



UNIVERSITI PUTRA MALAYSIA

***EXPRESSION AND ASSOCIATION OF miR-181a AND miR-663 AND
THEIR TARGET GENES IN HEAD AND NECK CANCER***

YAGHMA MASOOD

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By

YAGHMA MASOOD

**Thesis submitted to the School of Graduate Studies, Universiti Putra
Malaysia, in fulfillment of the requirements for the Degree of Doctor of
Philosophy**

February 2018

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To my parents, husband and daughters

For their unconditional love and support

This accomplishment belongs to you all as well

**Abstract of thesis presented to the Senate of Universiti Putra Malaysia
in fulfillment of the requirement for the degree of Doctor of Philosophy**

**EXPRESSION AND ASSOCIATION OF miR-181a AND miR-663 AND
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YAGHMA MASOOD

February 2018

**Chair: Cheah Yoke Kqueen, PhD
Faculty: Medicine and Health Sciences**

Head and neck cancer is the sixth most common malignancy worldwide and the fifth most common cancer in peninsular Malaysia. The over five-year survival rate for patients with HNC is only 40-50% because of distant metastasis, loco-regional recurrences, and secondary primary tumours. miRNAs have been shown to be able to regulate many cellular processes, including proliferation, differentiation, angiogenesis, cell development, etc. There is strong evidence that miRNAs may represent different targets for anticancer therapies. The aberrant expression of human microRNA-181a-2-3p and miR-663 has been implicated in the pathogenesis of various cancers. However, the role of hsa-miR-181a-2-3p and hsa-miR-663 in the pathogenesis of head and neck cancer and its clinical significance are still unclear. This study is the continuation of previous work done by our research group where novel expression of hsa-miR-181a-2-3p was found in head and neck cancer. To check and compare the expression of hsa-miR-181a-2-3p, hsa-miR-663 was selected, which already has established expression in HNC. Therefore, the aim of this study was to search for the molecular targets of hsa-miR-181a -2-3p and hsa-miR-663 and determine their expression and their common predicted targets in HNC. So, it was hypothesised that hsa-miR-181a-2-3p and hsa-miR-663 may play an important role in the progression of head and neck cancer and co-regulate few common targets which lead to the activation of cancer pathways in HNC development. To predict the targets of hsa-miR-181a -2-3p and hsa-miR-663, three different algorithms were used, including TargetScan, miRanda-mirSVR and RNA22 HAS. Two algorithms, TarBase and miRTarBase, were used to identify the validated targets of hsa-miR-181a-5p (a mature product of hsa-miR-181a) and hsa-miR-663. To further narrow down the list of targets identified from the *in silico* analysis, the target genes of hsa-miR-181a-2-3p and hsa-miR-663 were further validated by published literature, before using them in this research project. The web-based Database for Annotation, Visualization and Integrated Discovery tool (DAVID) was used to provide biological functional

interpretation of the validated targets of hsa-miR-181a-5p and hsa-miR-663. A total of 70 formalin-fixed paraffin embedded (FFPE) tissue specimens and 4 fresh frozen (FF) tissue samples from HNC patients (26 stage I, 15 stage II, 11 stage III and 22 stage IV HNC cases), and 12 non-cancerous FF samples were collected from the Peninsular Malaysian population. The expression of these miRNAs and their common predicted targets were determined by doing q-PCR in HNC cell line, non-cancerous samples and HNC samples.

Bioinformatic studies have showed that hsa-miR-181a and hsa-miR-663 might regulate a large number of target genes that are important in the regulation of critical cell processes, such as cell fate, cell survival, metabolism, and cell death. To date, 584 targets of hsa-miR-181a have been validated; and 61 of these targets are cancer genes. In addition, it was identified that 101 targets of hsa-miR-663 have been validated; and 15 of these targets are cancer genes. The precision of predictions by all the algorithms for hsa-miR-181a-2-3p and hsa-miR-663 targets was low. Based on the DAVID and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis, it is concluded that many of these genes are involved in tumorigenesis of various cancers, including HNC. Besides this, the main cancer pathways regulated by hsa-miR-181a and hsa-miR-663 could be PI3K/Akt, MAPK, and Wnt signaling pathways in head and neck cancer. Based on the amalgamation of *in silico* analysis and published literature, nine common predicted targets (ATM, BCL2, BCL2L2, CDKN1A, CDKN1B, DDIT4, p53, p73 and PARP1) of hsa-miR-181a-2-3p and hsa-miR-663 were chosen for further experimental investigation. Moreover, results in this study showed that advanced HNC had a significant higher expression level of hsa-miR-181a-2-3p and hsa-miR-663 than that in early stage of HNC, suggesting that it may have a critical role in tumor metastasis of advanced HNC. It was also found that BCL2 and PARP1 were also upregulated along with upregulation of hsa-miR-181a-2-3p and hsa-miR-663 in HNC compared to that in non-cancerous tissues. However, ATM, CDKN1A, CDKN1B, DDIT4, p53 and p73 expression were inversely correlated with hsa-miR-181a-2-3p and hsa-miR-663 expression.

