EGFR mutation in lung cancer: tumor heterogeneity and the impact of chemotherapy

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EGFR inhibitors have been examined as treatments for unselected NSCLC patients until the discovery that activating EGFR mutations render the tumors highly sensitive to these drugs (1,2). Since then, several studies have demonstrated that the presence of an *EGFR* activating mutation identifies a different population of NSCLC patients, with a significantly better prognosis, provided EGFR inhibitors are one of the treatment lines. Thus, testing for such mutations is recommended as part of the initial workup of advanced NSCLC patients.

EGFR mutation status is predictive of benefit from EGFR tyrosine kinase inhibitors (TKIs) in NSCLC, with significant advantages compared to chemotherapy in PFS and response rates in both first and second line. Conversely, patients with wild type (wt) *EGFR* tumors derive a greater benefit from chemotherapy in the first line setting. However, there is conflicting data regarding whether chemotherapy or EGFR TKIs is most beneficial in the treatment of wt *EGFR* after first line therapy. Specifically, identification of an *EGFR* mutation in tumors was not required for overall survival benefit from erlotinib or gefitinib as second- or third-line treatment (3,4). Erlotinib given as maintenance treatment improved OS also in patients with a wt *EGFR* (HR, 0.77; P=0.0243) (5). Chemotherapy-induced changes may partially explain the different results regarding first-line treatment or later treatment lines, as the *EGFR* mutation status is usually defined by the pre-chemotherapy tumor sample. In addition, only 66-83% of *EGFR* mutation positive patients respond to first line EGFR inhibitors, indicating that additional factors determine the sensitivity of tumors to EGFR inhibitors. Among many causes tested as modifying

the EGFR inhibitors sensitivity, *EGFR* mutation abundance was found to be predictive for benefit from gefitinib (6). In the study by Zhou *et al.* (6) high abundance was defined as identification of a sensitizing mutation by sequencing, while low abundance as identification only by the use of an ultra-sensitive technique, *A*mplification *R*efractory *M*utation *S*ystem (ARMS). Difference in mutation abundance can be explained by any combination of several factors: variations in the copy numbers of mutation positive *EGFR* gene in cancer cells, variability in the proportion of tumor cells to stroma cells in the tested specimen, and tumor heterogeneity.

The presence of tumor heterogeneity has recently been highlighted regarding driver mutations in renal cell cancer (7) and has been investigated regarding *EGFR* mutations in NSCLC, with conflicting results (8,9). An extensive recent study by Bai *et al.* (10) describes a three-pronged approach to the question of *EGFR* tumor heterogeneity, mostly looking at systemic chemotherapy-induced changes. The tests reported include examining *EGFR* mutation status in plasma free DNA and in tumors before and after chemotherapy, and EGFR mutation testing of multiple fragments of the same tumor. Each of these approaches demonstrates evidence that can be interpreted as an indication of tumor heterogeneity and variations in the prominent clones following anti-neoplastic treatments.

EGFR mutation testing in plasma free DNA as used by Bai *et al.* has been previously demonstrated to identify about 80% of tumor *EGFR* mutations (11). In 20% of patients *EGFR* mutation was detected before any treatment but not following first-line chemotherapy, while in 9% an *EGFR* mutation was detected in the plasma only after

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chemotherapy treatment. As could be expected, the loss of *EGFR* mutation detection was associated with tumoral response to treatment, probably associated with reduced tumor cells exposure to the circulation. The opposite change is more difficult to comprehend, but could indicate that one mechanism of chemotherapy resistance is emergence of an *EGFR*-mutation-bearing clone, thus the correlation reported with tumor progression. An obvious caveat of this set of results is the 20% rate of false negative *EGFR* mutation detection by the method used to examine plasma DNA.

The *EGFR* mutation status was determined in biopsy specimens taken at diagnosis and in pathology specimens resected following two cycles of neo-adjuvant chemotherapy treatment. The results reveal a 22% rate of discordance, the vast majority of cases involving an *EGFR* mutation at presentation and no mutation found following systemic neo-adjuvant chemotherapy. No method of mutation detection is 100% accurate, and variability in mutant *EGFR* allele amounts due to any of the above explanations could explain the discordance. Yet, the authors have used highly sensitive and reliable methods, thus highlighting the possibility that in a significant proportion of lung cancers harboring an *EGFR* mutation, a clone that lacks this driver mutation can appear. The authors suggest such phenomena would cause reduced benefit from EGFR TKI if given following chemotherapy treatment; however, several reports indicate no reduced OS for *EGFR* mutation-bearing patients not treated with EGFR TKIs at first line (12-14). Tumors responding to neo-adjuvant chemotherapy demonstrate in many cases fibrotic changes, reducing the percentage of tumor cells in the samples taken and potentially the chance of mutation detection.

