Best Orals – 2nd Prize

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ABSTRACT TITLE:
EGFR and KRAS mutation testing in circulating plasma DNA of lung cancer patients using a high-throughput system (Sequenom's MassARRAY technology) and a targeted High Resolution Melt Analysis: Is it useful for routine detection?

ABSTRACT TEXT:
Objective: The detection of genomic alterations in circulating cell-free DNA (cfDNA) is a non-invasive approach for potentially improving the monitoring of lung cancer patients. These genomic alterations are frequently multiple and should be then assessed before administration of targeted therapy. The aim of this work was to analyse the different associated mutations in cfDNA from lung cancer tumours expressing KRAS or EGFR mutations.
Method: Matched samples, FFPE tumour tissue and plasma DNA, from 67 patients with KRAS mutations and 25 patients having tumours mutated for EGFR, as determined by pyrosequencing, were evaluated. We used the Sequenom MassArray System and LungCarta panel for somatic mutation profiling in cfDNA, which was extracted on the QIAsymphony automated platform.
Results: KRAS and EGFR mutations detected in tissues were demonstrated in 25/65 (38%) and 14/25 (56%) in cfDNA from the corresponding plasma samples. 61/90 (68%) cfDNA samples, in which EGFR and KRAS mutations were identified, harboured multiple mutations, in particular on p53 [25/61 (41%)], STK11 [10/61 (16%)], DDR2 [4/61 (6%)], and MET [2/61 (3%)] gene.
Conclusion: The MassARRAY technology identifies several genomic alterations potentially associated with KRAS or EGFR mutations in cfDNA from lung cancer patients. This approach can open new avenues for future therapeutic strategies from liquid biopsy assessment