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[Medical] International Consortium Including Taiwan Team Identify Genomic Sites of Breast Cancer Genes
[Medical] International Consortium Including Taiwan Team Identify Genomic Sites of Breast Cancer Genes (Chinese Version)

Academia Sinica Newsletter (2009/07/30) The Breast Cancer Association Consortium (BCAC), an international breast cancer research cooperation which includes a Taiwan team headed by Research Fellow Chen-Yang SHEN from the Institute of Biomedical Sciences, Academia Sinica, recently identified genomic sites which may harbor breast cancer genes. Their findings are a major milestone in cancer research and have recently been published in three major scientific journals: Nature Genetics, the Journal of the National Cancer Institute and Human Molecular Genetics.

Breast cancer is one of the most common cancers in womenand its risk factors strongly suggest that hormonesare involved in the development of the disease. Early onset of menstrual periods, late menopause, and, having no history of pregnancy have been shown to significantly increase the risk of developing breast cancer. However, only one-half of the women who develop the diseasefit into these currently recognized at-risk groups, a fact that has prompted scientists to search for genes that may help increase understanding of the cancer.

In cooperation with surgeons in Taiwan, including Drs. Jyh-Cherng YU and Giu-Cheng HSU from the Tri-Service General Hospital, Dr. Shou-Tung CHEN from the Changhua Christian Hospital, Dr. Chiun-Sheng HUANG from the National Taiwan University Hospital and Dr. Ming-Feng HOU from Kaohsiung Medical University Chung-Ho Memorial Hospital, Dr. Chen-Yang SHEN and colleagues collected up a group of breast cancer patients to form the Taiwan Breast Cancer Study (TWBCS). The TWBCS was invited to join the BCAC in 2006, and participated in research that led to the identification of the first breast cancer gene (FGFR2) on chromosome ten, research that was published in Nature in 2007.

For the current study the team used a recent technical breakthrough, the genome-wide scan (GWS), a powerful gene discovery tool to identify disease genes. They uncovered multiple genomic sites that may harbor breast cancer genes on chromosomes two, three and seventeen. The discoveries could result in new anticancer drug targets and new preventive, therapeutic and diagnostic approaches.

"These findings emphasize the importance of local/international cooperation and long-term bio-banking of human specimens in modern medial research, in order to obtain an ample sample study subjects," said Dr. SHEN. "An ample sample is necessary to obtain consistent research results, by which further developments in cancer prevention and treatment can be achieved," he said.

"On the other hand," he continued, "the comparison of genetic profile between Taiwanese breast cancer and breast cancer in other countries and populations has identified the novelty of our patients."

The researchers emphasize that findings of the current study, based on the GWS, clearly suggest that many factors are involved in causing breast cancer and that both genetic and environmental factors play roles. The GWS approach provides a unique opportunity to comprehensively evaluate the relative importance of individual genes for each person, and may result in significant improvements in the efficacy of population-based programs for the prevention of, and intervention for, breast cancer. This technique may also be applied to other common cancers, and provide clues to understand the formation of common chronic diseases, including hypertension and diabetes.

Selected recent papers using the whole-genome scan to identify breast cancer genes published by the BCAC can be found in the following websites:

http://jnci.oxfordjournals.org/cgi/content/full/101/14/1012
http://www.nature.com/ng/journal/v41/n5/abs/ng.354.html
http://hmg.oxfordjournals.org/cgi/content/full/18/9/1692
http://www.nature.com/nature/journal/v447/n7148/full/nature05887.html

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