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Molecular markers with prognostic and predictive relevance in NSCLC

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Abstract

Lung cancer accounts for the majority of cancer-related deaths worldwide of which non-small-cell lung carcinoma alone takes a toll of around 85%. In the next years modest survival improvement can be expected by chemotherapy. Advances in understanding of the molecular pathogenesis of lung cancer have led to the identification of several specific targets for therapeutic agents. EGFR activating mutations (exons 18 to 21) and EML4-ALK rearrangement are clinically important markers able to select NSCLC patients which benefit from EGFR or ALK tyrosine kinase inhibitors (gefitinib, erlotinib, crizotinib).

Many other molecular abnormalities have been reported in other genes such as HER2, KRAS, KDR, FLT1, MET, BRAF, and more recently RET, ROS as well as FGFR1. DNA repair players are also potential predictors of standard anti-cancer therapies (ERCC1, RRM1, MSH2, BRCA1, PARP). We examined, in the context of NSCLC, the prognostic and predictive value of these mutations especially for drive therapeutic interventions.

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