Power in numbers: Meta-analysis to identify inhibitor-sensitive tumor genotypes

Geoffrey R. Oxnard1,3 and Pasi A. Jänne1,2,3,#

1Lowe Center for Thoracic Oncology and the 2Belfer Institute for Applied Cancer Science, Dana-Farber Cancer Institute; 3Department of Medicine, Brigham and Women’s Hospital, Boston, MA

Running title: Meta-analysis of tumor genotyping

Keywords: Tumor genotyping, lung cancer, kinase inhibitor

Corresponding author:
Pasi A. Jänne, MD PhD
Dana-Farber Cancer Institute
450 Brookline Ave; HIM 223.
Boston, MA 02215
pjanne@partners.org
Phone: 617-632-6076
FAX: 617-582-7683

Conflicts of interest:

G.R. Oxnard –

Consultant/Advisory Board

Minor ($10,000 or less)
Genentech and Boehringer-Ingelheim

P.A. Jänne –

Consultant/Advisory Board

(Minor $10,000 or less)
Astra Zeneca, Boehringer Ingelheim, Pfizer, Roche, Genentech, Sanofi

Other: Post marketing royalties from DFCI owned IP licensed to Lab Corp on EGFR mutation testing

(Major $10,000 or more)
Lab Corp
Summary

Widespread tumor genotyping has increased the complexity of lung cancer care, often identifying mutations of uncertain clinical significance. In the accompanying article, the authors perform a meta-analysis of the published literature on EGFR genotype and erlotinib/gefitinib sensitivity to develop a publically accessible database to inform patient care.

In this issue of Clinical Cancer Research, Yeh and colleagues present a new strategy to address the complexity of genotype-directed cancer therapy: using meta-analysis of the published literature to develop a database of actionable somatic EGFR mutations (1). Genotyping of EGFR is now a standard component of non-small cell lung cancer (NSCLC) care, as with KRAS and BRAF for colorectal cancer and melanoma, respectively. But when these biomarkers were first developed, early studies intentionally simplified the complexity of tumor genotype by dichotomizing cancers into “mutant” or “wildtype”. In this fashion, drug-sensitive phenotypes were identified: KRAS-wildtype colon cancers gain a survival benefit from cetuximab, EGFR-mutant lung cancers are best treated with EGFR tyrosine kinase inhibitors (TKIs), and BRAF-mutant melanomas gain unique benefit from vemurafenib.

However, closer scrutiny of the data reveals a greater degree of complexity. The pivotal studies of first-line gefitinib and erlotinib were limited to cancers carrying EGFR exon 19 deletions or L858R mutations. The landmark study of cetuximab efficacy in colorectal cancer only included sequencing of KRAS exon 2. And the BRIM3 trial of vemurafenib versus dacarbazine only randomized melanomas harboring V600E mutations. Is the drug-sensitive phenotype limited to the genotypes studied in these landmark randomized trials? This question is particularly important because genotyping does not only detect these genotypes – less common somatic
mutations are also detected, though many are not well established as clinical biomarkers. To achieve precision genotype-directed therapy, we must determine how to manage patients harboring these uncommon genotypes.

In the case of NSCLC, less common mutations constitute 10-15% of all EGFR-mutant lung cancer. Yet, their exclusion from many pivotal trials leaves clinicians uncertain as to whether they are best treated with targeted therapy or conventional chemotherapy. Because the low prevalence of these genotypes makes them difficult to study, several approaches (Figure 1) have been used to gain an understanding of their behavior:

- **Single-center experiences:** Several cancer centers in Asia and the United States have been routinely performing genotyping since EGFR mutations were first discovered nearly a decade ago. Based upon these experiences, it has been identified that G718X and L861Q mutations are associated with a 53-60% response rate (RR) to erlotinib or gefitinib (2), that exon 20 insertions are unlikely to respond and are associated with a poorer survival (2, 3), and that a subset of exon 19 deletions are less likely to respond to erlotinib or gefitinib (4). The primary limitation of single-center experiences is the possibility that results are specific to certain assays and may not generalize.

- **Multi-center experiences:** Collaborative efforts between multiple cancer centers can create an opportunity to study genotypes too rare to study as a single center. For example, combining the experiences of two large referral centers, a recent study of 12 patients with exon 19 insertions found these mutations to be associated with TKI-sensitivity (5). The most comprehensive multi-centered effort may be the French ERMETIC IFCT network, through which 1048 EGFR-mutant cancers were identified over a 6-year period (6); results have not yet been published. Multi-centered trials have occasionally included patients with
uncommon *EGFR* mutations, though generally a small number; the LUX-Lung 3 trial of afatinib versus chemotherapy included 37 patients with uncommon mutations, with objective responses seen in association with several uncommon genotypes (7).

