

Treatment Guideline for Advanced NSCLC Based on Driver Gene Mutations

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In 2004, three groups of researchers retrospectively found a close relationship between epidermal growth factor (*EGFR*) gene mutations and efficacy of the *EGFR*-tyrosine kinase inhibitor (TKI) used in molecularly targeted therapy in non-small cell lung cancer (NSCLC) [1-3]. Since 2009, prospective randomized Phase 3 studies clarified that progression free survival (PFS) with use of *EGFR*-TKI was superior to that of cytotoxic chemotherapies for advanced NSCLC patients with *EGFR* mutations [4-7]. Next, in 2007, echinoderm microtubule-associated protein-like 4-anaplastic lymphoma kinase (*EML4-ALK*) fusion gene was found to be another driver gene mutation of NSCLC, [8] and an *ALK* inhibitor, crizotinib, has been established to be active in terms of efficacy and PFS [9]. Both *EGFR*-TKI and *ALK* inhibitors are considered to have a positive effect on survival [10,11]. These suggest that the time for personalized treatments for advanced NSCLC has arrived. Furthermore, the results of Lung Cancer Mutation Consortium and other studies have clarified incidences of *EGFR*, *ALK*, *KRAS*, *Pi3KCA*, *BRAF* and other mutations [12], and might give chances of new targeted therapies. However, the majority of treatment guidelines for advanced NSCLC employ an old fashioned decision-tree (Figure 1A), in which the first decision step is histology (non-squamous cell carcinoma vs. squamous cell carcinoma) and, in the case of non-squamous cell carcinoma, the second decision step is detecting *EGFR* mutations and *ALK* fusion mutations.

First, biomarker tests should predict treatment benefit more precisely than a histological examination. *EGFR* mutation tests have proven to be reliable for use in clinical practice [13]. In particular, *EGFR* mutation testing as a biomarker has attained high levels of predictability, reliability, and feasibility, and can be performed with practical cost [14-16]. Second, histological examination is only modestly reliable; in the discrimination between non-squamous cell carcinoma and squamous cell carcinoma, inter-pathologists' correlation was found to be modest ($\kappa=0.55$) [17]. Therefore, in Japan, where approximately 50,000 patients were newly diagnosed as NSCLC in 2011, approximately 48,000 tests for *EGFR* mutations were performed, [16] indicating that most patients in Japan with NSCLC were screened. The cost of about 200 US dollars for the test is covered by national health insurance. In contrast, the infrastructure for testing *EML4-ALK* fusion genes is still being developed [18]. *EML4-ALK* fusion genes clearly predict clinical benefit with crizotinib treatment [9,11]. Nevertheless, there is no all-purpose testing procedure that has been established. Fluorescent in situ hybridization (FISH) and immunohistochemistry (IHC) need big tissue samples, indicating that there is some problem in terms of feasibility of sampling for advanced NSCLC, which has no indication for operation. Reverse transcription PCR (RT-PCR) for *EML4-ALK* mutations also has modest feasibility because of the need for adequate quantities of RNA immediately after getting clinical samples. Furthermore, there is some inconsistency among results by FISH, IHC and RT-PCR, [18] such as the level of reliability. Currently, FISH is more validated than IHC and RT-PCR [19]; however, FISH is the most expensive test and may not be suitable for massive screening. Therefore, the actual treatment guideline for advanced NSCLC at present in Japan as well as in Italy [20] designates *EGFR* testing as the first step, histological examination

(non-squamous cell carcinoma vs. squamous cell carcinoma) as the second step, and, in the case of non-squamous cell carcinoma, testing for *ALK* fusion genes (Figure 1B) is the 3rd decision step.

In future, when we get an easy, reliable and not-expensive screening test to investigate all of the "druggable" mutations, which have specific inhibitors, a final guideline having the first step of testing druggable mutations and, thereafter, the second step of histological examination will be born (Figure 1C). The value of testing for other driver gene mutations will be more appreciated in future treatment guidelines.

