Further molecular profiling of tumors harboring therapeutic targets within non-small cell lung cancer

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Abstract

Treatment of NSCLC has been overwhelmingly with molecular targeted therapies for several years, and the recent availability of biomarker testing to guide therapy choice has lead to the use of targeted drugs. This approach has been highly successful in EGFR and ALK rearranged tumors, which harbor specific driver mutations, but has been less successful in other subsets of NSCLC, which feature cancer drivers that are not known in the general population. In the current study, we have used a comprehensive tumor profiling approach to explore the spectrum of actionable alterations present within NSCLC tumors, with a particular focus on non-amplifiable targets that have not been extensively explored to date. The results of this study highlight the extent to which non-amplifiable targets are prevalent within NSCLC, and provide a novel opportunity for the identification of therapeutic approaches for patients with NSCLC.

Background

The identification of actionable, non-amplifiable alterations which can lead to significant clinical benefit has been the focus of extensive research in recent years. A number of such targets include mutations in the EGFR gene, as well as mutations in KRAS and other RAS genes, which are not present in all patients with NSCLC. However, these alterations are only identified in a small subset of patients with NSCLC and are not detectable using standard treatment approaches for other tumor types.

Comprehensive analysis of large sets of tumors containing a broad range of alterations which may be clinically relevant, although their occurrence at low frequency, may help to identify the occurrence of these alterations in a wider patient population. In the current study, we have used a comprehensive tumor profiling approach to explore the spectrum of actionable alterations present within NSCLC tumors, with a particular focus on non-amplifiable targets that have not been extensively explored to date. The results of this study highlight the extent to which non-amplifiable targets are prevalent within NSCLC, and provide a novel opportunity for the identification of therapeutic approaches for patients with NSCLC.

Methods

We used the Caris Molecular Intelligence assay to profile 6870 non-small cell lung cancer tumors from 2009 to 2014. The Caris Molecular Intelligence assay is a next-generation sequencing (NGS) panel that targets over 450 cancer-related genes, including all known actionable genes. The results of this study highlight the extent to which non-amplifiable targets are prevalent within NSCLC, and provide a novel opportunity for the identification of therapeutic approaches for patients with NSCLC.

Results:

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Conclusions:

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References:

