Genome wide profiling in oral squamous cell carcinoma identifies a four genetic marker signature of prognostic significance

Vui King Vincent-Chong1,2, Iman Salashahourifar3, Kar Mun Woo1, Anif Anwar4, Rozaimi Razali5, Ranganath Gudimella6, Zainal Aniff Abdul Rahman1,7, Siti Mazliah Ismail2, Thomas George Kalliankodi1,8, Anand Ramanathan1,2, Wan Mahadzir Wan Mustafa9, Manil Thomas Abraham9, Keng Kiong Tay9, Rosnah Binti Zain1,2*

1 Oral Cancer Research and Coordinating Centre, Faculty of Dentistry, University of Malaya, Kuala Lumpur, Malaysia. 2 Department of Oral and Maxillofacial Clinical Sciences, Faculty of Dentistry, University of Malaya, Kuala Lumpur, Malaysia. 3 Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran. 4 Sengenics Sdn Bhd, High Impact Research (HIR) Building, University of Malaya, Kuala Lumpur, Malaysia. 5 Department of Oral and Maxillofacial Surgery, Hospital Kuala Lumpur, Kuala Lumpur, Malaysia. 6 Department of Oral and Maxillofacial Surgery, Hospital Tengku Ampuan Rahimah, Klang, Selangor Darul Ehsan, Malaysia. 7 Department of Oral Surgery, Hospital Umum Kuching, Kuching, Sarawak, Malaysia.

* rosnahbz12@yahoo.com

Abstract

Background

Cancers of the oral cavity are primarily oral squamous cell carcinomas (OSCCs). Many of the OSCCs present at late stages with an exceptionally poor prognosis. A probable limitation in management of patients with OSCC lies in the insufficient knowledge pertaining to the linkage between copy number alterations in OSCC and oral tumourigenesis thereby resulting in an inability to deliver targeted therapy.

Objectives

The current study aimed to identify copy number alterations (CNAs) in OSCC using array comparative genomic hybridization (array CGH) and to correlate the CNAs with clinico-pathologic parameters and clinical outcomes.

Materials and methods

Using array CGH, genome-wide profiling was performed on 75 OSCCs. Selected genes that were harboured in the frequently amplified and deleted regions were validated using quantitative polymerase chain reaction (qPCR). Thereafter, pathway and network functional analysis were carried out using Ingenuity Pathway Analysis (IPA) software.

Results

Multiple chromosomal regions including 3q, 5p, 7p, 8q, 9p, 10p, 11q were frequently amplified, while 3p and 8p chromosomal regions were frequently deleted. These findings were in