Studi Ekspresi Gen hTERT RNA pada Sampel Jaringan Normal dan Kanker Kolorektal Menggunakan Metode Reverse Transcription Quantitative Polymerase Chain Reaction (RT-qPCR) = Study of hTERT RNA Gene Expression in Normal and Colorectal Cancer Tissue Samples using Reverse Transcription Quantitative Polymerase Chain Reaction (RT-qPCR) Method

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Abstrak

Kanker kolorektal merupakan keganasan sel yang tumbuh dari jaringan usus besar, seperti kolon dan rektum. Kasus kanker kolorektal di Indonesia menempati urutan ketiga dengan 12,8 insiden per 100.000 penduduk usia dewasa dan memiliki nilai mortalitas sebesar 9,5% dari seluruh kasus jenis kanker. Lambatnya diagnosis kanker sejak dini dan prognosis yang buruk menyebabkan tingginya mortalitas kanker kolorektal di Indonesia dibandingkan pada beberapa negara maju. Oleh karena itu, diperlukan identifikasi biomarker, seperti deteksi ekspresi RNA yang berfungsi sebagai pemberi informasi genetik dan subjek regulasi transkripsi, untuk memahami jalur pensinyalan karsinogenesis kolorektal dalam meningkatkan prognosis dan prediksi respons terapeutik terhadap pasien. Telomerase Reverse Transcriptase (hTERT) merupakan subunit utama dari enzim telomerase yang memiliki peran dalam menjaga kestabilan kromosom, sehingga mengindikasi adanya pengaruh ekspresi hTERT yang tinggi terhadap perkembangan kanker kolorektal. Penelitian ini menggunakan sampel jaringan normal dan kanker kolorektal yang diperoleh dari pasien pengidap kanker kolorektal dengan nilai ekspresi gen hTERT diperoleh menggunakan reverse transcription-quantitative polymerase chain reaction (RT-qPCR). Nilai Cycle Threshold (CT) diperoleh dan dilakukan analisis statistik menggunakan aplikasi JAMOVI. Berdasarkan rumus ekspresi gen 2-IICT, ekspresi meningkat jika memiliki perhitungan ekspresi <1 dan ekspresi menurun jika memiliki perhitungan ekspresi 1<. Hasil menunjukkan bahwa sebesar 50% pasien pengidap kanker kolorektal mengalami peningkatan ekspresi gen hTERT RNA, sedangkan 50% lainnya mengalami penurunan ekspresi. Peningkatan ekspresi gen hTERT RNA pada jaringan kanker adalah sebesar 18,97 kali lebih tinggi dibandingkan jaringan normal. Namun, berdasarkan analisis statistik, ekspresi hTERT tidak menunjukkan perbedaan yang signifikan antara jaringan normal dan kanker dikarenakan jumlah sampel yang sedikit. ......Colorectal cancer is a malignancy that grows from the tissues of the large intestine, such as the colon and rectum. Colorectal cancer cases in Indonesia ranks third with 12.8 incidents per 100,000 adult population and has a mortality rate of 9.5% of all cancer cases. The delay in early cancer diagnosis and poor prognosis lead to higher colorectal cancer mortality in Indonesia compared to some developed countries. Therefore, it is necessary to identify biomarkers, such as detection of RNA expression that serves as a genetic information provider and transcriptional regulatory subject, to understand the signaling pathways of colorectal carcinogenesis in improving prognosis and predicting therapeutic response in patients. Human Telomerase Reverse Transcriptase (hTERT) is the main subunit of the telomerase enzyme that has a role in maintaining chromosome stability, thus indicating the effect of high hTERT expression on the development of colorectal cancer. This study used normal tissue samples and colorectal cancer obtained from patients with colorectal cancer with hTERT gene expression values ââobtained using reverse transcription-quantitative polymerase chain reaction (RT-qPCR). Cycle Threshold (CT) values ââwere obtained, and statistical analysis was performed using the JAMOVI application. Based on the 2-IICT gene expression formula, the expression increased if it had an expression count <1 and the expression decreased if it had an expression count of 1<. The results showed that 50% of patients with colorectal cancer had an increased expression of the hTERT RNA gene, while the other 50% had decreased expression. The increase in hTERT RNA gene expression in cancer tissue was 18.97 times higher than normal tissue. However, based on statistical analysis, hTERT expression did not show a significant difference between normal and cancer tissues due to the small number of samples.