UNIVERSITI TEKNOLOGI MARA

PROTEOMIC PROFILING FOR POTENTIAL BIOMARKERS OF OSTEOSARCOMA PATIENTS

ZULAIKA BINTI ROSLAN

Thesis submitted in fulfilment
of requirements for the degree of
Master of Science

Faculty of Medicine

August 2016

CONFIRMATION BY PANEL OF EXAMINERS

I certify that a Panel of Examiners has met on 21st April 2016 to conduct the final examination of Zulaika Binti Roslan on her Master of Science thesis entitled "Proteomic Profiling for Potential Biomarkers of Osteosarcoma Patients" in accordance with Universiti Teknologi MARA Act 1976 (Akta 173). The Panel of Examiners recommends that the student be awarded the relevant degree. The Panel of Examiners was as follows:

Azian Binti Abdul Latiff
Professor
Faculty of Medicine
Universiti Teknologi MARA
(Chairman)

Zulkhairi Hj. Amom
Professor
Faculty of Health Sciences
Universiti Teknologi MARA
(Internal Examiner)

Mohd Fadzelly Abu Bakar
Associate Professor
Faculty of Science, Technology and Human Development (FSTPi)
Universiti Tun Hussein Onn Malaysia (UTHM)
(External Examiner)

DR MOHAMMAD NAWAWI
DATO' HAJI SEROJI
Dean
Institute of Graduate Studies
Universiti Teknologi MARA
Date: 9th August 2016

ABSTRACT

Osteosarcoma (OS) is a common malignant bone tumour mainly occurs in children and young adults between the ages of 10 to 30 years. Although the advance of technology and improvement in chemotherapy treatment for OS has significantly improved the survival rate in recent years, its poor prognosis and unknown etiology continues to remain the major challenge in managing the disease progression. Therefore, the objectives of this study are to establish the serum protein profile of OS patients, to investigate the differential protein expression in pre and post-chemotherapy and to identify the potential protein biomarkers relevant in OS cell migration. Serum and bone tissues biopsies were collected from healthy volunteers, pre- and post-chemotherapy OS patients. In this study, OS serum protein profile was established using a 4-plex iTRAQ analysis. Approximately 217 proteins with 104,214 spectra were acquired which includes low abundance proteins involved in biological processes and other protein classes. In addition, VCAM-1 was significantly altered ($p<0.05$) and shown to be highly expressed in post-chemotherapy OS serum. VCAM-1 and ICAM-3 expression was then verified using western blot and immunohistochemistry staining to observe their roles in OS cell migrations. To date, this is the first differential protein expression study to use OS patients' serum at different stages for the protein profiling. The comprehensive data on the differentially expressed protein was successfully generated and the comparative study has revealed a significant amount of protein expressed has been significantly altered. This data could provide a new insight on the fundamental OS biological processes and further use as a potential biomarker for better OS prognosis.

ACKNOWLEDGEMENT

Firstly, I wish to thank god for giving me the opportunity to embark on my master and completing it. My gratitude and thanks go to my supervisor Dr. Sharaniza Ab. Rahim, my co-supervisors Dr. Mudiana Muhamad, Assoc. Prof. Dr. Azura Mansor and Dr. Effat Omar. Thank you for your endless supports and encouragement and most importantly your trusts in me. I would also like to express my gratitude to , Prof. Dr. Tunku Kamarulzaman, as the PI of the HIR grant in University Malaya and the staff in Institute for Molecular Medicine and Biotechnology (IMMB) especially En. Yusri Idros for providing their assistances and guidance.

My sincere thanks also goes to my bestfriends miza, shaq, zana, and didi. Without your precious supports and endless nights of coffee sessions, I would not been able to finish this thesis.

Finally, this thesis is dedicated to the loving memory of my late father. His supports and visions in life was what made me who I really am today. I also want to express my special thanks to my mom and family, for enduring this journey together. May Allah bless all of us. Alhamdulillah for this piece of victory.

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