Taken together, these results suggest that hsa-miR-181a-2-3p and hsa-miR-663 may serve as an oncogene in head and neck cancer. Furthermore, hsa-miR-181a-2-3p and hsa-miR-663 might be used as new biomarkers together with their common predicted targets in the prediction of prognosis of HNC in clinical practice. More functional and mechanistic studies are needed to validate the role of hsa-miR-181a-2-3p and hsa-miR-663 in the development, progression, and metastasis of HNC.

Abstrak tesis yang dikemukakan Kepada Senat Universiti Putra Malaysia
sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

**EKSPRESI DAN HUBUNGKAIT miR-181a DAN miR-663 DENGAN GEN
SASARAN DALAM KANSER KEPALA DAN LEHER**

Oleh

YAGHMA MASOOD

Februari 2018

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Kanser kepala dan leher adalah kanser keenam yang paling biasa di seluruh dunia dan kanser kelima yang paling umum di Semenanjung Malaysia. Kadar survival selama lima tahun untuk pesakit kanser kepala dan leher hanya 40-50% kerana metastasis jauh, kawasan setempat yang berulang, dan tumor utama sekunder. miRNA telah terbukti mampu mengawal selia banyak proses selular, termasuk percambahan, pembezaan, angiogenesi, pembangunan sel, dan lain-lain. Terdapat bukti kukuh bahawa miRNAs boleh mewakili pelbagai sasaran untuk terapi antikanser. Ekspresi tidak normal gene manusia microRNA-181a-2-3p dan miR-663 telah terlibat dalam patogenesis pelbagai kanser. Walau bagaimanapun, peranan hsa-miR-181a-2-3p dan hsa-miR-663 dalam patogenesis kanser kepala dan leher dan kepentingan klinikalnya masih tidak jelas. Kajian ini adalah kesinambungan daripada kajian terdahulu yang dilakukan oleh kumpulan penyelidikan kami di mana ekspresi novel hsa-miR-181a-2-3p didapati dalam kanser kepala dan leher. Untuk menyemak dan membandingkan ekspresi hsa-miR-181a-2-3p, hsa-miR-663 telah dipilih, yang telah pun menyatakan ekspresi dalam kanser kepala dan leher. Oleh itu, matlamat kajian ini adalah untuk mencari sasaran molekul hsa-miR-181a-2-3p dan hsa-miR-663 dan menentukan ekspresi mereka dan sasaran ramalan mereka yang biasa dalam kanser kepala dan leher. Hipotesis kajian ini adalah hsa-miR-181a-2-3p dan hsa-miR-663 mungkin memainkan peranan penting dalam perkembangan kanser kepala dan leher dan mengawal selia beberapa sasaran umum yang membawa kepada pengaktifan laluan kanser dalam pembangunan kanser kepala dan leher.

Untuk menentukan sasaran hsa-miR-181a-2-3p dan hsa-miR-663, tiga algoritma yang berbeza iaitu Target Scan, miRanda-mirSVR dan RNA22 HAS telah digunakan. Dua algoritma iaitu TarBase dan miRTarBase digunakan untuk mengenalpasti sasaran-sasaran sah hsa-miR-181a-2-3p

(produk matang hsa-miR-181a) dan hsa-miR-663. Untuk mengecilkan senarai sasaran yang dikenalpasti daripada analisis *in silico*, gen-gen sasaran hsa-miR-181a-2-3p dan hsa-miR-663 telah disahkan menggunakan kajian-kajian terdahulu sebelum digunakan dalam kajian ini. Aplikasi web “Database for Annotation, Visualization and Integrated Discovery (DAVID)” telah digunakan untuk terjemahan fungsi biologi sasaran-sasaran sah hsa-miR-181a-2-3p dan hsa-miR-663. Tujuh puluh spesimen tisu dan 4 sampel tisu segar beku daripada pesakit HNC (26 peringkat I, 15 peringkat II, 11 peringkat III dan 22 peringkat IV kes-kes HNC), dan 12 sampel bukan kanser telah dikumpul daripada populasi di Semenanjung Malaysia. Ekspresi miRNA serta sasaran jangkauan umum mereka telah ditentukan melalui q-PCR untuk barisan sel HNC, sampel HNC serta sampel bukan kanser.

