Identification of the circulating-tumor-cell specific genes in the osteosarcoma

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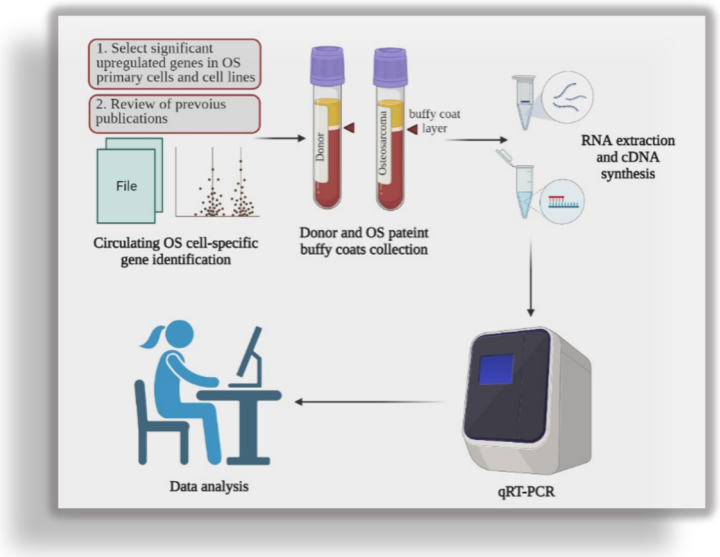
Abstract: Osteosarcoma (OS) is an aggressive bone tumor that frequently occurred in persons aged 15-25. Patients who developed metastasis are associated with a poor prognosis. Finding Circulating-Tumor Cells (CTCs), which indicate an intermediate metastasis using current markers, may not represent tumor metastasis. This study aimed to detect CTCs using a simple molecular technique as Quantitative Real-Time PCR (qRT-PCR), which could be applied in general laboratories. Herein, most of the candidate genes were obtained from the and retrieving by calculating differential gene expression from published gene expression and submitted to the Gene Expression Omnibus (GEO), and some of the candidate genes were obtained from previous data reviewing. The expression of candidate genes in OS patient (n=74) and non-cancer donor (n=79) samples were analyzed by qRT-PCR. A diagnostic model for detecting specific gene expression was derived with a multivariable fractional polynomial (MFP) algorithm. A model incorporating four OS-specific genes including *COL1A2*, *PLS3*, *Ezrin* and *VIM* possessed an outstanding discriminative ability via the area under the receiver operating characteristic curve (ROC) of 0.99 (95%CI 0.97, 1.00). Using the ROC curves revealed that the area under the curve (AUC) was at 0.99 (95%CI: 0.97-1.00). At the probability cut-off value of 0.3, the sensitivity and specificity of the model's detection for OS detection were 100% (95%CI 94.8, 100.0), 96.49% (95%CI 87.9, 99.6), respectively. These four genes also showed a possibility for metastatic prediction. Overall, our presented technique is an alternative tool for the micro-metastasis predictors.

Graphical abstract:



Keywords: Osteosarcoma, Circulating tumor cells, Biomarker, mRNA expression, qRT-PCR

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