

## **PERBEDAAN EKSPRESI circBCBM1 MENURUT SUBTIPE MOLEKULER KANKER PAYUDARA METASTASIS JAUH**

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### **ABSTRAK**

**Latar Belakang:** Kanker payudara merupakan kanker dengan insidensi tertinggi di dunia dan penyebab kematian yang signifikan di Indonesia, terutama akibat metastasis. Pemilihan terapi pada pasien dengan metastasis menjadi tantangan karena dipengaruhi juga oleh status reseptor hormon dan ekspresi HER2 yang menjadi penentu subtype kanker payudara, sehingga pengembangan terapi personal menjadi penting saat ini. Circular RNA (circRNA), khususnya circBCBM1, diketahui berperan sebagai onkogen dan berhubungan dengan metastasis kanker payudara. Namun, perbedaan ekspresi circBCBM1 berdasarkan subtype molekuler kanker payudara metastasis masih belum diteliti, padahal subtype kanker payudara juga berperan dalam

perkembangan metastasis. Oleh karena itu, penelitian ini bertujuan menganalisis perbedaan ekspresi circBCBM1 menurut sub tipe kanker payudara metastasis.

**Metode:** Penelitian dilakukan dengan metode potong lintang menggunakan sampel blok parafin dari pasien kanker payudara metastasis di Rumah Sakit Umum Pusat (RSUP) dr. Kariadi tahun 2020 – 2024. Sampel dipilih melalui *consecutive sampling* dan dibagi berdasarkan 3 sub tipe kanker payudara: Luminal, HER-2 *enriched*, dan TNBC, kemudian dihitung ekspresi gen circBCBM1 melalui metode RT-qPCR. Pengolahan data dilakukan dengan analisis bivariat uji ANOVA satu arah.

**Hasil:** Dari 57 sampel, ditemukan bahwa rerata circBCBM1 tertinggi ditemukan pada kelompok TNBC, diikuti oleh sub tipe Luminal dan HER-2 *enriched*. Dari hasil uji circBCBM1 berdasarkan sub tipe kanker payudara metastasis didapatkan nilai  $p = 0,042$  ( $p < 0.05$ ) sehingga ditemukan perbedaan rerata circBCBM1 yang signifikan secara statistik.

**Kesimpulan:** Penelitian ini menemukan perbedaan rerata ekspresi circBCBM1 yang signifikan jika dilihat menurut sub tipe molekuler pasien kanker payudara metastasis jauh. Rerata ekspresi circBCBM1 paling tinggi ditemukan pada kelompok sub tipe TNBC, sejalan dengan sifat TNBC yang paling agresif dibanding sub tipe lainnya.

**Kata kunci:** circBCBM1, sub tipe kanker payudara, metastasis, ekspresi gen, circRNA

## ABSTRACT

**Background:** Breast cancer is one of the most prevalent cancers worldwide and a significant cause of mortality in Indonesia, particularly due to metastasis. Treatment selection in metastatic breast cancer remains challenging as it is influenced by hormone receptor status and HER2 expression, which determine breast cancer molecular subtypes. Therefore, the development of

molecular biomarkers is essential for personalized therapy. Circular RNAs (circRNAs), particularly circBCBM1, are known to function as oncogenes and are associated with breast cancer progression and metastasis. However, the differences in circBCBM1 expression among molecular subtypes of metastatic breast cancer have not been widely investigated, despite the important role of breast cancer subtypes in metastatic progression. Therefore, this study aimed to analyze differences in circBCBM1 expression across molecular subtypes of metastatic breast cancer.

**Methods:** This cross-sectional study used paraffin block specimens from metastatic breast cancer patients at Dr. Kariadi Central General Hospital from 2020 to 2024. Samples were selected using consecutive sampling based on inclusion and exclusion criteria and were classified into three breast cancer subtypes: Luminal, HER2-enriched, and TNBC. The expression of circBCBM1 was calculated by RT-qPCR method. Data were analyzed using bivariate analysis with a one-way ANOVA test.

**Results:** Among the 57 samples included in this study, the highest mean circBCBM1 expression was found in the TNBC group, followed by the Luminal and HER2-enriched subtypes. Analysis of circBCBM1 expression differences among metastatic breast cancer subtypes showed a  $p$ -value = 0.042 ( $p < 0.05$ ), indicating a statistically significant difference in mean circBCBM1 expression among the three breast cancer subtypes.

**Conclusion:** This study demonstrated a significant difference in mean circBCBM1 expression according to the molecular subtype of metastatic breast cancer patients. The highest mean circBCBM1 expression was observed in the TNBC subtype, consistent with the more aggressive nature of TNBC compared to other subtypes.

**Keyword:** circBCBM1, breast cancer subtypes, metastasis, gene expression, circRNA