- **Meta-analysis:** To circumvent the logistical challenges of multi-centered genotyping efforts, meta-analyses can use the published literature to systematically collect and analyze independent datasets. The best established meta-analysis of genomic data is the Catalogue Of Somatic Mutations In Cancer (COSMIC) database run by the Sanger Institute (8). A central aim of this effort is to identify the frequency of somatic mutations, but the database does not associate these genotypes with sensitivity to targeted therapies.

The article by Yeh et al (1), accompanying this editorial, represents the first published meta-analysis, to our knowledge, describing the published literature on *EGFR* genotype and TKI-sensitivity. Searching PubMed, the authors identified and reviewed 2085 manuscripts published between June, 2005 and May, 2011. They limited their analysis to the 146 papers (7%) which included individual patient-level detail on *EGFR* genotype and RECIST response to erlotinib or gefitinib. This included 1021 patients with 207 different *EGFR* genotypes. Importantly, the meta-analysis includes many patients from the well-characterized Taiwanese experience (2). The authors associated 72% of these individual genotypes with disease control based upon a disease control rate (DCR) of at least 50%.

Are the findings from this meta-analysis consistent with other published literature? Yes, particularly since several key articles have been incorporated into the analysis. The authors, however, categorize treatment outcomes into disease control (complete response, partial response or stable disease) and disease progression, an approach that may overestimate the clinical effect of EGFR inhibitors against a particular *EGFR* genotype. High rates of objective
response to targeted therapy have been seen repeatedly with oncogene-addicted cancer types.

What's more, a meta-analysis of EGFR TKI trials found that RR more closely correlates with survival prolongation than does DCR (9). Clarity on this issue is particularly important if clinicians are going to use this information to decide whether to use a first-line TKI or chemotherapy for a NSCLC patient harboring a rare EGFR genotype.

What new can be learned from this meta-analysis about rarer EGFR mutations? Currently, 67% of genotypes studied occurred in a single patient and only 12 occurred in more than 4 patients. One reason this series includes fewer patients than might be expected is because many larger papers, including most describing trial results, do not publish patient-level data on genotype and response. To overcome this weakness, the authors have established a database aiming to collect such data going forward: the DNA-mutation Inventory to Refine and Enhance Cancer Treatment (DIRECT). It is anticipated that more information on rarer genotypes will become available as the database grows. At present, the most intriguing data is that, of 9 patients with the poorly described S768I mutation (8 of these occurring with various co-mutations), 6 had a response to TKI.

Perhaps the biggest limitation to the success of the DIRECT database will be the challenge of quality control. Is it appropriate to collectively study mutations identified in different laboratories using different assays? For example, one highly sensitive assay for T790M was removed from the market due to problems with false positive results (10); such “T790M-positive” cases might not exhibit resistance to TKI, while T790M detected using Sanger sequencing in a clinical laboratory is clearly associated with TKI resistance (and risk of an underlying germline mutation) (11). Some genotyping assays only test for a limited set of mutations, potentially missing important co-mutations that would be identified using direct sequencing. Lastly, a rare mutation identified in a research laboratory could potentially represent a sequencing artifact rather than a
true oncogenic alteration. A strategy to help interpret the clinical relevance of the mutations in DIRECT would be to capture the type of assay used and whether it was performed in a clinically certified laboratory. This is especially relevant given the poorer outcomes described when gefitinib was given to lung cancer patients with low abundance $EGFR$ mutations only detected using a highly sensitive assay (12). While for some rare genotypes, collective study using meta-analysis may be our only option for characterizing drug sensitivity, results from a single-center experience will inherently be more transparent until all centers utilize a single genotyping assay and share a similar degree of expertise.
Figure Legend

Figure 1. Approaches to studying and interpreting tumor genotypes. Genotyping performed as part of routine clinical care occasionally identifies uncommon genotypes which may lend sensitivity to targeted therapy (top). However, not all data on specific genotypes and their association with drug sensitivity reaches the published literature (middle). Common genotypes are often included in prospective trials (blue), less common genotypes may be described in observational series (red), and the rarest genotypes may only be presented as case reports (green). Meta-analysis can allow collective study of these individual published experiences (bottom), though the completeness of the data inherently depends upon selection criteria as well as publication biases.
Acknowledgements

This study is supported in part by a grant from the National Institutes of Health RO1CA114465 (P.A.J.) and the National Cancer Institute Lung SPORE P50CA090578 (P.A.J., G.R.O.).
References


Genotyping at individual institutions

Prospective trials for common genotypes

Selection criteria

Meta analysis attempts to collectively describe the entire population based upon available data.

Observational series describing uncommon genotypes

Case reports of rare genotypes

Publication biases
Power in numbers: Meta-analysis to identify inhibitor-sensitive tumor genotypes

Geoffrey R. Oxnard and Pasi A. Jänne

Clin Cancer Res  Published OnlineFirst February 12, 2013.