Poster
#1153P

Classification of multifocal lung adenocarcinomas subtypes using next-generation sequencing in pN0M0 lung adenocarcinomas

Xin Zhang[1], Changbo Sun[1,2], Liang Wang[3], Yuan Miao[3], Liming Wang[1], Xiaoxi Fan[1], Peng Yang[4], Yang Xu[4], Xue Ren[4], Xue Wu[4], Shun Xu[1]

[1]Department of Thoracic Surgery, The First Hospital of China Medical University, Shenyang, Liaoning, China; [2]Deparment of Thoracic Surgery, The University of Tokyo Graduate School of Medicine, Tokyo, Japan; [3]Department of Pathology, The First Hospital of China Medical University, Shenyang, Liaoning, China; [4]Nanjing Geneseeq Technology Inc., Nanjing, China

中国医科大学附属第一医院
THE FIRST HOSPITAL OF CHINA MEDICAL UNIVERSITY

BACKGROUND

The incidence of multifocal lung adenocarcinomas (MLAs) increased remarkably over the past decade, owing to the advancement in imaging technology. The classification of MLAs subtypes, including multiple primary lung adenocarcinomas (MPLAs) and intrapulmonary metastases (IPMs), has great clinical significance in staging and treatment decisions. However, the application of molecular approaches in MLAs diagnosis, especially in pN0M0 patients, has not been well-investigated.

METHODS

We retrospectively investigated 45 pN0M0 MLAs patients (101 lesion pairs). Five additional patients with intrathoracic metastases were used as controls for IPMs, while 223 patients with unifocal lung adenocarcinomas were randomly paired (489 pairs) as controls for MPLAs. Two diagnostic approaches, comprehensive histologic assessment (CHA) and broad panel next-generation sequencing (NGS), were performed and compared.

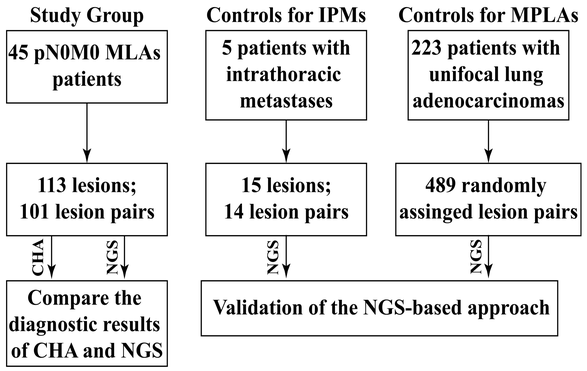

Figure 1. The schematics of the study. MLAs, multifocal lung adenocarcinomas; IPMs, intrapulmonary metastases; MPLAs, multiple primary lung adenocarcinomas; CHA, comprehensive histologic assessment; NGS, next-generation sequencing.

Patient Features	Number	%
Age		
≤60	24	53.3
＞60	21	46.7
Sex		
Male	13	28.9
Female	32	71.1
Family history		
Lung cancer	9	20
Other cancer	8	17.8
None	28	62.2
Smoking history		
Current/former	12	26.7
Never	33	73.3
Number of lesions		
2	31	68.9
3	6	13.3
4	7	15.6
5	1	2.2
Location of lesions		
Ipsilateral same lobe	17	37.8
Ipsilateral other lobe	22	48.9
Contralateral lobe	6	13.3

Table 1 Clinicopathological characteristics of the MLAs patients in the study group (n=45).

RESULTS

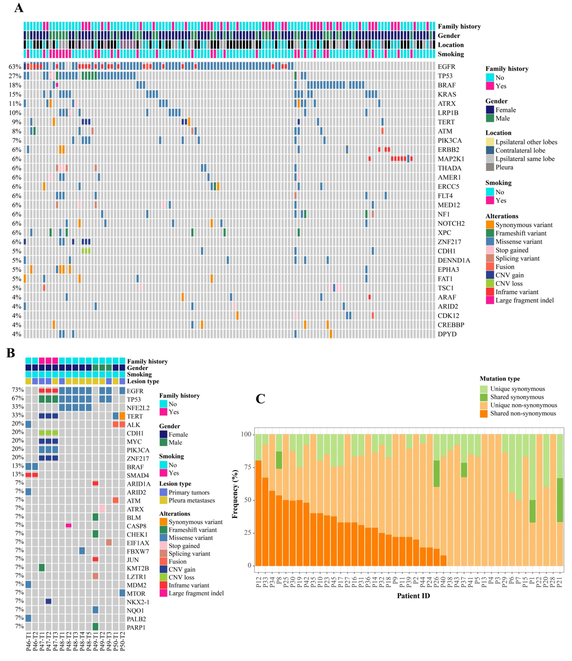

Figure 2 Analyzing the genetic features in the study group. (A) The genetic alterations detected in 113 lesions of the study group (n=45). (B) The genetic alterations detected in 15 lesions of the control group (n=5). (C) Distribution of somatic mutations among the 113 lesions in the study group.

Patients (p value=0.22)		NGS prediction		Total
		MPLAs	IPMs	
CHA prediction	MPLAs	26 (83.9%)	8 (61.5%)	34
	IPMs	5 (16.1%)	5 (38.5%)	10
Total		31	13	44

Table 2 The comparison of CHA prediction with NGS prediction at the patient level.

Lesion pairs (p value=0.03)		NGS prediction		Total
		MPLAs	IPMs	
CHA prediction	MPLAs	77 (91.7%)	11 (68.8%)	88
	IPMs	7 (8.3%)	5 (31.2)	12
Total		84	16	100

Table 3 Comparison of CHA prediction with NGS prediction at the lesion level.

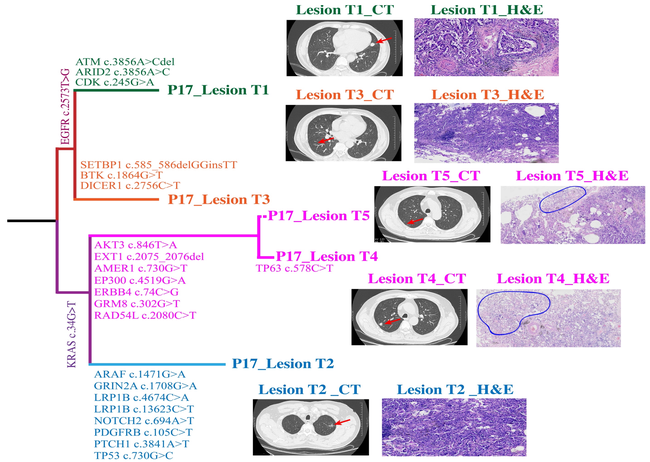

Figure 3 The phylogenetic and imaging analyses of patient P17. The CT scans of the five lesions were shown, with red arrows to indicate the position of tumors. The hematoxylin and eosin (H&E) images were illustrated on the right, and the evidence of spread through air spaces (STAS)-caused metastasis was highlighted using blue circle.

CONCLUSIONS

We characterized MLAs classification in pN0M0 patients using both CHA and NGS. Our results demonstrated considerable discordance between the diagnostic results from the two methods, suggesting the importance to classify MLAs using unbiased molecular approaches.

DISCLOSURE: Peng Yang, Yang Xu, Xue Ren, and Xue Wu are employees of Nanjing Geneseeq Technology Inc.. All other authors declare no conflict of interest.

CONTACT: Xin Zhang, M.D., The First Hospital of China Medical University
Email: zhangxin7@cmu1h.com