INTRODUCTION

Oral cavity squamous cell carcinoma (OCSCC) is the eighth most common cancer worldwide, accounting for 2% of the overall incident cases of cancer.1 Although this malignancy is a serious problem in many parts of the globe, its incidence is much higher in countries with a high rate of alcohol and/or tobacco use.2,3

Distant metastasis (DM) from OSCC portends a dismal prognosis, with the chance of a 5-year disease-free survival probability of 17% or less.4 And, in many cases, patients have been previously identified as having metastatic disease when first seen by medical professionals.5 However, clinicians often have difficulty determining whether a patient has disease progression or not.6

Therefore, successfully identifying patients with DM is critical for determining treatment options.7 More specifically, the survival of patients with OSCC is affected by the presence of distant metastasis, which is the primary cause of death in OSCC patients.8 The presence of DM at the time of diagnosis is a significant predictor of poor survival outcomes.9

METHODS AND MATERIALS

Study population and design

A study protocol was approved by the Institutional Review Board of the Chang Gung Memorial Hospital (99-01128) and all provided written informed consent to take part in the study. The study protocol was reviewed by the institutional review board of the Taiwan Oral Oncology Research Group. The study was conducted in accordance with the Declaration of Helsinki and approved by the institutional review board of the Hospital.

HPV genotyping

DNA was extracted from paraffin-embedded tumor samples as previously described.10 HPV DNA was amplified with MY09/11borinated GP5+ primers which target the L1 region. In positive cases, the HPV L1 gene was genotyped using an HPV kit (EzyChipE; King Lab Co., Ltd., Taiwan) that can differentiate between 37 HPV types.

HPV viral load

HPV-16 and HPV-18 viral loads were quantified using real-time qPCR. All of the reactions were performed in duplicate on a 7300 Real-Time PCR System (Applied Biosystems, Foster City, CA). To evaluate HPV viral loads, frozen tumor tissues were ground using a tissue homogenizer, and the resulting tissue lysates were analyzed using the qPCR method. The qPCR method was used to determine the viral load of the sample.

HPV viral load was determined to be positive if the viral load was ≥ 1.0E5 genome copies per mL.

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