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Interaction of CCND1 Genotype and Smoking Habit in Taiwan Lung Cancer Patients

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The *cyclin D1* (*CCND1*) is critical in the transition of cell cycle from G1 to S phase and unbalanced cell cycle regulation is a hallmarker of carcinogenesis. The study aimed at investigating the association of *CCND1* genotypes with lung cancer risk in Taiwan and examining the gene-environment interaction among *CCND1* genotype and smoking habits. The genotype of *CCND1* A870G (rs9344) and C1722G (rs678653) were determined by polymerase chain reaction (PCR) and restriction fragment length polymorphism (RFLP) analysis of DNA from the blood. The study recruited 358 lung cancer patients and 716 cancer free health controls. The results showed that there were significant differences between lung cancer and control groups in the distribution of the genotypes (P=0.0003) and allelic frequency (P=0.0007) in the *CCND1* rs9344 genotype. Individuals who carried AG or GG genotype had 0.59- and 0.52-fold of odds ratio of developing lung cancer compared to those who carried the AA genotype (95%CI=0.44-0.78 and 0.35-0.79, respectively). There was also an obvious interaction of *CCND1* rs9344 genotype with personal smoking habit on lung cancer risk (P=0.0009). These findings support the conclusion that the cell cycle regulation may play a role in lung cancer development and that *CCND1* rs9344 polymorphism together with smoking habit maybe a useful biomarker for lung cancer prediction.

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Association of Caveolin-1 Genotypes with Nasopharyngeal Carcinoma Susceptibility in Taiwan

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Caveolin-1 (*Cav-1*), which has been proposed as a candidate tumor suppressor, plays a regulatory role in several signaling pathways. High expression of *Cav-1* in nasopharyngeal carcinoma (NPC) may enhance tumor cell migration and correlate with poor prognosis of the patients, while the genetic alterations of *Cav-1* during nasopharyngeal carcinogenesis are still largely unknown. The aim of this study was to evaluate the association between NPC susceptibility and *Cav-1* genotypes. One hundred and seventy six patients with NPC and 176 age- and gender-matched healthy controls recruited in Taiwan were genotyped and analyzed by PCR-restriction fragment length polymorphism. There were significant differences between the NPC and control groups in the distributions of the genotypic (P=0.0019) and allelic frequencies (P=2.5*10-4) in the *Cav-1* T29107A (rs7804372) polymorphism. In this first report of *Cav-1* involvement in NPC the A allele of *Cav-1* T29107A is found to be protective against the development of NPC and may be a novel useful genomic marker for early screening and prediction of NPC.

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Association of Alpha B-Crystallin (CRYAB) Genotypes with Breast Cancer Susceptibility in Taiwan

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Alpha B-Crystallin (CRYAB) is purported to be a metastasis suppressor protein, and lack or lower CRYAB expression is a prognostic biomarker for several types of cancer, such as that of the prostate and head and neck. However, the association of genomic variation of *CRYAB* and breast cancer is not well studied. The aim of this study was to evaluate the association of polymorphic genotypes of *CRYAB* with breast cancer within a Taiwanese population. In this hospital-based study, 1232 patients with breast cancer and an equal number of healthy controls in central Taiwan were genotyped via polymerase chain reaction and restriction fragment length polymorphism (PCR-RFLP) and the association of *CRYAB* A-1215G (rs2228387), C-802G (rs14133) and intron 2 (rs2070894) polymorphisms with breast cancer risk in a central Taiwanese population was investigated. Those individuals with *CRYAB* C-802G CG and GG genotypes had 1.50- and 2.22-fold risk for breast cancer than those with the CC genotype. As for the A-1215G and intron 2 polymorphisms, there was no significant association of the genotype with breast cancer risk. In allelic frequency analysis, the G allele *CRYAB* C-802G conferred a significantly (P=5.63×10-10) increased risk of breast cancer. Our results provide evidence that the G allele of *CRYAB* C-802G is correlated with breast cancer risk and this polymorphism may be a useful marker for early detection of breast cancer in clinical practice.