References

1. Lynch TJ, Bell DW, Sordella R, Gurubhagavatula S, Okimoto RA, et al. (2004) Activating mutations in the epidermal growth factor receptor underlying responsiveness of non-small-cell lung cancer to gefitinib. *N Engl J Med* 350: 2129-2139.
2. Paez JG, Jänne PA, Lee JC, Tracy S, Greulich H, et al. (2004) *EGFR* mutations in lung cancer: correlation with clinical response to gefitinib therapy. *Science* 304: 1497-1500.
3. Pao W, Miller V, Zakowski M, Doherty J, Politi K, et al. (2004) *EGF* receptor gene mutations are common in lung cancers from "never smokers" and are associated with sensitivity of tumors to gefitinib and erlotinib. *Proc Natl Acad Sci U S A* 101: 13306-13311.
4. Maemondo M, Inoue A, Kobayashi K, Sugawara S, Oizumi S, et al. (2010) Gefitinib or chemotherapy for non-small-cell lung cancer with mutated *EGFR*. *N Engl J Med* 362: 2380-2388.
5. Mitsudomi T, Morita S, Yatabe Y, Negoro S, Okamoto I, et al. (2010) Gefitinib versus cisplatin plus docetaxel in patients with non-small-cell lung cancer harbouring mutations of the epidermal growth factor receptor (WJTOG3405): an open label, randomised phase 3 trial. *Lancet Oncol* 11: 121-128.
6. Zhou C, Wu YL, Chen G, Feng J, Liu XQ, et al. (2011) Erlotinib versus chemotherapy as first-line treatment for patients with advanced *EGFR* mutation-positive non-small-cell lung cancer (OPTIMAL, CTONG-0802): a multicentre, open-label, randomised, phase 3 study. *Lancet Oncol* 12: 735-742.
7. Rosell R, Carcereny E, Gervais R, Vergnenegre A, Massuti B, et al. (2012) Erlotinib versus standard chemotherapy as first-line treatment for European patients with advanced *EGFR* mutation-positive non-small-cell lung cancer (EURTAC): a multicentre, open-label, randomised phase 3 trial. *Lancet Oncol* 13: 239-246.
8. Soda M, Choi YL, Enomoto M, Takada S, Yamashita Y, et al. (2007) Identification of the transforming *EML4-ALK* fusion gene in non-small-cell lung cancer. *Nature* 448: 561-566.

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9. Shaw AT, Kim DW, Nakagawa K, Seto T, Crinó L, et al. (2013) Crizotinib versus chemotherapy in advanced ALK-positive lung cancer. *N Engl J Med* 368: 2385-2394.
10. Takano T, Fukui T, Ohe Y, Tsuta K, Yamamoto S, et al. (2008) EGFR mutations predict survival benefit from gefitinib in patients with advanced lung adenocarcinoma: a historical comparison of patients treated before and after gefitinib approval in Japan. *J Clin Oncol* 26: 5589-5595.
11. Kwak EL, Bang YJ, Camidge DR, Shaw AT, Solomon B, et al. (2010) Anaplastic Lymphoma Kinase Inhibition in Non-Small-Cell Lung Cancer. *N Engl J Med* 363: 1693-1703.
12. MG Kris, BE Johnson, DJ Kwiatkowski (2011) Identification of driver mutations in tumor specimens from 1,000 patients with lung adenocarcinoma: The NCI's Lung Cancer Mutation Consortium (LCMC). *J Clin Oncol* 29: (2011 ASCO Annual Meeting suppl; abstr CRA7506)
13. Nagai Y, Miyazawa H, Huqun, Tanaka T, Udagawa K, et al. (2005) Genetic heterogeneity of the epidermal growth factor receptor in non-small cell lung cancer cell lines revealed by a rapid and sensitive detection system, the peptide nucleic acid-locked nucleic acid PCR clamp. *Cancer Res* 65: 7276-7282.
14. Goto K, Satouchi M, Ishii G, Nishio K, Hagiwara K, et al. (2012) An evaluation study of EGFR mutation tests utilized for non-small-cell lung cancer in the diagnostic setting. *Ann Oncol* 23: 2914-2919.
15. Rosell R, Moran T, Queralt C, Porta R, Cardenal F, et al. (2009) Screening for epidermal growth factor receptor mutations in lung cancer. *N Engl J Med* 361: 958-967.
16. Hagiwara K, Kobayashi K (2013) Importance of the cytological samples for the epidermal growth factor receptor gene mutation test for non-small cell lung cancer. *Cancer Sci* 104: 291-297.
17. Grilley-Olson JE, Hayes DN, Moore DT, Leslie KO, Wilkerson MD, et al. (2013) Validation of interobserver agreement in lung cancer assessment: hematoxylin-eosin diagnostic reproducibility for non-small cell lung cancer: the 2004 World Health Organization classification and therapeutically relevant subsets. *Arch Pathol Lab Med* 137: 32-40.
18. Tetsuya Mitsudomi, Yasushi Yatabe, Hirotohi Akita, Akihiko Genma, Manabu Soda, et al. Biomarker Committee, the Japan Lung Cancer Society Guidance for ALK Gene Testing in Lung Cancer Patients.
19. Tsoo MS, Hirsh FR, Yatabe Y (2000) IASLC Atlas of ALK Testing in Lung Cancer.
20. Marchetti A, Ardizzoni A, Papotti M, Crinó L, Rossi G, et al. (2013) Recommendations for the analysis of ALK gene rearrangements in non-small-cell lung cancer: a consensus of the Italian Association of Medical Oncology and the Italian Society of Pathology and Cytopathology. *J Thorac Oncol* 8: 352-358.