The third set of evidence Bai *et al.* present include a large-scale analysis of *EGFR* mutation status in different parts of 79 tumors. The authors report a staggering 38% rate of tumor heterogeneity in terms of *EGFR* mutation. This corroborates a few additional smaller studies (15), but contrasts with others (8). In cases where *EGFR* mutation positive tumors were found to have foci with no *EGFR* mutation, an obvious potential explanation is that some of the foci were taken of stromal normal cells or of fibrotic areas. The authors do not detail the procedure of micro-dissection chosen nor how did they verify that only tumor cells were examined. Tumors identified initially as wt *EGFR* where low abundance of mutant *EGFR* was found in some foci might actually represent multi-clonal tumor evolution, although at a rate lower than suggested

by the authors. EGFR inhibitors secondary resistance that develops in tumors found initially to harbor a sensitizing *EGFR* mutation does not involve overgrowth of a wt *EGFR* clone in most cases (16,17). This fact itself suggests that the presence of such clones is not as common as can be expected from the results reported by Bai *et al.*

EGFR mutations were found in the normal epithelium in *EGFR* mutation positive tumors' vicinity (18), indicating this genetic abnormality is one of the earliest events of malignant transformation for such tumors and that all tumor cells that arise in such cases would harbor this driver mutation. However, the possibility of an *EGFR* mutation evolving at different stages in some tumors, giving rise to *EGFR* mutation heterogeneity cannot be ruled out. A convincing way to demonstrate this requires positive identification of alternative clones, through the presence of different driver mutations in different parts of the same tumor, either in the *EGFR* gene or in other oncogenes or tumor suppressor genes. Such events were found to be rare by one report (8). Performing micro-dissection of small tumor foci, and using molecular biology tools currently available, deep sequencing of small amounts of tissue samples would allow a definite answer to the important question of lung cancer intra-tumoral heterogeneity in general, and specifically to the question of EGFR heterogeneity.

Acknowledgements

References

1. Paez JG, Jänne PA, Lee JC, et al. EGFR mutations in lung cancer: correlation with clinical response to gefitinib therapy. Science 2004;304:1497-500.
2. Lynch TJ, Bell DW, Sordella R, et al. Activating mutations in the epidermal growth factor receptor underlying responsiveness of non-small-cell lung cancer to gefitinib. N Engl J Med 2004;350:2129-39.
3. Zhu CQ, da Cunha Santos G, Ding K, et al. Role of KRAS and EGFR as biomarkers of response to erlotinib in National Cancer Institute of Canada Clinical Trials Group Study BR.21. J Clin Oncol 2008;26:4268-75.
4. Douillard JY, Shepherd FA, Hirsh V, et al. Molecular predictors of outcome with gefitinib and docetaxel in previously treated non-small-cell lung cancer: data from the randomized phase III INTEREST trial. J Clin Oncol

2010;28:744-52.

5. Cappuzzo F, Ciuleanu T, Stelmakh L, et al. Erlotinib as maintenance treatment in advanced non-small-cell lung cancer: a multicentre, randomised, placebo-controlled phase 3 study. Lancet Oncol 2010;11:521-9.

6. Zhou Q, Zhang XC, Chen ZH, et al. Relative abundance of EGFR mutations predicts benefit from gefitinib treatment for advanced non-small-cell lung cancer. J Clin Oncol 2011;29:3316-21.

7. Gerlinger M, Rowan AJ, Horswell S, et al. Intratumor heterogeneity and branched evolution revealed by multiregion sequencing. N Engl J Med 2012;366:883-92.

8. Yatabe Y, Matsuo K, Mitsudomi T. Heterogeneous distribution of EGFR mutations is extremely rare in lung adenocarcinoma. J Clin Oncol 2011;29:2972-7.

9. Chen ZY, Zhong WZ, Zhang XC, et al. EGFR mutation heterogeneity and the mixed response to EGFR tyrosine kinase inhibitors of lung adenocarcinomas. Oncologist 2012;17:978-85.

10. Bai H, Wang Z, Chen K, et al. Influence of chemotherapy on EGFR mutation status among patients with non-small-cell lung cancer. J Clin Oncol 2012;30:3077-83.

11. Bai H, Mao L, Wang HS, et al. Epidermal growth factor receptor mutations in plasma DNA samples predict tumor response in Chinese patients with stages IIIB to IV non-small-cell lung cancer. J Clin Oncol 2009;27:2653-9.

12. Maemondo M, Inoue A, Kobayashi K, et al. Gefitinib or chemotherapy for non-small-cell lung cancer with mutated EGFR. N Engl J Med 2010;362:2380-8.

13. Fukuoka M, Wu YL, Thongprasert S, et al. Biomarker analyses and final overall survival results from a phase III, randomized, open-label, first-line study of gefitinib versus carboplatin/paclitaxel in clinically selected patients with advanced non-small-cell lung cancer in Asia (IPASS). J Clin Oncol 2011;29:2866-74.

14. Rosell R, Moran T, Queralt C, et al. Screening for epidermal growth factor receptor mutations in lung cancer. N Engl J Med 2009;361:958-67.

15. Taniguchi K, Okami J, Kodama K, et al. Intratumor heterogeneity of epidermal growth factor receptor mutations in lung cancer and its correlation to the response to gefitinib. Cancer Sci 2008;99:929-35.

16. Sequist LV, Waltman BA, Dias-Santagata D, et al. Genotypic and histological evolution of lung cancers acquiring resistance to EGFR inhibitors. Sci Transl Med 2011;3:75ra26.

17. Bar J, Onn A. Overcoming molecular mechanisms of resistance to first-generation epidermal growth factor receptor tyrosine kinase inhibitors. Clin Lung Cancer 2012;13:267-79.

18. Tang X, Shigematsu H, Bekele BN, et al. EGFR tyrosine kinase domain mutations are detected in histologically normal respiratory epithelium in lung cancer patients. Cancer Res 2005;65:7568-72.