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Title: Endobronchial ultrasound-guided sampling can be used for successful molecular sampling in routine clinical practice

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Body: Treatment in oncology is becoming increasingly driven by tumour genetics and biomarker status. In non-small cell lung cancer, mutations within the gene encoding for the tyrosine kinase domain of the epidermal growth factor receptor (EGFR) are associated with improved response to tyrosine kinase inhibitors. This has led to need for genetic analysis for this mutation in lung cancer patients. Initial studies assessed EGFR status in surgical biopsies. Many patients have advanced disease at presentation and there is a requirement to be able to perform this analysis on fine needle aspirates. Whilst studies have shown cytological samples specifically prepared are suitable for this analysis, few studies have assessed the ability to perform molecular analysis on routine samples. We hypothesised that molecular analysis would be possible from routine samples collected at our institution. All procedures performed between 2008 and 2011 were reviewed. Using patient and pathology records, data was collected on patient demographics, adequacy of samples, cytological diagnosis and molecular analyses performed. Cancer was diagnosed in 352 out of 741 cases (48%). Molecular analysis was performed in 70 cases (20% cancer cases). Molecular analysis included PCR, flow cytometry and FISH and occurred in varying cancer diagnoses including: lymphoma (B cell and Hodgkins), melanoma, sarcoma and lung and breast cancer. In a subgroup, EGFR analysis was possible in 87% (47/54) of cases with mutations present in 34% (16/47). Samples from EBUS-TBNA can be used for molecular analysis in routine clinical practice. Their use extends not only to lung but other metastatic cancers of the thorax.