

BACKGROUND

- Circulating tumor DNA (ctDNA), is a surrogate material for somatic mutation (mut.) detection, such as *EGFR* in NSCLC patients
- However, the applicability for the detection of *ALK* and *ROS1* fusions and resistance mutations is poorly described

OBJECTIVE

- To evaluate an amplicon-based *ctDNA* assay for detecting *ALK/ROS1* fusions and mut. in a cohort of *ALK/ROS1+* NSCLC patients

PATIENTS AND METHODS

- *ALK* and *ROS1* rearranged NSCLC patients were prospectively enrolled from Dec. 2016 to Dec. 2017 in our institution
- The analysis of *ALK & ROS1* mutations, *EML4-ALK* (variant 1,2,3) and *ROS1* fusions (with partner genes *CD74*, *SLC34A2*, *SDC4* and *EZR*) in *ctDNA* were performed using InVisionFirst Lung™

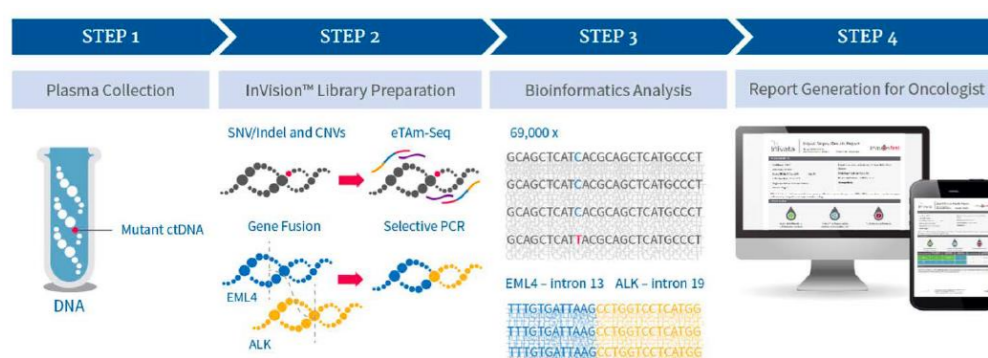


Figure 1. The InVisionFirst Lung™ assay identifies *ALK* and *ROS1* gene fusions using an amplicon-based technology to selectively amplify genomic breakpoints, the sequence of the junctions are then identified using NGS, allowing the genomic breakpoint in *ctDNA* to be mapped. In a recent analytical validation study (Plagnol V. et al, PLoS ONE 2008), this methodology detected *EML4-ALK* and *SLC34A2-ROS1* breakpoints in *ctDNA* reference material at a VAF of 0.0625%, with 100% specificity

