



Correspondence

Evaluation of miR-16 as an internal control in the patients with breast cancer



To the editor,

We read with great interest the results as reported by Liu et al [1] using quantitative real-time polymerase chain reaction assays with miR-16 as a normalizer. They found that serum levels of miR-21 and miR-125b were decreased in breast cancer patients who responded to chemotherapy compared with nonresponders, and that lower expression of these microRNAs was associated with better disease-free survival in the patients with breast cancer.

Because of the critical impact of the accurate determination of microRNA levels on the biological interpretation of data, the choice of the normalization agent is of great importance. Although miR-16 was used as an internal control in this study, several studies have shown that it is not a suitable internal control for serum microRNA normalization in breast cancer. Stuckrath et al [2] identified miR-16 as a differentially regulated microRNA in the plasma samples of breast cancer patients (*t* test, adjusted $P = .047$; limma test, adjusted $P = .003$), and they also found that plasma levels of miR-16 were significantly increased in breast cancer patients before and after chemotherapy compared with healthy women (both, $P = .0001$). Shin et al [3] reported that miR-16 was downregulated in the plasma samples of triple-negative breast cancer (TNBC) patients compared with healthy controls ($P < .001$), and they also introduced miR-16 as a biomarker that could differentiate non-TNBC patients from those with TNBC ($P < .001$). Hu et al [4] demonstrated that miR-16 was differentially expressed in the serum samples of breast cancer patients compared with

controls in the discovery ($n = 96$) and validation ($n = 152$) stages ($P < .0001$). Further studies have elucidated the role of miR-16 in therapeutic response, such as the research of Li et al [5], which indicated that miR-16 levels were significantly increased in the trastuzumab-sensitive patients compared with trastuzumab-resistant patients ($P < .05$).

Soheil Madadi

Meysam Soleimani

*Department of Pharmacognosy and Pharmaceutical
Biotechnology, School of Pharmacy*

Hamadan University of Medical Sciences, Hamadan, Iran

E-mail address: m.soleimani@umsha.ac.ir

<https://doi.org/10.1016/j.humpath.2018.10.034>

References

- [1] Liu B, Su F, Chen M, et al. Serum miR-21 and miR-125b as markers predicting neoadjuvant chemotherapy response and prognosis in stage II/III breast cancer. *HUM PATHOL* 2017;64:44-52.
- [2] Stuckrath I, Rack B, Janni W, Jager B, Pantel K, Schwarzenbach H. Aberrant plasma levels of circulating miR-16, miR-107, miR-130a and miR-146a are associated with lymph node metastasis and receptor status of breast cancer patients. *Oncotarget* 2015;6:13387-401.
- [3] Shin VY, Siu JM, Cheuk I, Ng EK, Kwong A. Circulating cell-free miRNAs as biomarker for triple-negative breast cancer. *Br J Cancer* 2015;112:1751-9.
- [4] Hu Z, Dong J, Wang LE, et al. Serum microRNA profiling and breast cancer risk: the use of miR-484/191 as endogenous controls. *Carcinogenesis* 2012;33:828-34.
- [5] Li H, Liu J, Chen J, et al. A serum microRNA signature predicts trastuzumab benefit in HER2-positive metastatic breast cancer patients. *Nat Commun* 2018;9:1614.