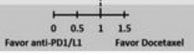
single agent in the second-line therapy of NSCLC. Whether combination of PD-L1 and clinicopathologic characters could circle out optimal beneficiaries are still unknown. **Method:** We performed a meta-analysis of randomized control trials that compared immune-checkpoint inhibitors against chemotherapy in second-line therapy. Data including smoking status, EGFR status, KRAS status and histology were extracted as subgroup analyze to estimate the potential predictor of efficacy for anti PD-1/L1. **Result:** Five clinical trials that compared immune-checkpoint inhibitors against chemotherapy for second-line therapy were included. Both PD-L1 positive (HR=0.64, 95%CI=0.56-0.73, P<0.00001) and PD-L1 negative (HR=0.88, 95%CI=0.78-1.00, P=0.05) favored anti PD-1/L1. Subgroup analyze indicated that adenocarcinoma (ADC) as well as squamous cell carcinoma (SCC) preferred anti PD-1/L1. Never smokers may not benefit from anti PD-1/L1 but current/ever smokers did (HR=0.70, 95%CI=0.63-0.79, P<0.00001). Patients with EGFR mutation could not gain benefit from anti PD-1/L1 while the EGFR wild type could (HR=0.67, 95%CI=0.60-0.76, P<0.00001). Both KRAS mutation (HR=0.60, 95%CI=0.39-0.92, P=0.02) and wild type/unknown (HR=0.81, 95%CI=0.67-0.97, P=0.02) were apt to anti PD-1/L1. **Conclusion:** Regardless of PD-L1 status, immune-checkpoint inhibitors could achieve better efficacy than chemotherapy in second-line therapy. Current/ever smokers without EGFR mutations may benefit more from anti PD-1/L1. Combination of PD-L1 and strongly relevant clinicopathologic characters should be considered to tailor optimal patients for anti PD-1/L1. **Keywords:** biomarker and clinicopathologic characters, Immunotherapy, non-small cell lung cancer

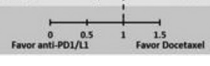
A

Subgroup of trials	Weight	Hazard Ratio	HR (95%CI)	P value
PD-L1				
positive	47.4%		0.64 (0.56, 0.73)	<0.00001
negative	52.6%		0.88 (0.78, 1.00)	0.05
EGFR				
mutation	10.8%		1.12 (0.80, 1.56)	0.51
wild type/unknown	89.2%		0.67 (0.60, 0.76)	<0.00001
KRAS				
mutation	15.1%		0.60 (0.39, 0.92)	0.02
wild type/unknown	84.9%		0.81 (0.67, 0.97)	0.02



B

Subgroup of trials	Weight	Hazard Ratio	HR (95%CI)	P value
Gender				
male	64.9%		0.74 (0.66, 0.84)	<0.00001
female	35.1%		0.80 (0.68, 0.94)	0.006
Age				
<65yrs	56.8%		0.75 (0.64, 0.88)	0.0004
65-75yrs	35.0%		0.62 (0.51, 0.76)	<0.00001
>75yrs	8.2%		0.99 (0.65, 1.50)	0.97
Smoking status				
Non-smoker	15.1%		0.81 (0.60, 1.10)	0.17
Current/former smoker	84.9%		0.70 (0.63, 0.79)	<0.00001
ECOG PS				
0	28.5%		0.70 (0.58, 0.85)	0.0002
1	71.5%		0.67 (0.60, 0.75)	<0.00001
Histology				
Adenocarcinoma	71.3%		0.71 (0.63, 0.80)	<0.00001
Squamous carcinoma	28.7%		0.67 (0.56, 0.81)	<0.0001