Kajian bioinformatik kami telah menunjukkan bahawa hsa-miR-181a dan hsa-miR-663 mungkin mengawalselia sebahagian besar gen-gen sasaran yang memainkan peranan penting dalam kawalan proses-proses sel kritikal seperti takdir sel, kemandirian sel, metabolisme serta kematian sel. Sehingga kini, 584 sasaran hsa-miR-181a telah disahkan dan 61 daripadanya merupakan gen kanser. Selain itu, kami juga telah mengenalpasti 101 sasaran hsa-miR-663 yang telah disahkan dan 15 daripadanya adalah gen kanser. Ketepatan jangkauan semua algoritma sasaran hsa-miR-181a-2-3p dan hsa-miR-663 adalah rendah. Berdasarkan DAVID dan laluan analisis “Kyoto Encyclopedia of Genes and Genomes (KEGG)”, kebanyakan gen ini terlibat dalam genesis tumor kebanyakan kanser termasuklah HNC. Selain itu, laluan-laluan kanser utama yang dikawalselia oleh hsa-miR-181a dan hsa-miR-663 mungkin merupakan laluan-laluan signal PI3K/Akt, MAPK dan Wnt dalam kanser leher dan kepala. Berdasarkan gabungan analisis *in silico* dan kajian-kajian terdahulu, 9 sasaran jangkauan umum (ATM, BCL2, BCL2L2, Cdkn1a, CDKN1B, DDIT4, p53, p73 dan PARP1) hsa-miR-181a-2-3p dan hsa-miR-663 telah dipilih untuk eksperimen penyelidikan seterusnya. Tambahan pula, keputusan kami menunjukkan HNC yang sudah teruk mempunyai level ekspresi hsa-miR-181a-2-3p dan hsa-miR-663 yang lebih tinggi dan signifikan berbanding HNC di peringkat awal, yang mungkin menunjukkan bahawa ia mungkin memainkan peranan yang penting dalam metastasis barah HNC yang sudah teruk. Kami juga mendapati bahawa BCL2 dan PARP1 juga telah meningkat seiring dengan peningkatan kawalan hsa-miR-181a-2-3p dan hsa-miR-663 dalam HNC berbanding tisu-tisu bukan kanser. Walau bagaimanapun, ekspresi ATM, CDKN1A, CDKN1B, DDIT4, p53 dan p73 mempunyai korrelasi yang berkadar songsang dengan ekspresi hsa-miR-181a-2-3p dan hsa-miR-663.

Apabila digabungkan, keputusan-keputusan ini mencadangkan bahawa hsa-miR-181a-2-3p dan hsa-miR-663 mungkin berfungsi sebagai gen kanser dalam kanser leher dan kepala. Selain itu, hsa-miR-181a-2-3p dan hsa-miR-663 serta sasaran-sasaran jangkauan umum mereka mungkin akan digunakan sebagai penanda biologi dalam menentukan nasib HNC dalam bidang klinikal. Kajian-kajian fungsi dan mekanisme perlu dilakukan lebih lagi

untuk mengesahkan fungsi hsa-miR-181a-2-3p dan hsa-miR-663 dalam penghasilan, kemajuan, dan metastasis HNC.



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I certify that a Thesis Examination Committee has met on 20 February 2018 to conduct the final examination of Yaghma Masood on her thesis entitled "Expression and Association of miR-181a and miR- 663 and their Target Genes in Head and Neck Cancer" in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Doctor of Philosophy.

