Somatic mutations of the tyrosine kinase domain of epidermal growth factor receptor and tyrosine kinase inhibitor response to TKIs in non-small cell lung cancer: an analytical database.

Murray S, Dahabreh IJ, Linardou H, Manoloukos M, Bafaloukos D, Kosmidis P.

Source

Department of Molecular Biology, Metropolitan Hospital, N. Faliro, 18547, Athens, Greece. smbhsam@hotmail.com

Abstract

BACKGROUND:

After the discovery of somatic mutations in the tyrosine kinase domain (exons 18-24) of the epidermal growth factor receptor (EGFR) correlating with responses of non-small cell lung cancer (NSCLC) to the tyrosine kinase inhibitors (TKIs) gefitinib and erlotinib, there has been increasing interest in utilizing this molecular marker for treatment selection. We aimed to analytically catalogue the mutational spectrum of somatic mutations in EGFR and format a database allowing correlation of specific mutations with clinico-pathologic factors and response to TKIs.

METHODS:

A computerized search of MEDLINE (January 1, 2004 to June 30, 2007) was performed to identify articles reporting on NSCLC patients harboring somatic mutations in EGFR. Demographic, clinico-pathologic, mutational, and response data were extracted and tabulated.

RESULTS:

A total of 202 eligible articles were identified. We report data on 12,244 patients with 3381 somatic EGFR mutations. The majority of mutations have been reported on only one occasion (158 of 254, 62.2%), and only nine mutations occur at a rate of >or=1%. L858R and delE746-A750 account for 32.84% and 24.28% of all mutations, respectively; with 50% of mutations being exon 19 deletions or "deletional-insertions." There is a clear association between the presence of mutations and response to TKI.

CONCLUSIONS:

We have generated a free access, nonprofit online analytical database of somatic EGFR mutations in NSCLC. Cumulative information will be made available through a routine update of both database tables and associated graphical representations. Direct updates and submissions through the online site (www.somaticmutations-EGFR.org) are encouraged, as are comments and suggestions.

Comment in

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