P1.01-028
Characteristics of Cell Free DNA in Lung Cancer Patients

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Background: A third generation EGFR tyrosine kinase inhibitor, osimertinib, is effective for T790M positive lung cancer patients. Although the tissue re-biopsy of primary or metastatic tumors was required to use osimertinib, cell free DNA (cfDNA) has been recently approved for detection of T790M in Japan. We have reported that cfDNA size distribution was different between lung cancer and healthy individuals using a capillary electrophoresis system, that is one peak around the size of 170 bp in healthy individuals, and two peaks, 170 bp and 5 kb in advanced lung cancer patients. The purpose of this study is to clarify the clinical and biological characteristics of each sized cfDNA. **Method:** The plasma collected from 92 lung cancer patients, 18 benign pulmonary disease patients, 20 healthy individuals at Saga University Hospital were analyzed. cfDNA extraction was performed from 1000μl plasma by automated DNA extraction system using cellulose magnetic beads. We first compared the DNA concentrations and cfDNA size among three groups. The DNA concentrations were quantified by Quantus®, the fluorescent measurement of dsDNA intercalated dye, and cfDNA size was analyzed by the Agilent 2100 Bioanalyzer®. We next separately isolated cfDNA 170 bp and 5 kb fragments, and detected the epidermal growth factor receptor (*EGFR*) L858R point mutation by mutation-biased PCR and quenched probe system (MBP-QP) method. **Result:** The DNA concentration was higher in lung cancer patients compared to those in benign pulmonary disease and healthy individuals. Divided by histological types, DNA concentrations were highest in small cell carcinoma, and were increased in patients with advanced stages. Especially, DNA concentrations were higher in presence of metastasis, and 5 kb fragments were significantly increased in these cases. L858R positive patients showed higher DNA concentration with more obvious difference in 5 kb fragments. L858R was detected in both cfDNA fragments, 170 bp and 5 kb, which were separately isolated, suggesting that both sized DNA fragments contain circulating tumor-derived DNA (ctDNA). **Conclusion:** cfDNA concentrations were associated with progression of lung cancers, and bimodal characteristic was observed in terms of cfDNA size. Although the 170 bp short fragments of cfDNA are well known as an apoptotic product, the origin of 5 kb long fragments is still unclear. We have continuously examined how ctDNA was released from tumor cell. **Keywords:** plasma DNA integrity, lung cancer, cell free DNA(cfDNA)

P1.01-029
Lymphocyte Monocyte Ratio as a Prognostic Factor in Non-Small Cell Lung Cancer

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Background: Chronic state of inflammation is an important factor in advanced cancer which is used by tumor cells for maintaining survival and growth. Hematological parameters such as neutrophil/lymphocyte ratio (NLR), thrombocyte/ lymphocyte ratio (TLR) and lymphocyte / monocyte ratio (LMR) are reliable indicators of systemic inflammation. We aimed to elucidate the effect of hematological parameters and clinical features of patients on the prognosis

of advanced stage non-small cell lung cancer (NSCLC). **Method:** We included 102 stage IV NSCLC patients who presented to the oncology clinic 2010-2016. Pretreatment clinical parameters and NLR, TLR, and LMR were retrieved from the medical records. The cut off values, calculated with ROC analysis, for NLR, LMR, TLR were 2.5, 3 and 183, respectively. All patients were divided into two groups according to cut off values and analyzed accordingly. **Result:** Median OS and PFS were 10 and 6 months respectively. In univariate analysis high NLR, high TLR and low LMR were found to be significantly associated with survival . Among clinical parameters having ECOG performance score 0-1 , older age (≥70 years) single metastatic disease were prognostic. In multivariate cox regression analysis only the number of metastatic lesions and LMR were found to be independent predictors for survival. **Conclusion:** Although the interaction between tumor cells and the host immune system is a very complex process, LMR, NLR and TLR are hematological parameters that can be easily derived from total blood counts and can be used in daily clinical practice. Among these markers, we suggest that LMR holds the greatest potential as a viable prognostic factor in the setting of metastatic NSCLC. **Keywords:** Advanced stage, Non-Small Cell Lung Cancer (NSCLC), Lymphocyte monocyte ratio (LMR)

P1.01-030
Predictive Biomarkers in Non-SmallCell Carcinoma and Their Clinical Association

