



ALK and ROS-1 NSCLC patients treatment approach based on genomic profile by liquid biopsy

Lung cancer is the leading cause of cancer-related death in the world. Anaplastic lymphoma kinase (*ALK*) and *ROS-1* gene rearrangements occur in ~5% and 1–2% of patients with advanced NSCLC, respectively, mainly in lung adenocarcinomas.

ALK and ROS-1 tyrosine kinase inhibitors (TKIs) have become the new standard of care in the first-line treatment of advanced *ALK* and *ROS-1* positive NSCLC patients. As there are several TKIs available, the optimal sequential ALK and ROS-1 TKI strategy at progression is relevant, and this may have an impact on patients' outcome.

Almost one-third of advanced NSCLC patients do not have adequate tumor tissue for genomic profiling. Liquid biopsy as circulating tumor DNA analysis (ctDNA) may provide real-time information on the molecular evolution of the disease upon personalised therapy. Currently, next generation sequencing (NGS) is considered the optimal method for detecting *ALK* and *ROS-1* mutations from ctDNA.

Although intra-tyrosine kinase *ALK*-mutations are the main mechanism of acquired resistance (AR) to ALK TKIs, there is a preliminary specific resistance mutation profile with a subsequent therapeutic implication based on the ALK TKI chosen. In first generation ALK TKI crizotinib-refractory tumors, the efficacy of next generation ALK TKIs (brigatinib, ensartinib, ceritinib, lorlatinib) is independent of the occurrence of acquired *ALK*-mutations. However, the upfront administration of second generation ALK TKIs (alectinib, brigatinib) or third generation ALK TKI (lorlatinib), have challenged the current blinded sequential treatment strategy guided by clinicians.

AR to ROS-1 TKIs can occur through either pharmacological or biological mechanism, which consist mainly of acquisition of secondary point mutations in the *ROS1* kinase domain, activation of by pass tracks and phenotypic changes. After progression to first-line ROS-1 TKI crizotinib, secondary mutations can be overcome with repotrectinib or lorlatinib. However, the new first line entrectinib approval and other novel drugs under development, will require a more robust understanding of the resistance pattern that will have subsequent treatment impact.

Considering the crucial prognostic and predictive value of secondary *ALK* and *ROS-1* resistance mutations for the selection of the optimal sequential TKI, serial ctDNA analysis may provide real-time information on the disease molecular evolution upon ALK and ROS-1 TKI therapy. The characterization of mechanisms of AR will be clinically relevant to develop new personalised treatment strategies to overcome resistance in the near future.

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