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LIST OF ABBREVIATIONS/ANNOTATIONS

Abbreviations

ATM	Ataxia Telangiectasia Mutated
AMOs	Anti-mirnaoligonucleotides
ACTB	Cyclophilin, Actin Beta
ANOVA	One-Way Analysis of Variance
ASOs	Antisense Oligonucleotides
BLAST	Basic Local Alignment Search Tool
BCL2	B-Cell Lymphoma 2
BCL2L2	Bcl2 Like 2
CDKN1A	Cyclin Dependent Kinase Inhibitor 1A
CDKN1B	Cyclin Dependent Kinase Inhibitor 1B
Ct	Threshold Cycle
cDNA	Complementary DNA
CO ₂	Carbon Dioxide
CLASH	Cross-Linking, Ligation and Sequencing Hybrids
DDIT4	DNA Damage-Inducible Transcript 4
DNA	Deoxyribonucleic Acid
dsDNA	Double Stranded Deoxyribonucleic Acid
DAVID	Database for Annotation Visualization and Integrated Discovery
DMSO	Dimethyl Sulfoxide
DMEM	Dulbecco's Modified Eagle's Medium
EMT	Epithelial Mesenchymal Transition
FF	Fresh Frozen
FFPE	Formalin Fixed Paraffin Embedded
FBS	Fetal Bovine Serum
FASTA	Fast Adaptive Shrinkage Thresholding Algorithm
GAPDH	Glyceraldehyde- 3-Phosphate Dehydrogenase
GO	Gene Ontology
HNC	Head and Neck Cancer
HPV	Human Papilloma Virus
hsa-miRNA	Human microRNA
HNSCC	Head and Neck Squamous Cell Carcinoma
ISH	In Situ Hybridisation
JAK/STAT	Janus Kinase/Signal Transducer and Activator of Transcription
JNK	c-Jun NH ₂ -terminal Kinase
KEGG	Kyoto Encyclopedia of Genes and Genomes Pathways
LNA	Locked Nucleic Acid
T _a	Annealing Temperature
MAPK	Mitogen Activated Protein Kinase
mRNA	Messenger Ribonucleic Acid
miRNA	MicroRNA
ncRNA	Non-Coding RNA
NCBI	National Centre for Biotechnology Information
NGS	Next Gene Sequencing
OC	Oral Cancer

ORF	Open Reading Frame
PTEN	Phosphatase and Tensin Homolog
PI3K/AKT	Phosphoinositide 3-kinase/Protein kinase B
pre-miRNA	Precursor miRNA
Pri-miRNA	Primary miRNA
PCR	Polymerase Chain Reaction
piRNA	Piwi-Interacting RNA
PAR-CLIP	Photoactivatable Ribonucleoside-Enhanced Crosslinking and Immunoprecipitation
PARP1	Poly(Adp-Ribose) Polymerase 1
p53	Tumor Protein p53
p73	Tumor Protein p73
q-PCR	Real Time Quantitative PCR
RNA	Ribonucleic Acid
RT-PCR	Reverse Transcriptase Polymerase Chain Reaction
RISC	RNA-Induced Silencing Complex
RNAi	RNA-Mediated Interference
RNase	Ribonuclease
SACC	Salivary Adenoid Cystic Carcinoma
snoRNA	Small Nucleolar RNA
SCC	Squamous Cell Carcinoma
SNP	Single Nucleotide Polymorphisms
SD	Standard Deviation
UTR	Untranslated Region
UDSP	Universal Degenerate Specific Primer
VEGF	Vascular Endothelial Growth Factor

Annotations

%	Percentage
Δ	Delta
°C	Degree Celsius
μl	Micro Liter
μm	Micrometer
cm	Centimeter
mg	Milligram
ml	Milliliter
mm	Millimeter
mM	MicroMolar
ng/μl	Nanogram/micro Liter
μg	Microgram
μM	MicroMolar

CHAPTER 1

INTRODUCTION

1.1 Introduction

Head and neck cancer (HNC) constitutes cancers that arise most often from the oral cavity, larynx, and oropharynx. It is the sixth most common malignancy worldwide, representing a major international health problem (Harris et al., 2012) and accounts for 650,000 new cases annually (Siegel, Naishadham, & Jemal, 2012). In South-Central Asia, HNC is the second most common cancer (Ferlay et al., 2010). It is the fifth most common cancer among the Peninsular Malaysian population. In 2006, nearly 3000 cases of head and neck cancers were reported in Peninsular Malaysia. Malaysia is a multiracial country, consisting of three major types of ethnicities; Malay, Chinese, and Indian. Prevalence of head and neck cancers in Malaysia varies according to these three major types of ethnicities; oral, laryngeal and pharyngeal cancers are more common in Indians, followed by Malays, and Chinese. On the other hand, nasopharyngeal cancer is most common among the Chinese followed by the Malays, and Indians (Razak, Saddki, Naing, & Abdullah, 2009).

