Abstract Group: 11.1. Lung Cancer

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Title: Multigene mutation analysis of mediastinal and hilar lymph nodes sampled by endobronchial ultrasound-guided needle aspiration

Dr. Thomas 3317 Vandemoortele 3317.thomas.vandemoortele@umontreal.ca MD 1, Dr. Isabelle 7900 Nanni-Metellus isabelle.nanni@ap-hm.fr MD 2, Dr. Elise 7901 Kaspi elise.kaspi@ap-hm.fr 3, Dr. Véronique 7902 Secq veronique.secq@ap-hm.fr MD 4, Dr. Sophie 7903 Laroumagne sophie.laroumagne@ap-hm.fr MD 1, Dr. Patrice 7904 Roll patrice.roll@ap-hm.fr MD 3, Dr. Elisa 7905 Roca elisaroca@gmail.com MD 1, Dr. Hervé 7906 Dutau herve.dutau@ap-hm.fr MD 1, Prof. Dr Philippe 7907 Astoul pastoul@ap-hm.fr MD 1 and Dr. Andrée 7908 Robaglia andree.robaglia@ap-hm.fr MD 3. 1 Thoracic Oncology, Pleural Diseases and Interventional Pulmonology, Hôpital Nord, Marseille, France; 2 Biologic Oncology Transfer Laboratory, Medical Faculty, Marseille, France; 3 Cellular Biology Laboratory, Hôpital La Timone, Marseille, France and 4 Department of Anatomopathology Laboratory, Hôpital Nord, Marseille, France.

Body: Background: The presence of an Epidermal Growth Factor Receptor (EGFR) activating mutation guide treatment selection in advanced Non-Small Cell Lung Cancer (NSCLC), whereas (BRAF) mutations play a role in metastatic melanoma. We aimed to determine the feasibility of routine multigene mutation analysis for EGFR, KRAS, BRAF and PI3KCA in EndoBronchial UltraSound-guided (EBUS) TransBronchial Needle Aspiration (TBNA) in patients with NSCLC and melanoma. Methods: Data was prospectively collected from patients undergoing EBUS-TBNA from March 2011 until September 2012. Smears were studied after using Papanicolaou and May-Grünwald Giemsa stains. Genetic mutations were analyzed in metastatic lymph nodes diagnosed by EBUS TBNA in 40 patients with NSCLC and melanoma. Methods: Data was prospectively collected from patients undergoing EBUS-TBNA from March 2011 until September 2012. Smears were studied after using Papanicolaou and May-Grünwald Giemsa stains. Genetic mutations were analyzed in metastatic lymph nodes diagnosed by EBUS TBNA in 40 patients with NSCLC and melanoma. Methods: Data was prospectively collected from patients undergoing EBUS-TBNA from March 2011 until September 2012. Smears were studied after using Papanicolaou and May-Grünwald Giemsa stains. Genetic mutations were analyzed in metastatic lymph nodes diagnosed by EBUS TBNA in 40 patients with NSCLC and melanoma. Methods: Data was prospectively collected from patients undergoing EBUS-TBNA from March 2011 until September 2012. Smears were studied after using Papanicolaou and May-Grünwald Giemsa stains. Genetic mutations were analyzed in metastatic lymph nodes diagnosed by EBUS TBNA in 40 patients with NSCLC and melanoma. Results: Mutigene mutation analysis was completed for samples from 40 patients (97.6%). Mutations were detected in 11 patients (26.8%) : 3 (7.3%) EGFR exon 19 deletion, 6 (14.6%) KRAS mutation, 1 (2.4%) BRAF, and 1 (2.4%) PI3KCA mutation. Only one sample could not be processed for the detection of KRAS mutation. All the samples were adequate for the other mutations detection. Molecular biology analyses were performed both on cytological samples and biopsy samples in 7 patients (17.1%), with a perfect correlation between these. Conclusions: Mutations of the EGFR, KRAS, BRAF and PI3KCA genes can be detected in cytological samples routinely obtained with EBUS TBNA.