mutations are related with efficacy of chemotherapy and gefitinib, cisplatin-based chemotherapy. XRCC3 241 genotyping and EGFR non-small cell lung cancer are associated with clinical outcome to months, OS 15 months vs. 5.7 months, ORR 91% vs. 9%; P < 0.01).

Conclusions: RRMI and BRCA1 mRNA expression levels in non-small cell lung cancer are associated with clinical outcome to cisplatin-based chemotherapy, XRCC 3 241 genotyping and EGFR mutations are related with efficacy of chemotherapy and gefitinib, respectively.

3

Association between MicroRNA Polymorphisms, Expressions, Lung Cancer Development and Prognosis
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Recent evidence indicates that small non-coding RNA molecules known as microRNAs (miRNAs) can function as tumor suppressors or oncogenes. Mutation, mis-expression or altered mature miRNA processing are implicated in lung carcinogenesis and lung tumor progression. Recent findings that human serum contains stably expressed microRNAs (miRNAs) imply a great potential of serum miRNA signature as disease fingerprints. In addition, single nucleotide polymorphisms (SNPs) in pre-miRNAs could alter miRNA processing, expression, and/or target mRNA binding. Therefore, we hypothesized that serum mRNA expression profiles can be used as a novel non-invasive biomarker for non-small cell lung cancer (NSCLC) diagnosis and prognosis, and polymorphisms (SNPs) in pre-miRNAs are associated with lung cancer susceptibility and survival by modifying the miRNA expressions and binding affinities. To test these hypotheses, we used Solexa sequencing techniques followed by quantitative RT-PCR assay to obtain the expression pattern of serum miRNAs for NSCLC with different characteristics and related control. In addition, we genotyped four SNPs in pre-miRNAs identified to date in a case-control study of lung cancer to evaluate the associations of these SNPs with lung cancer susceptibility and survival. The preliminary results showed that (1) Four miRNAs (miR-486, miR-30d, miR-1 and miR-499) were well correlated with NSCLC survival by individual qRT-PCR on discovery stage samples. The 4-miRNA signature was consistently an independent predictor of survival in further training and validation samples and the predictive effects were more evident in stage I and II samples and in squamous cell NSCLC; (2) rs11614913 in hsa-mir-196a2 was significantly associated with NSCLC susceptibility and survival, and the variant homozygote CC increased the risk of lung cancer and was a significantly unfavorable prognostic factor of NSCLC. In addition, the rs11614913 CC was associated with a significantly increased mature hsa-mir-196a expression in lung tissues but not the precursors, suggesting an enhanced processing of pre-hsa-mir-196a to its mature form. Furthermore, in vitro binding assays revealed that rs11614913 variant can affect target mRNA binging to its mature hsa-mir-196a2-3 p. Therefore, we concluded that profiling of serum miRNAs can serve as a novel sensitive and specific non-invasive biomarker for both diagnosis and prognosis of NSCLC. SNP rs11614913 in hsa-mir-196a2 may be an independent susceptibility and prognostic biomarker for NSCLC.

4

Potential Efficacy of Multi-targeted Tyrosine Kinase Inhibitors in Non-small-cell Lung Cancer
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Outcomes of treatment for patients suffering from metastatic non-small cell lung cancer (NSCLC) are poor with chemotherapy. Recent years, novel agents such as erlotinib, gefitinib, cetuximab and bevacicizumab, which target specific, aberrant molecular pathways in NSCLC have been undergoing evaluation in clinical trials. These targeted agents targeting a single molecule in a signaling pathway involved in NSCLC have impacted the natural history of the disease. While modest, the activity of these single-target agents’ results in improved clinical outcomes, highlighting the promising potential of these agents that target biological pathways in patients with NSCLC. While NSCLC is a highly heterogeneous disease, it is likely that agents with multiple targets (e.g. sunitinib, sorafenib, ZD6474, AZD2171 and AMG 706) may have greater activity than those with single-target activity through inhibition of other pathways that may act as salvage or escape mechanisms for malignant cells. New multi-targeted therapeutic agents currently under clinical evaluation have shown promising effects as single agents, and preclinical studies have indicated that this efficacy may be due at least in part to the inhibition of multiple pathways that may result in a synergistic anti-tumor effect.

5

Comparing the Diagnostic Value of FLT and FDG PET/CT in Assessment of Regional Lymph Nodes in Thoracic Esophageal Squamous Cell Carcinoma
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Purpose: Using pathological examination as golden standard to determine whether FLT PET/CT can detect regional lymph nodes metastases in untreated thoracic esophageal squamous cell carcinoma. In view of the reported high sensitivity of FDG PET/CT for the evaluation of thoracic nodules of esophageal carcinoma, we additionally performed FDG PET/CT for direct comparison with that of FLT.

Materials and methods: From March 2008 to January 2009, 22 patients with thoracic esophageal squamous cell carcinoma underwent...