EDITORIAL

Cancer Prevention
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RESEARCH ARTICLES

Trends in Lung Cancer and Cigarette Smoking: California Compared to the Rest of the United States
John P. Pierce, Yuyan Shi, Sara B. McMenemy, Tarik Benmarhnia, Dennis R. Trinidad, David R. Strong, Martha M. White, Sheila Kealey, Erik M. Hendrickson, Matthew D. Stone, Sandy Kwong, Xueying Zhang, and Karen Messer

Interventions to Reduce Future Cancer Incidence from Diesel Engine Exhaust: What Might Work?
Renee N. Carey, Lin Fritschi, Timothy R. Driscoll, Susan Peters, Deborah C. Glass, Geza Benke, and Alison Reid

Obesity-associated Breast Inflammation among Hispanic/Latina Breast Cancer Patients

Genome-Wide Meta-analysis of Gene-Environmental Interaction for Insulin Resistance Phenotypes and Breast Cancer Risk in Postmenopausal Women
Su Yon Jung, Nick Mancuso, Herbert Yu, Jeanette Papp, Eric Sobel, and Zuo-Feng Zhang

Evaluation of the Associations Between Cervical Microbiota and HPV Infection, Clearance, and Persistence in Cytologically Normal Women
Wu Ritu, Wu Enqi, Siping Zheng, Jiandong Wang, Yaqin Ling, and Yan Wang

Interaction Between Susceptibility Loci in MAVS and TRAF3 Genes, and High-risk HPV Infection on the Risk of Cervical Precancerous Lesions in Chinese Population
Di Xiao, Dandan Liu, Zihao Wen, Xiuiai Huang, Chengli Zeng, Zixing Zhou, Yajing Han, Xiaohong Ye, Jing Wu, Yao Wang, Congrong Guo, Meiling Ou, Shiqi Huang, Chuican Huang, Xiangcai Wei, Guang Yang, and Chunxia Jing

Acknowledgment to Reviewers

ABOUT THE COVER

HPV infection is very common in sexually active women, and the infecting HPVs can usually be spontaneously eliminated from individuals within 6 to 18 months. Only a small proportion of infected women retain the virus, and this could lead to the development of cervical intraepithelial neoplasia (CIN) and cervical carcinoma. The mechanism by which some individuals develop a persistent HPV infection that goes on to develop into clinically significant disease, however, remains largely unclear. Emerging evidence shows that the cervicovaginal microbiota play a substantial role in the infection and clearance of HPV in the reproductive tract and constitute a new biomarker reservoir to predict the persistence or regression of HPV. The cover shows the cervical communities of cytologically normal women from Beijing, China were classified into 5 community state types (CST) in hierarchical clustering analyses based on the Jensen–Shannon distance matrix and Ward linkage. Each point represents a sample. The CST1 (in red) is dominated by Lactobacillus iners; CST2 (in yellow) by Lactobacillus crispatus; CST3 (in green) by Lactobacillus crispatus, Gardnerella, ADEV, and a variety of Pseudomonas spp. CST4 (in blue) by Gardnerella ADEV, and Lactobacillus iners; and CST5 (in purple) by Salmonella enterica, a variety of Lactobacillus spp., Pseudomonas spp., Prevotella spp., and Streptococcus spp., respectively. See the article by Ritu et al. (beginning on page 43) for more information.

American Association for Cancer Research