Tobacco and alcohol consumption have been identified as important causes of head and neck cancer (Hashibe et al., 2007; Hashibe et al., 2009). Furthermore, studies have also reported that genetic factors, including family history and genetic variants, in multiple biological pathways, were involved in the development of HNC (Geisler & Olshan, 2001). Furthermore, in South-Central Asia, approximately 90% of HNC cases are attributable to the use of tobacco in various unrecorded forms, habitual chewing of Betel quid/ areca nut, and excessive alcohol drinking. It is the second leading cause of cancer death among males in South-Central Asia (Ferlay et al., 2010). In recent years, the demographics of the disease are moving to non-smoking younger men and women (Jakymiw et al., 2010; P. E. Petersen, 2009).

Despite considerable advances in multimodality therapy, including surgery, radiotherapy and chemotherapy, the major problem is that the overall five-year survival rate for patients with HNC is only 40-50% (J. Y. Chan & Wei, 2013; Takes et al., 2012). This has remained relatively unchanged over the past 3 to 4 decades because of distant metastasis, loco-regional recurrences and secondary primary tumours (Leemans, Braakhuis, & Brakenhoff, 2011). However, the exact mechanism of developing HNC has not been fully explored. Better understanding of the molecular mechanisms underlying invasion and metastasis is urgently needed to improve the diagnosis, approaches to therapy, and prevention of HNC (Kinoshita, Nohata, Fuse, et al., 2012).

Head and neck cancer is a heterogeneous group of cancer. The heterogeneity of this cancer is increased by the growing rate of human papillomavirus (HPV)-associated tumour (Beck & Golemis, 2016). Studies have emphasised that HNC molecular heterogeneity are based on many factors like, methylation profiles, mutated genes, miRNA expression which may represent new targets for cancer therapies (Pezzuto et al., 2015) .

MicroRNAs (miRNAs) have been shown to play vital roles in various biological and pathological processes (Jackson & Standart, 2007). These functions include growth, invasion, angiogenesis, proliferation, and differentiation (Bartel, 2004; R. C. Lee, Feinbaum, & Ambros, 1993). Growing evidences suggest that miRNA play important roles in the initiation, development, metastasis and prognosis of human cancers including HNC (Guo et al., 2012; Jakymiw et al., 2010). miRNAs are small endogenous nonprotein-coding single stranded RNA molecules with an average length of 19–25 nucleotides (Esquela-Kerscher & Slack, 2006). They function by regulating the genes expression at the transcriptional or posttranscriptional level via binding 3' UTR of mRNA. The regulation of the genes is done either by suppressing the translation of protein coding genes or by degrading the mRNAs (Bartel, 2004; Kutter & Svoboda, 2008). A single miRNA can bind and regulate as many as 200 protein coding genes, often encoding proteins with related functions. On the other hand, many miRNAs could bind to a single gene promote (Nohata, Hanazawa, Kinoshita, Okamoto, & Seki, 2013). Some down regulated miRNAs could function as tumor suppressors by negatively regulating oncogenes whereas upregulated miRNAs could function as oncogenes by repressing tumor suppressors. This upregulation and downregulation of miRNAs have been shown to contribute to cancer development (Esquela-Kerscher & Slack, 2006).that a number of studies have reported the effect of miRNAs in the pathogenesis of cancers including HNC. Remarkably, miRNAs act as a valuable tool in therapeutics, diagnostics and prognostics in many types of cancer. There is strong evidence that miRNAs may also represent different targets for anticancer therapies. The aberrant expression of human miR-181a-2-3p and miR-663 has been implicated in the pathogenesis of various cancers. They either serve as an oncogene or a tumor suppressor in the pathogenesis of many cancers. A systematic search of the literature revealed that only one research was done on hsa-miR-181a-2-3p in head and neck cancer. Only two studies have shown expression of hsa-miR-663 in nasopharyngeal carcinoma. Limited work has been done on hsa-miR-181a-2-3p and hsa-miR-663 in the pathogenesis of HNC; and their clinical significance is still unclear. Moreover, this study is the continuation of previous work done by our research group where novel expression of hsa-miR-181a-2-3p was found in head and neck cancer. To check and compare the expression of hsa-miR-181a-2-3p, hsa-miR-663 was selected, which already has established expression in HNC.

