Monitoring response to therapy in patients with cancer: is circulating DNA the answer?

Michael J. Duffy^{1,2}, John Crown³

¹UCD School of Medicine and Medical Science, Conway Institute, University College Dublin, Dublin, Ireland; ²Clinical Research Centre, ³Department of Medical Oncology, St Vincent's University Hospital, Dublin, Ireland

Corresponding to: Professor Michael J. Duffy. UCD Clinical Research Centre, St Vincent's University Hospital, Dublin 4, Ireland. Email: michael.j.duffy@ucd.ie.



Submitted May 14, 2013. Accepted for publication Jul 12, 2013. doi: 10.3978/j.issn.2305-5839.2013.07.02 **Scan to your mobile device or view this article at:** http://www.atmjournal.org/article/view/2324/3178

One of the most frequent uses of tumor markers is in monitoring response to therapy in patients with advanced malignancy. Although serial imaging is the gold standard method for assessing response, the use of circulating markers has several advantages including non-invasive measurement, relatively low costs and convenience for patients. Proposed markers for monitoring therapy in patients with breast cancer include CA 15-3, CEA, TPA, TPS and circulating tumor cells (CTC) (1,2). Although the best marker for monitoring remains to be determined, CA 15-3 is the most widely used in clinical practice.

Recently, Dawson et al. (3) described the use of circulating tumor-derived DNA for monitoring response to therapy in 52 patients with advanced breast cancer. The circulating DNA measured was mostly derived from 2 mutant genes in the patients' tumors, i.e., from PIK3CA and TP53 (p53). Circulating tumor-derived DNA was compared with CA 15-3 and CTC. Although 52 patients were recruited, only 30 had identifiable tumor-related genetic alterations suitable for monitoring. Of these 30, 29 (97%) of the patients had detectable alterations in the circulation. In contrast, CTC were present in 26/30 (87%) and elevated levels of CA 15-3 in 21/27 (78%). Furthermore, serum DNA and CTC but not CA 15-3 were found to be prognostic of outcome.

The authors concluded that serum measurement of tumor-derived DNA showed a greater dynamic range and better correlation with alterations in tumor mass compared with CTC or CA 15-3. In addition, serum DNA gave the earliest indication of response to treatment in 10/19 patients.

Oncologists involved in everyday clinical practice may

ask the question, what is the practical relevance of this proof of concept study? In particular, they may ask if the measurement of circulating tumor DNA is ready for prime time (4)?

Although the measurement tumor-derived DNA in serum appears to have a number of advantages vis-à-vis existing markers, it also has a number of limitations. Thus, in the study of Dawson et al. (3), detectable circulating tumor DNA was only present in 29 of the 52 recruited patients. Most of this informative DNA was derived from the 2 most frequently mutated genes in breast cancer, i.e., PIK3CA and TP53 (5,6). It could be argued that if DNA from additional mutant genes was evaluated, sensitivity could be increased. However, apart from PIK3CA and TP53, other genes in breast cancers appear to be mutated in less than 10% of cases (5,6). A further caveat is that determining gene mutation status is relatively expensive and time consuming and would not be practical in most diagnostic laboratories at present.

There may however, be specific situations in which measurement of tumor derived-DNA will provide information that is not available from the existing markers. Thus, preliminary findings suggest that mutations in PIK3CA genes result in resistance to trastuzumab (7,8). Detecting these mutations in a readily available fluid such as blood might thus be able to provide a non-invasive and early indication of resistance to this therapeutic antibody. In this context, it should be noted mutant KRAS DNA was recently found in blood from patients with advanced colorectal cancer that developed resistance to the anti-EGFR monoclonal antibody, panitumumab (9). In 3 of 9 patients, the mutated DNA was identified prior to

Duffy and Crown. Circulating DNA in cancer monitoring

Page 2 of 2

radiological evidence of disease progression.

Early detection of therapy resistance mutations via a non-invasive method, as found in this study (9) could lead to prompt cessation of an ongoing ineffective treatment and result in the administration of a new drug which might be more efficacious. Of course these preliminary finding with circulating tumor DNA in breast and colorectal cancer require confirmation before this technology can be recommended for prime time.

For now and for the short term, oncologist will therefore have to rely on the existing markers for monitoring therapy in patients with cancer, including breast cancer. Research into circulating tumor DNA should be continued. Provided the findings of Dawson *et al.* (3) can be confirmed in larger studies, these assays should be simplified and made available in a relatively inexpensive and convenient-to-use format.

Acknowledgements

The authors wish to thank Science Foundation Ireland, Strategic Research Cluster Award (08/SRC/B1410) to Molecular Therapeutics for Cancer Ireland, and the Irish Cancer Society BREAST CANCER PREDICT programme, for funding their work.

Disclosure: The authors declare no conflict of interest.

References

1. Duffy MJ, Evoy D, McDermott EW. CA 15-3: uses and

Cite this article as: Duffy MJ, Crown J. Monitoring response to therapy in patients with cancer: is circulating DNA the answer? Ann Transl Med 2013;1(3):24. doi: 10.3978/j.issn.2305-5839.2013.07.02

limitation as a biomarker for breast cancer. Clin Chim Acta 2010;411:1869-74.

- Sturgeon CM, Duffy MJ, Stenman UK, et al. National Academy of Clinical Biochemistry Laboratory Medicine practice guidelines for use of tumor markers in testicular, prostate, colorectal, breast and ovarian cancers. Clin Chem 2008;54:e11-79.
- Dawson SJ, Tsui DW, Murtaza M, et al. Analysis of circulating tumor DNA to monitor metastatic breast cancer. N Engl J Med 2013;368:1199-209.
- 4. Lippman M, Osborne CK. Circulating tumor DNA-ready for prime time? N Engl J Med 2013;368:1249-50.
- Cancer Genome Atlas Network. Comprehensive molecular portraits of human breast tumours. Nature 2012;490:61-70.
- Banerji S, Cibulskis K, Rangel-Escareno C, et al. Sequence analysis of mutations and translocations across breast cancer subtypes. Nature 2012;486:405-9.
- Chandarlapaty S, Sakr RA, Giri D, et al. Frequent mutational activation of the PI3K-AKT pathway in trastuzumab-resistant breast cancer. Clin Cancer Res 2012;18:6784-91.
- Wang L, Zhang Q, Zhang J, et al. PI3K pathway activation results in low efficacy of both trastuzumab and lapatinib. BMC Cancer 2011;11:248.
- Diaz LA Jr, Williams RT, Wu J, et al. The molecular evolution of acquired resistance to targeted EGFR blockade in colorectal cancers. Nature 2012;486:537-40.