



Somatic copy-neutral loss of heterozygosity and copy number abnormalities in Malaysian sporadic colorectal carcinoma patients

Y.Y. Yam¹, B.P. Hoh^{1,2}, N.H. Othman^{3,4}, S. Hassan⁵, M.M. Yahya⁵,
Z. Zakaria⁵ and R. Ankathil¹

¹Human Genome Centre, School of Medical Sciences,
Universiti Sains Malaysia, Health Campus, Kubang Kerian,
Kelantan, Malaysia

²Institute for Medical Molecular Biotechnology, Faculty of Medicine,
Universiti Teknologi MARA, Sungai Buloh Campus, Selangor, Malaysia

³Clinical Research Platform, Universiti Sains Malaysia, Health Campus,
Kubang Kerian, Kelantan, Malaysia

⁴Department of Pathology, School of Medical Sciences,
Universiti Sains Malaysia, Health Campus, Kubang Kerian,
Kelantan, Malaysia

⁵Department of Surgery, School of Medical Sciences,
Universiti Sains Malaysia, Health Campus, Kubang Kerian,
Kelantan, Malaysia

Corresponding author: R. Ankathil
E-mail: rankathil@hotmail.com

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ABSTRACT. Colorectal cancer is one of the most common cancers in many countries, including Malaysia. The accumulation of genomic alterations is an important feature of colorectal carcinogenesis. A better understanding of the molecular events underlying the stages of colorectal carcinogenesis might be helpful in the detection and management of the disease. We used a commercially available single-nucleotide polymorphism genotyping array to detect both copy number

abnormalities (CNAs) and copy-neutral loss of heterozygosity (LOH) in sporadic colorectal carcinomas. Matched tumor and normal tissues of 13 colorectal carcinomas (Dukes' stages A-D) were analyzed using a 250K single nucleotide polymorphism array. An additional assay was performed to determine the microsatellite instability status by using the National Cancer Institute-recommended BAT-26 panel. In general, copy number gain (92.3%) was most common, followed by copy number loss (53.8%) and copy-neutral LOH (46.2%). Frequent CNAs of gains and losses were observed on chromosomes 7p, 8, 13q, 17p, 18q, and 20q, and copy-neutral LOH was observed on chromosomes 2, 6, 12, 13q, 14q, 17, 20p, 19q, and 22q. Even though genomic alterations are associated with colorectal cancer progression, our results showed that DNA CNAs and copy-neutral LOH do not reflect disease progression in at least 50% tumors. Copy-neutral LOH was observed in both early and advanced tumors, which favors the involvement of these genomic alterations in the early stages of tumor development.

Key words: Sporadic colorectal cancer; Copy number abnormality; Copy-neutral loss of heterozygosity