1.1.1 Problem Statement

Head and neck cancer is the sixth most common malignancy worldwide and the fifth most common cancer in peninsular Malaysia. The over five-year survival rate for patients with HNC is only 40-50% because of distant metastasis, loco-regional recurrences and secondary primary tumours. MiRNAs have been shown to be able to regulate many cellular processes, including proliferation, differentiation, angiogenesis, cell development, etc. There is a strong evidence that miRNAs may represent different targets for anticancer therapies. The aberrant expression of human miR-181a-2-3p and miR-663 has been implicated in the pathogenesis of various cancers. The role of hsa-miR-181a-2-3p and hsa-miR-663 in the pathogenesis of HNC is yet to be investigated upon. Therefore, it is important to address the following hypothesis and objectives.

1.1.2 Hypothesis

It was hypothesised that hsa-miR-181a-2-3p and hsa-miR-663 may play an important role in the progression of head and neck cancer and co-regulate few common targets which lead to the activation of cancer pathways in HNC development.

1.1.3 Aim

The aim of this study was to search for the molecular targets of hsa-miR-181a -2-3p and hsa-miR-663 and determine their expression and their common predicted targets in HNC.

1.1.4 Specific Objectives

The specific objectives of this study were to:

- 1) identify the predicted target genes of hsa-miR-181a-2-3p and hsa-miR-663 in HNC by using three different computational algorithms for miRNA target prediction;
- 2) identify the validated target genes of hsa-miR-181a-5p and hsa-miR-663, and their predicted cancer pathways (using DIANA) involved in the progression and development of HNC;
- 3) validate the role of hsa-miR-181a-2-3p and hsa-miR-663 and their selected common predicted targets in human HNC cell line and tissues; and
- 4) investigate the association between expression of miRNAs (hsa-miR-

181a-2-3p and hsa-miR-663), their selective common predicted targets, and clinopathological factors in HNC.

To address the above hypothesis and objectives, the HNC samples were obtained from Malaysian human population. The current study will provide a better understanding of the effect of hsa-miR-181a-2-3p and hsa-miR-663, and their selective common predicted targets in the progression and development of HNC. Hence, the study may contribute to a better accuracy in diagnosis, prognosis, and improving decision making by oncologists in the treatment of HNC patients.



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BIODATA OF STUDENT

Yaghma Masood was born in Rampur, India. She was the second child from four siblings. She had primary and secondary education from Abdullah Girls' Senior Secondary School, Aligarh, India. Yaghma Masood is a Dentist and a lecturer at the Department of Dentistry and Oral Health, La Trobe University, Australia. She was graduated with first class in Bachelor of Dental Surgery from Aligarh Muslim University, Aligarh, India in 2005. She received her master's degree with merit in Experimental Oral Pathology in 2007 from Barts and the London, Queen Mary University of London, UK. In 2008, she joined Universiti Teknologi MARA as a Lecturer. Due to her strong interest in research, she continued her further studies for PhD. In 2013, She enrolled in Doctor of Philosophy program at Faculty of Medicine and Health Sciences, Universiti Putra Malaysia. Her research focus in PhD was on the role of microRNAs in head and Neck Cancer. During her candidature, she published one article as first author at international level with impact factor 2.249. She has submitted two more articles for publication. Her other research interests include oral cancer, dental caries and oral health related quality of life. Yaghma is a co-investigator for three research grants for the research projects on oral cancer, dental caries and oral health related quality of life. She has published more than 15 peer reviewed journal articles and book chapters, many of which are in leading journals. He is also a reviewer for many reputed journals including Angle Orthodontics.

LIST OF PUBLICATION

Published Articles

Masood Y., Kqueen CY., Rajadurai P. Role of miRNA in Head and Neck Squamous Cell Carcinoma. 2014. Expert Review of Anticancer Therapy, 2014; 1-15. (ISI Impact Factor 2.279).

Articles with Prepared Manuscript and under Submission

Masood Y., Mohtarrudin N., Subha TS., Rajadurai P., Kqueen CY. Hsa-microRNA-181a-2-3p as biomarker for head and neck cancer in patients: a bioinformatic and clinical study and the therapeutic implication.

Masood Y., Mohtarrudin N., Subha TS., Rajadurai P., Kqueen CY. Hsa-microRNA-663 as biomarker for head and neck cancer in patients: a bioinformatic and clinical study and the therapeutic implication.



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