

Pair-wise comparison analysis of differential expression of mRNAs in early and advanced stage primary colorectal adenocarcinomas

Abstract

Objectives: To characterise the mRNA expression patterns of early and advanced stage colorectal adenocarcinomas of Malaysian patients.

Design: Comparative expression analysis. **Setting and participants:** We performed a combination of annealing control primer (ACP)-based PCR and reverse transcription-quantitative real-time PCR for the identification of differentially expressed genes (DEGs) associated with early and advanced stage primary colorectal tumours. We recruited four paired samples from patients with colorectal cancer (CRC) of Dukes' A and B for the preliminary differential expression study, and a total of 27 paired samples, ranging from CRC stages I to IV, for subsequent confirmatory test. The tumouric samples were obtained from the patients with CRC undergoing curative surgical resection without preoperative chemoradiotherapy. The recruited patients with CRC were newly diagnosed with CRC, and were not associated with any hereditary syndromes, previously diagnosed cancer or positive family history of CRC. The paired non-cancerous tissue specimens were excised from macroscopically normal colonic mucosa distally located from the colorectal tumours. **Primary and secondary outcome measures:** The differential mRNA expression patterns of early and advanced stage colorectal adenocarcinomas compared with macroscopically normal colonic mucosa were characterised by ACP-based PCR and reverse transcription-quantitative real-time PCR.

Results: The RPL35, RPS23 and TIMP1 genes were found to be overexpressed in both early and advanced stage colorectal adenocarcinomas ($p < 0.05$). However, the ARPC2 gene was significantly underexpressed in early colorectal adenocarcinomas, while the advanced stage primary colorectal tumours exhibited an additional overexpression of the C6orf173 gene ($p < 0.05$).

Conclusions: We characterised two distinctive gene expression patterns to aid in the stratification of primary colorectal neoplasms among Malaysian patients with CRC. Further work can be done to assess and compare the mRNA expression levels of these identified DEGs between each CRC stage group, stages I–IV.