RESULTS

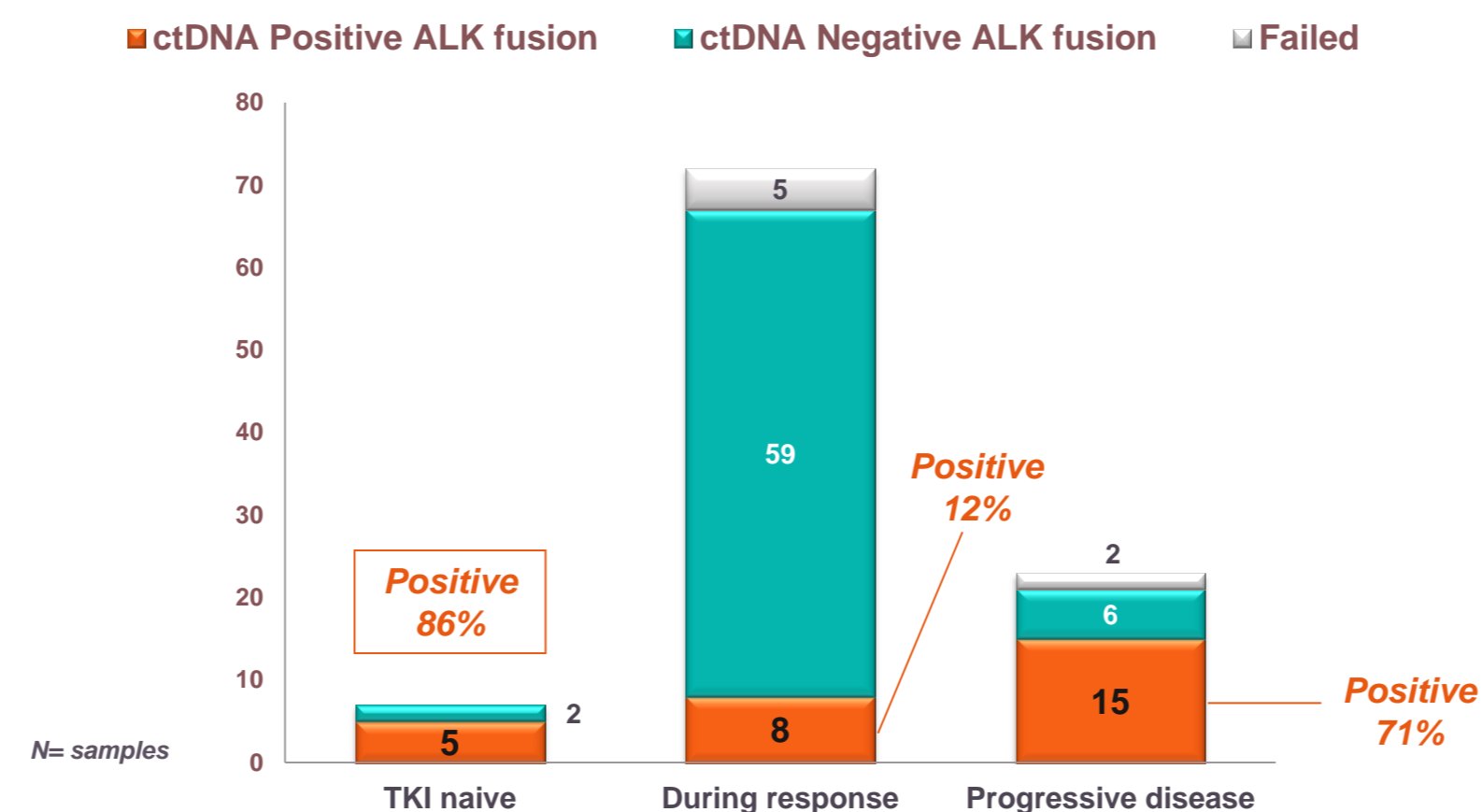
- **51 patients were included.** Patient characteristics are included in **Table 1**
- *ALK & ROS1* status was confirmed by *ALK* immunohistochemistry (IHC) (n=26) and FISH (n=40)
- The median prior tyrosine kinase inhibitors (TKI) received was 2 (0-4)
- **Blood samples (n=102) were collected at different time points:**
 - treatment-naïve (n=7)
 - on treatment (n=95)
 - at progressive disease (PD) (n=23), particularly at PD to tyrosine kinase inhibitors (n=17)

Characteristics	Overall population (n=51, %)
Age	Median (range) 52 (22-73)
Sex	Male 24 (47%) Female 27 (53%)
Stage at diagnosis	I-II 2 (4%) IIIA-IIIB 7 (14%) IV 56 (82%)
Histology	Adenocarcinoma 50 (98%) Large cells carcinoma 1 (2%)
Smoking	Non smoker 27 (53%) Former smoker 19 (37%) Current smoker 4 (8%)
Molecular diagnosis	IHC 26 (51%) FISH 40 (78%)
Type of fusion	<i>ALK</i> fusion 43 (84%) <i>ROS1</i> fusion 8 (16%)
Therapy at collection	Treatment-naïve 7 (14%) Crizotinib 9 (18%) Next-gen TKI 29 (57%) Others 6 (12%)

Table 1: Baseline characteristics

ALK & ROS1 fusion

ctDNA fusion detection at different time points



- In treatment-naïve patients, *ALK & ROS1* *ctDNA* fusions were detected in 86% of patients (5/6 *ALK* fusion; 1/1 *ROS1* fusion)
- Sensitivity for *ALK* was 83% and 100% for *ROS1*, in treatment naïve patients

