Introduction New lung nodules observed after prior radical cancer treatment present a complex and increasingly common problem for lung cancer MDTs. Existing research shows lung cancer is common with previous smoking-related cancers, potentially due to shared risk factors or long-term effects of anti-cancer therapies. Radiomics involves computational high-throughput extraction of mathematical features from medical images. Study of AI and machine learning approaches using radiomics data aims to improve lung nodule stratification/malignancy prediction, but this clinical niche remains understudied.

Methods A retrospective series of CT thorax scans of patients with new lung nodules/lesions >5mm and previous radically treated cancer within 10 years curated for the AI-SONAR study, were anonymised and handcrafted manual segmentation performed. Voxel dimension parameters were standardised and 70:30 training/test set split applied. Radiomic feature extraction was performed on each nodule/lesion. Two-step feature reduction identified key radiomic features (<5) and a Radiomics Predictive Vector (RPV) generated and tested for accuracy in differentiating each malignant class. We further compared 88 different machine learning and feature selections combinations assessing for model AUC performance. Validation of both analysis approaches was performed on a public composite dataset.

Results 200 cases identified comprised 100 metastatic lung tumours (MS) and 100 second primary lung cancers (SPLC). Following feature reduction, two key radiomic features were identified to generate an RPV: 1) FOS_lmode_LLL 2) SNS_sph. The RPV achieved a training set performance AUC of 0.77, sensitivity 0.77, specificity 0.71 and F1 model precision score of 0.75. Test set RPV performance demonstrated an AUC of 0.82, sensitivity 0.83, specificity 0.70 and F1 score of 0.74. Analysis using contrast only cases (N=158) showed loss in RPV model performance, AUC 0.55/0.48 and F1 score 0.29/0.26 in training/test sets respectively.

Conclusion Our early work highlights that a radiomics based machine learning model may provide information to guide clinicians in timely diagnosis and management of new indeterminate lung nodules/lesions in patients with a previous radically treated cancer. Next steps involve a larger dataset analysis with additional data modalities. The scope of impact would be an opportunity to improve hospital resource use, patient anxiety and mitigate delays in early cancer diagnosis.

P76 COMPARISON OF ENDOBRONCHIAL ULTRASOUND (EBUS) FINE NEEDLE ASPIRATION (FNA) AND FINE NEEDLE BIOPSY (FNB) FOR CANCER DIAGNOSIS: A SINGLE CENTRE PROSPECTIVE STUDY

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Introduction EBUS is a key tool in the investigation of lung cancer and other metastatic malignancy. In the era of targeted treatment, acquisition of sufficient tissue for Next Generation Sequencing (NGS) is vital and fine needle biopsy (FNB) may offer an advantage over traditional fine needle aspiration (FNA). More real world experience of EBUS-FNB is required.

Methods A prospective study of FNB and FNA was undertaken at a tertiary centre between 12/2019–03/2020 and 03/2023–06/2023 in patients undergoing linear EBUS for investigation of suspected pathological mediastinal/hilar lymphadenopathy or pulmonary mass with either a Fransseen FNB or FNA needle or both. The histopathologist was blinded to the needle type used. Data was collected on patient demographics, EBUS nodal descriptors and pathology reports including sample quality [good, moderate or poor] and tissue adequacy for NGS.

Results 72 specimens (60 nodes, 12 lung masses) were obtained from 32 patients (23 via FNA 22G, 2 via FNA 21G and 47 via FNB 22G) (table 1). Ultrasound appearance was
recorded for 70 target lesions, 60% were homogenous while 40% were heterogeneous. Commonest lymph node stations sampled were station 7 (51.7%) and 4R (23.3%). Thirteen patients had tissue sampled via both FNA and FNB needles. Diagnoses included cancer (31% in FNB and 41.2% in FNA group), sarcoidosis (24.1% in FNB and 11.8% in FNA group) and benign lymphadenopathy (34.5% in FNB and 23.5% in FNA group).

Pathologist preference for specimen quality was significantly better with FNB vs FNA (55.3% vs 28%, fisher’s exact test p=0.04). Tissue architecture preservation was better with FNB vs FNA (57.4% vs 12%, fisher’s exact test p=0.0002). However, diagnostic yield did not significantly differ between either needle (fisher’s exact test p=0.77). In patients with Non-Small Cell Lung Cancer (NSCLC), suitability for NGS (Using the Oncomine Precision Assay on the Genexus platform) was better with FNB than FNA (75% vs 30%, fisher’s exact test p=0.03). No significant complications were observed.

Conclusion FNB provides a better quality specimen with preserved architecture than FNA. FNB samples were more suitable for NGS testing in lung cancer diagnosis.

REFERENCE

P77 EBUS TBNA FOR MOLECULAR TESTING IN LUNG CANCER – HOW MUCH IS ENOUGH?
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Background With the advent of immunotherapy and tyrosine kinase inhibitors, molecular testing has become routine and essential to guide oncological treatments. Endobronchial ultrasound and transbronchial needle aspirate (EBUS-TBNA) is a safe and accurate method for sampling mediastinal malignancies to diagnose and stage lung cancers. Sufficient tissue sampling for drug sensitivity testing (DST) is essential to ensure timely diagnosis and treatment. However, there is no clear guidance on the recommended number of passes per lymph node needed to facilitate this.

One study concluded that a median of 4 passes was needed to obtain sufficient tissue in adenocarcinomas. However, this required rapid on-site cytopathology evaluation (ROSE) and didn’t include DST for squamous carcinomas.

Standard practice at Royal United Hospital Bath is to perform 3 lymph node passes.Samples are deemed sufficient based on microscopic appearances determined by the endoscopist. The objective of our audit was to determine if our practice provided adequate tissue for successful DST in line with national standards, which should be greater than 90% of samples.

Method A total of 251 cases were audited between 2018–2023. Of these, 107 were diagnostic of lung adenocarcinoma, squamous cell carcinoma and non-small cell lung cancer NOS and sent for DST.

Exclusion criteria included other diagnoses, samples not sent for DST, and cases with more than 3 lymph node passes recorded on the EBUS report. Samples in which some drug sensitivity testing could take place but there was not enough tissue for all the required tests were categorised as insufficient.

Results Of the 107 cases, 98 (91.6%) were adequate samplings for DST and 9 (8.4%) were insufficient. All insufficient cases had a diagnosis of adenocarcinoma.

Conclusion Performing 3 lymph node passes were sufficient for DST without the support of ROSE and matched national standards in providing enough tissue sample for DST. This potentially can reduce the procedure duration for patients whilst maintaining diagnostic standards.

REFERENCES

P78 A ROSE BY ANY OTHER NAME WOULD SMELL AS SWEET: EVALUATION OF BIOMEDICAL SCIENTIST LED RAPID ON-SITE EVALUATION IN AN UK TEACHING HOSPITAL EBUS SERVICE
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Background Endobronchial ultrasound-guided transbronchial needle aspiration (EBUS-TBNA) is an established method to investigate hilar and mediastinal lymph node pathology. Rapid On-site Evaluation (ROSE) of lymph node aspirates is thought to be advantageous by ensuring adequate sampling, and can provide a rapid provisional diagnosis. However, ROSE can be associated with significant costs and resource use including cytopathologist time. Our consultant led service in a tertiary centre, has access to ROSE of EBUS-TBNA performed by 2 senior biomedical scientists (BMS), which provides limited microscopic evaluation to provide feedback of specimen adequacy in real time.

We aimed to evaluate the accuracy of BMS led ROSE of EBUS-TBNA, by comparing the initial ROSE assessment to the final pathology report by a cytopathologist.