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Multigenic prognosis assessment model for nasopharyngeal carcinoma via a modified meta-analysis approach

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Abstract

Objectives: Currently, clinically relevant multigene-based prognostic assessment models for nasopharyngeal carcinoma (NPC) are limited. This paper reports a novel NPC prognosis assessment model based on multiple established NPC-associated biomarkers.

Methods: We used a modified meta-analysis approach to retrieve eligible studies and analyse the data. Different prognostic biomarkers and hazard ratios (HRs) with 95 % confidence intervals (CIs) of overall survival (OS) data were extracted and tabulated from eligible studies. We then used the formula based on Parmar et al. to determine OS (expressed as HR with 95 % CI). Prognosis assessment risk scores assigned to the logarithm of HR were the basis for interpreting the multigene prognosis assessment model. Finally, we explained the biological significance of this model using a multigenic NPC oncogenesis network system.

Results: We constructed a multigenic NPC prognosis assessment model consisting of 10 prognostic biomarkers to determine the OS rate in NPC patients. Based on the biomarkers' expression patterns, the model could determine 1,023 possible OS rates of NPC patients. The risk score derived determines the prognosis status of the NPC patients. The higher the total risk assessment score, the poorer the prognosis. An NPC-associated network involving all ten biomarkers was also derived.

Conclusions: We provided a novel multigenic NPC prognosis assessment model comprising ten prognostic biomarkers on OS rate in NPC patients. A conceptual molecular-based pathophysiological network of NPC oncogenesis supported the biological relevance of this model.

Keywords: biomarkers; gene expression; nasopharyngeal carcinoma; overall survival rate; prognosis.

Introduction

Nasopharyngeal carcinoma (NPC) is a malignancy that originates from the epithelial tissue at the upper section of the pharynx behind the nose [1]. Although rare in North America and Europe, it is prevalent in certain parts of Asia, particularly in Southeast Asia [2]. Based on the World Health Organization (WHO), there are three histological subtypes of NPC. Type I and Type II/Type 2a constitute the keratinizing and non-keratinizing differentiated squamous cell carcinoma, respectively, and Type III/Type 2b is the undifferentiated basaloid squamous cell carcinoma [3]. Type III/2b is linked to Epstein-Barr virus (EBV) infection and is usually chemo-sensitive [3]. Aetiology for NPC includes genetic susceptibility (family history), EBV infection, environmental pollutants, lifestyle and dietary factors [4]. The cancer is often misdiagnosed due to the late presentation of clinical signs and symptoms and has a higher rate of metastasis than other types of head and neck cancer [3]. Early stages of malignancy usually involve the invasion of cancerous cells to surrounding tissue and their metastasis to the cervical lymph nodes [5]. A majority of NPC cases (more than 70 %) are diagnosed at the advanced stage (Stages III and IV) and have a reduced survival rate [6]. The current treatment for NPC is concurrent chemoradiotherapy (CCRT) with or without neo-adjuvant/adjuvant [7]. However, recurrence and metastasis still occur in approximately 9–18 % of NPC patients [8]. Accurate prognosis assessment, thus, represents an urgent aspect of managing NPC patients to monitor and improve treatment response and survival. A multigenic assessment model could achieve this.

Cancers are multigenic problems requiring the knowledge of multiple biomarkers to evaluate/predict treatment outcomes and OS. Currently, there are some NPC prognosis assessment strategies. These include a prognostic nomogram

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