions, and healthy individuals.

Telomere Length and Chronic Lymphocytic Leukemia

Ojha *et al.* _____ Page 1043

Chronic lymphocytic leukemia (CLL) is the most common leukemia in the Western world. Shorter mean telomere length in leukemic cells has been associated with more aggressive disease, and polymorphisms in telomere maintenance genes impact telomere length and contribute to CLL susceptibility. Ojha and colleagues used genome data from patients with CLL and healthy control populations and examined eight single nucleotide polymorphisms (SNPs) in genes definitively associated with leukocyte telomere length (LTL). Three of the eight LTL-associated SNPs were associated with CLL risk. The role of telomere length in CLL etiology may be distinct from its role in disease progression.

Selenium/Vitamin E Supplementation, Genotype, and Prostate Cancer

Chan *et al.* _____ Page 1050

Randomized trials supported the hypothesis that selenium and vitamin E lower prostate cancer risk, but the Selenium and Vitamin E Cancer Prevention Trial (SELECT) showed no benefit of either supplement. To investigate if genetic variants involved in selenium or vitamin E metabolism or transport may underlie the complex associations of selenium/vitamin E and prostate cancer, Chan and colleagues undertook a case-cohort study of SELECT participants randomized to placebo, selenium, or vitamin E. This study found statistically significant interactions between selenium assignment, SNPs in *CAT*, *SOD2*, *PRDX6*, *SOD3*, and *TXNRD2*, and high-grade prostate cancer risk, indicating that the effect of selenium or vitamin E supplementation on high-grade prostate cancer risk may vary by genotype.

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Highlights of This Issue

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