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Background: Recognition of molecular targets, such as *EGFR, ALK, ROS* and *MET* involved in cell signaling have led to the development of new targeted therapies. Widespread use of predictive markers has generated new data on prevalence and clinicopathological correlates. However, there is a lack of comprehensive data from Indian subcontinent. This study identifies clinical, histomorphologic and molecular correlates of biomarker positive NSCCl. **Method:** Archival data of NSCC patients diagnosed with stage IV disease was retrieved. Those who tested positive for one of the four biomarkers EGFR, ALK, MET, ROS from January 2010 to December 2016 were included. EGFR testing was done using Qiagen EGFR TherascreenRGQ PCR KIT. ALK-1 protein was tested by FDA approved immunohistochemistry.Ros-1 gene rearrangement was assessed using Dual Color Break Apart DNA probe (Zytolight). C- MET gene amplification assay was done using Zytolight labeled LSI MET DNA probe(green) and cen-7 probe(orange). Epidemiological patient profile and tumor histomorphology on small biopsies was correlated with molecular signature and assessed with treatment response and overall survival. **Result:** Of the total 1938 lung cancer patients included in our study, 347 patients were observed to exhibit positivity for either one among four molecular markers. Among 347 patients, 77.8% had EGFR mutation. Of these del 19 was commonest and observed in 55% cases, L858R in 27.6% cases, Exon 20 Insertion in 5% and G719X in 3% cases. 7% of these EGFR mutants showed dual mutation.ALK-1 protein overexpression was seen in 19.3% . ROS rearrangement was present in 0.8%. MET amplification was observed in 2%. Predominant histological type was adenocarcinoma (87.6%) with predominant solid pattern. The median overall survival for EGFR, ALK, ROS, MET were 13.44,11.5, 17.2 and 15.1 months respectively. Sex, age, histology, mutation type and performance status affected overall survival. **Conclusion:** Biomarker testing has improved outcome and provides new insight to cancer clinicopathological profile. **Keywords:** NSCLC, Predictive biomarker, Morphology

	EGFR			
	DEL 19 L858R EXON 20I G719X DUAL OTHERS(L861Q) (T790M)	ALK	ROS	MET
CASES	151 76 14 10 19 01	67	03	07
%	55 27.6 5 3 7 0.3 19.3 0.8 2			
OS	13.4 12.5 14.5 13 12.6 11 11.5 17.2 15.1			

P1.01-031
Utilization and Timing of Foundation Medicine (FMI) Testing in U.S. Advanced Non-Small Cell Lung Cancer (aNSCLC) Patients

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Background: Actionable insights generated by FMI's hybrid capture-based next-generation sequencing (NGS) comprehensive genomic profiling services are increasingly important for navigating cancer care in aNSCLC patients. FMI and other NGS platforms support treatment decisions by detecting a variety of genetic alterations implicated in oncogenesis. We describe: 1) the characteristics of aNSCLC patients receiving FMI testing and 2) the utilization patterns and timing of FMI testing in relation to treatment and other molecular tests using a real world oncology electronic health record (EHR) database. **Method:** Flatiron Health has a longitudinal, demographically and geographically diverse database containing EHR data, reflecting routine clinical practice, from over 265 cancer clinics in the US. Inclusion criteria were aNSCLC diagnosis and ≥2 clinic visits within the Flatiron network on or after January 1, 2011. Data pertaining to molecular testing was available on 5 biomarkers (EGFR, ALK, KRAS, ROS1, PDL1) and used to identify 3 mutually exclusive testing groups: FMI, other NGS and non-NGS. **Result:** As of March 31, 2017, the aNSCLC cohort included 33,473 patients. Of 1,395 patients with FMI testing, 738 (53%) also had ≥1 non-FMI test (43% EGFR, 40% ALK, 20% ROS1, 17% PDL1, 16% KRAS). In FMI-tested patients, 45% received results before starting a first line of therapy (vs. 57% of other NGS tested and 79% of non-NGS tested patients). Table 1 details patient and testing characteristics for FMI tested patients, along with first treatments received after FMI testing. **Conclusion:** Patients with FMI testing tended to be younger, non-smokers, and have squamous histology compared to patients receiving non-FMI tests. Nearly 50% of all FMI testing occurred prior to first treatment. Patients receiving FMI testing earlier were less likely to have a non-FMI biomarker test beforehand. Regardless of when FMI testing occurred, ~20-30% of patients received a NCCN-recommended targeted therapy immediately after the FMI test. **Keywords:** Oncology electronic health record (EHR), next generation sequencing (NGS), advanced non-small cell lung cancer (aNSCLC)