EML4-ALK variant

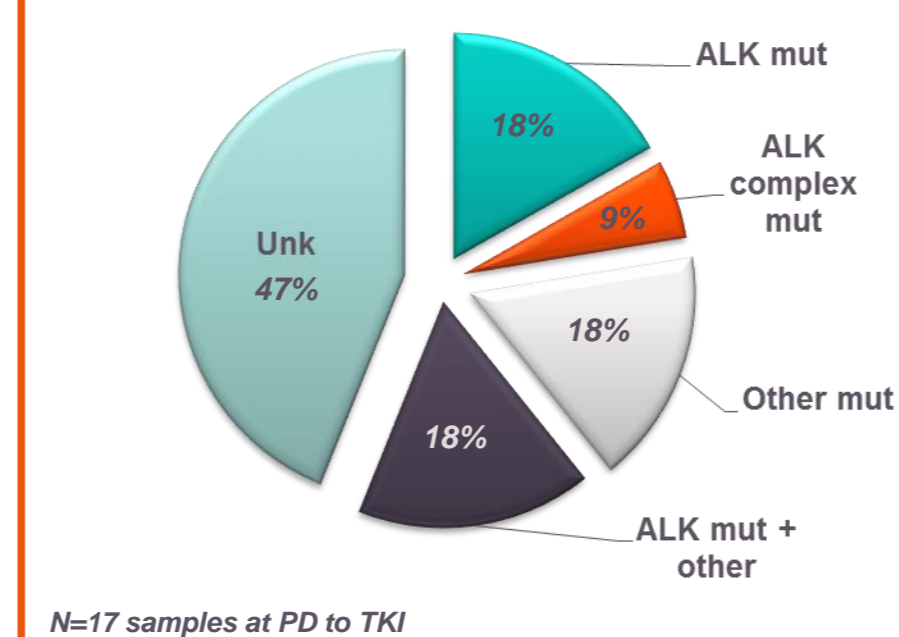
Fusion	Variant	Frequency observed N (%)
<i>EML4-ALK</i>	1	1 (14%)
<i>EML4-ALK</i>	2	-
<i>EML4-ALK</i>	3	5 (83%)

ROS1 gen partner

Fusion	Gen Partner	Frequency observed N (%)
<i>ROS1</i>	<i>CD74</i>	1 (100%)

ALK resistance mutations

Resistance mechanisms (%)

