Null Results in Brief

Lack of Association between CCND1 G870A Polymorphism and Risk of Esophageal Squamous Cell Carcinoma

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Introduction

ESCC, like most malignant tumors, is primarily a consequence of abnormal cell proliferation induced by uncontrolled cell cycle. Cyclin D1 plays an important role in the transition from G1 to S phase of the cell cycle and has oncogenic properties. Overexpression of this protein is thought to be related to the development of a variety of tumors, including ESCC (1). The gene encoding cyclin D1, CCND1, has a common G870A polymorphism at codon 242 in exon 4 that increases the frequency of alternate splicing, leading to an altered protein (2). The altered cyclin D1 does not contain the sequences involved in protein turnover and, thus, may have a longer acting half-life. It has been suggested that this polymorphism in the CCND1 gene confers susceptibility to certain cancers (3–5).

In this study, we analyzed DNA samples from a hospital-based case-control study in a Chinese population to test the hypothesis that the CCND1 G870A polymorphism may be a genetic risk modifier for ESCC.

Materials and Methods

This study included 321 patients with ESCC and 345 age- and gender-matched healthy controls. Patients were consecutively recruited from January 1998 to December 2000 at the Cancer Hospital, Chinese Academy of Medical Sciences (Beijing, China). Population controls were accrued from a database of nutritional survey conducted in the same regions. Most of the cases and controls have been characterized in a molecular epidemiological study described elsewhere (6). The CCND1 G870A genotypes were determined by PCR-restriction fragment length polymorphism method as described previously (4). The ORs and their 95% CIs were calculated by logistic regression model with the genotype confers susceptibility to certain cancers (3–5).

In the need for additional studies on polygene analysis.

Results and Discussion

The allele frequencies, among controls and 0.457 and 0.543,

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Cases (n = 321)</th>
<th>OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>GG</td>
<td>68 (21.2)</td>
<td>1.00</td>
</tr>
<tr>
<td>GA</td>
<td>157 (48.9)</td>
<td>0.80 (0.53–1.21)</td>
</tr>
<tr>
<td>AA</td>
<td>96 (29.9)</td>
<td>0.80 (0.51–1.25)</td>
</tr>
</tbody>
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References

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