Relationship between viral factors, axillary lymph node status and survival in breast cancer

許淳森

Tsai JH;Hsu CS;Tsai CH;Su JM;Liu YT;Cheng MH;Wei JC;Chen FL;Yang CC

摘要

Abstract

Purpose　Our previous study based on the results of polymerase chain reaction and Southern hybridization for the detection of Human papilloma virus (HPV), Cytomegalovirus (CMV), Epstein-Barr virus (EBV), Herpes simplex virus (HSV)-1, HSV-2, and Human herpesvirus (HHV)-8 DNA in non-familial breast cancer patients suggest that the viruses associated with breast cancer are HHV-8 > EBV ($P < 0.01$). Therefore, efforts were made to further investigate the association between breast cancer with nodal status and viral infections.

Methods　Sixty-two breast cancer patients and their mammary specimens were enrolled in this retrospective study. The presence of these six potential oncogenic viruses was analyzed to establish the relationship between nodal status and treatment outcome. Statistical analyses were used for the assessment of variables, including viral positivity and clinical feature.

Results　Viral positivity was not significantly different comparing node-positive and node-negative patients ($P > 0.05$). When the viral factors were not entered for statistical analyses, no variable was significantly related to overall survival. However, tumor stage, tumor size, nodal status , and estrogen receptor were significantly related to relapse-free survival ($P < 0.05$). For viral factors, the number of infecting viruses is related to the overall and relapse-free survivals. Only when V0 or V(0, 1) was grouped for comparison with other multiply virus-infected subgroups, were the overall and relapse-free survivals significantly different ($P < 0.005$ or $P < 0.001$). The results suggest that HSV-1, HHV-8, EBV, CMV, and HPV were related to overall survival, however, only HHV-8 and CMV were related to relapse-free survival ($P < 0.05$ or $P < 0.01$).

Conclusion　Virus factor is significantly related to human breast cancer, not only in terms of the oncogenetic process, but also in overall and relapse-free survivals.