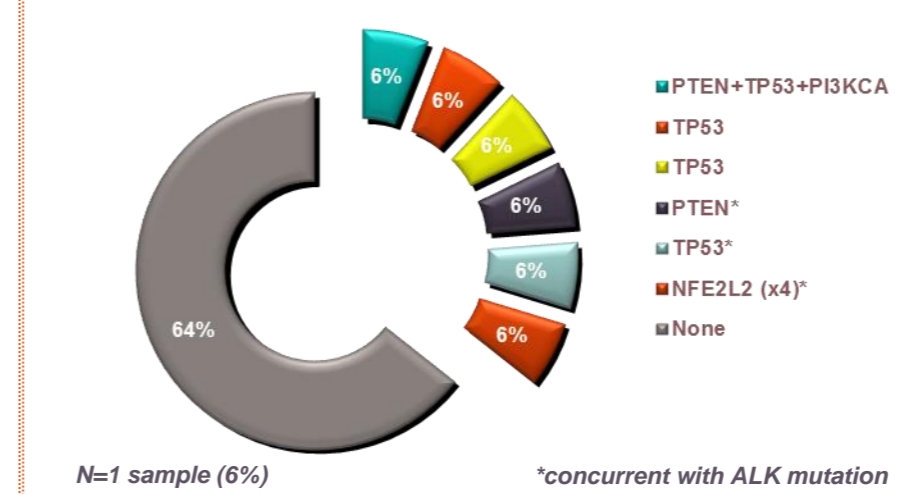


N=17 samples at PD to TKI

ALK resistance mutations

- 41% presented *ALK* mut. at PD to TKI (7/17)
 - *ALK* G1202R was the most common mutation (71%)
 - A single *ALK* mut. (n=3)
 - *ALK* complex mut. (n=1)
 - *ALK* + other mut. (n=3)
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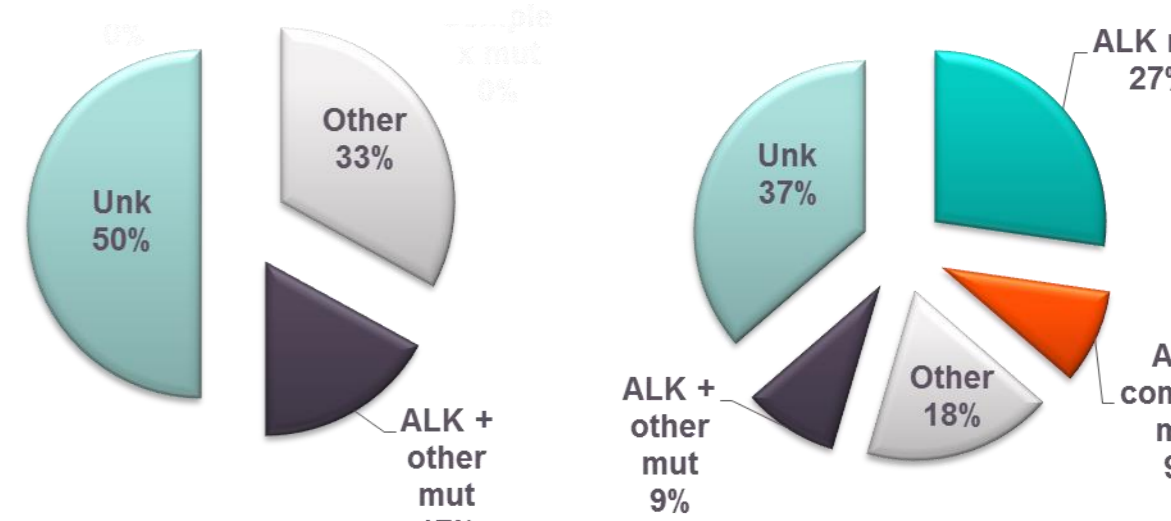
Other concurrent mutations



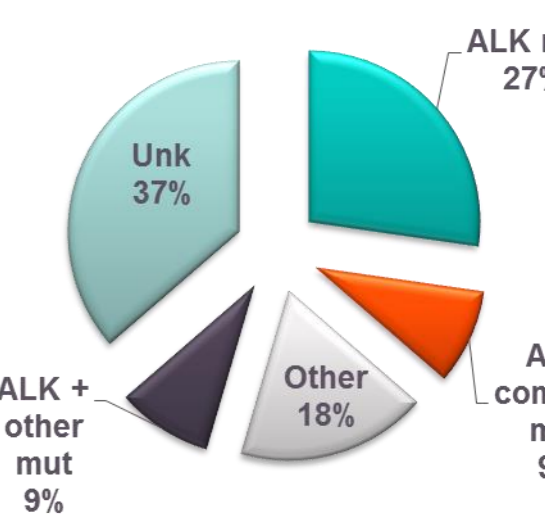
- 35% of all patients presented other concurrent mutations at PD (6/17)
- TP53 and PTEN were the most common mutations (4/6 and 2/6 respectively)

Crizotinib vs. Next-generation TKI

PD to crizotinib, n=6



- Higher incidence of *ALK* mut. at PD to next-gen TKI vs. crizotinib (45% vs. 17%)



CONCLUSION

- Routine liquid biopsy detects *ALK/ROS1* fusions in untreated NSCLC pts and reflects treatment sensitivity in TKI exposed pts.
- It is also an accurate tool to assess TKI resistance, detecting *ALK* and other potential resistance mutations, that reflect the tumor heterogeneity.