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Consortium develops technology to identify genetic and environmental causes of cancers

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Through the development of a novel, inexpensive genotyping microarray, the OncoArray, Dartmouth investigators have led a key collaborative research study that will revolutionize our knowledge of the causes of common cancers.

The OncoArray is comprised of 230,000 single nucleotide polymorphisms (SNPs), each representing a difference in a single DNA building block, or nucleotide. These variations act as biological markers, helping scientists locate genes that are associated with cancer and leading to a better understanding of risk of development and inheritance of disease genes.

One primary difficulty relates to the need to coordinate a consortium that has collected SNP samples and data from throughout the world. To resolve this challenge, Dartmouth researchers, led by Christopher Amos, PhD, Dartmouth Professor and Interim Director of Norris Cotton Cancer Center, formed a consortium of multiple institutions, funded by multiple sources. The consortium has developed approaches for quality control of SNP selection, site selection, and genotyping and ancestry analysis accuracy. "We are seeking to understand the causes of common cancer including genetic and environmental, and their interactions," explains Amos. Details of the consortium's goal and purpose, "The OncoArray Consortium: a Network for Understanding the Genetic Architecture of Common Cancers," were recently published in *Cancer Epidemiology Biomarkers*.

The consortium genotyped 447,705 samples out of a total of 494,763 SNPs that passed quality control steps with a success rate of 97%. Results from these analyses will enable researchers to identify and map new susceptibility loci associated with multiple cancers, assess disease-specific risk, and model genetic, environmental, and lifestyle-related exposures. "The new platform we developed for genotyping was highly successful in allowing us to query over 440,000 people with high accuracy and low cost. This approach will allow us to identify a very large number of new genetic factors influencing cancer risk and to tease apart the roles of environmental factors," explains Amos. "Preliminary studies have identified more than 100 new loci contributing to common cancers including lung, colon, breast, ovarian, and prostate cancers. Additionally, the new technology was applied to studies of glioma, head and neck, and testicular cancers and has provided key insights."

Amos anticipates that several dozen papers will result from consortium analyses. The first of these papers that analyzes susceptibility loci for oral cavity and pharyngeal cancer, has already published this month in Nature Genetics.

More information: C. I. Amos et al, The OncoArray Consortium: a Network for Understanding the Genetic Architecture of Common Cancers, *Cancer Epidemiology Biomarkers & Prevention* (2016). DOI: 10.1158/1055-9965.EPI-16-0106

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