Pulmonary Pathology Journal Club

(Articles from September 2025)

Presented by

Joanne Yi, MD

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Articles for Discussion

Ganapaty S, Cavazzi E, Manchen PJ, Butt YM, Smith ML, Tazelaar HD, Roden AC, Larsen BT. *Surgical pathology of diffuse parenchymal lung disease in patients with polymyalgia rheumatica*. Histopathology. 2025;87(3):453–463. doi:10.1111/his.15483

Background: Polymyalgia rheumatica (PMR) is a chronic inflammatory rheumatic disorder affecting mostly older patients between ages 70-80, characterized by stiffness and aching of the neck, shoulders, and hips. PMR is strongly associated with giant cell arteritis and sometimes with rheumatoid arthritis, but not with other types of rheumatologic disorders. Pulmonary involvement has been thought to be rare and details are not well documented in the literature. Given the recent radiologic observation with frequent GGO in PMR patients, pulmonary involvement might have been under recognized

Aims: To characterize diffuse parenchymal lung disease (DPLD) in PMR

Methods:

- Retrospective review of lung biopsies or autopsies from PMR patients with DPLD at Mayo Clinic archives during 2000-2024 (mostly consult service)
- Included those with sufficient clinical and radiologic information for demographic, tx hx, imaging findings, f/u outcomes
- Excluded infection, concomitant RA, or purely smoking related DPLD
- Review of HE, GMS, AFB for acute/chronic injury patterns, fibrosis type (UIP, NSIP, unclassifiable), small airway changes, vasculitis, and alveolar hemorrhage

Results

- N=11 (8F, 3M), mean age 74.4 $\pm$ 5.1 (median 75, range 66-82), 6 never smoker, 5 former smoker, develop 6-7 years after the dx of PMR
- Comorbidities: GERD, obesity, OSA, hypertension
- CT: bilateral GGOs, reticulation, often lower predominant, 1 case w/ honeycombing
- Pathology (Table 4): acute lung injury (73%) in the form of OP (45%), DAD/AFOP (18%), acute DAH with capillaritis (18%); chronic patterns showing mixed cellular/fibrotic NSIP (27%), UIP (9%), unclassifiable (36%); other features including alveolar hemosiderosis w/o vasculitis (36%), chronic pleuritis (27%), fibroblast foci (36%), honeycomb change (45%)

Take home message: DPLD is a rare but real manifestation of PMR. Organizing pneumonia and NSIP patterns predominate; UIP is rare. DAH with capillaritis can occur,

Kalchiem-Dekel O, Rakočević R, Toumbacaris N, Tan KS, Nadig TR, Adusumilli PS, Dycoco J, Lee RP, Oberg CL, Gray KD, Park BJ, Rocco G, Chaft JE, Solomon SB, Jones DR, Chawla M, Husta BC, Baine MK, Bott MJ. Robotic-assisted bronchoscopy for histopathologic subtyping of primary lung adenocarcinoma. *Lung Cancer.* 2025;207:108681. doi:10.1016/j.lungcan.2025.108681

Background:

- Subtyping of lung ADC for high-grade patterns (micropapillary, solid, cribriform, fused glandular) and mucinous differentiation is important for px and therapy
- However, limited tissue by preop bx makes precise grading and subtyping difficult
- Shape-sensing robotic-assisted bronchoscopy (ssRAB) gives a minimally invasive access to peripheral pulmonary lesions, integrating navigation, real-time imaging, and often allow an acquisition of adequate tissue for molecular profiling. (*this technique is recently showcased in the Nature. here is the paper for your information: Zhang Q et al. Shape sending robotic assisted bronchoscopy versus virtual bronchoscopic navigation in the diagnosis of peripheral pulmonary nodules. Nature Scientific Reports 2025;15:23950)*
- However, its performance for histopathologic pattern recognition is not well known.

Aims: To evaluate the performance of ssRAB-acquired biopsies in reflecting the histologic patterns and mucinous features with confirmation by surgical resection specimens

Methods:

- Retrospective review of all ssRAB procedures at MSK (Oct 2019 – Dec 2023) with dx of primary lung ADC using transbronchial forceps biopsy (TBFB) and/or transbronchial cryobiopsy (TBCB); TBNA only cases were excluded
- Histopathology evaluated per 2021 WHO Classification and IASLC grading system:
    - "High-grade" = ≥20% of solid (SOL), micropapillary (MIP), cribriform (CRIB), or fused glandular (GLAN) patterns
    - "Mucinous" = invasive mucinous adenocarcinoma (IMA) or mixed features
- Pattern by bx vs. subsequent surgical resection (when available)
- Logistic regression to identify predictors of successful pattern recognition
    - Sensitivity/specificity for biopsy vs. resection concordance.
    - Multivariable model: sampling type (cryobx vs. forceps), lesion characteristics, and imaging guidance.

Results

- ssRAB-acquired bx specimens (n=242) from 210 pts; subsequent resection (n=66)
- Median age 71 years; 65% female; 71% ever-smokers.
- Median lesion diameter: 23 mm.
- 66% of lesions: solid radiographically; 67%:located beyond the 6th AW generation.
- TBNA 97%; TBFB 95%; TBCB 21%
- Histopathologic pattern identified in 71% (172/242) of bx specimens with an overall accuracy of 68% for poorly diff histology on resection
- Cryobx improved pattern identification (92%) vs. (76% for forceps; $p = 0.04$).
- High-grade patterns identified in 44% and mucinous features in 19% of samples.
- Reasons for pattern non-identification: Crush artifact (39%); Low tumor cell content (21%); Nondiagnostic sampling (40%)
- Concordance with Surgical Resection (n = 66)

Feature	Accuracy	Sensitivity	Specificity	PPV	NPV
Poorly differentiated adenocarcinoma (≥20% high-grade)	68%	63%	72%	61%	74%
Mucinous features (IMA or mixed)	95%	89%	96%	80%	98%

- After excluding neoadjuvant cases, accuracy for poorly differentiated adenocarcinoma improved to 72%.
- No significant effect of location, size, or imaging guidance on concordance rates.
- Adverse events:1.4% pneumothorax; 0.4% bleeding requiring tube thoracostomy.

Take home message

- ssRAB can reliably identify high-grade and mucinous subtypes in lung ADC in comparison with resection histology and provides tissue quality comparable to transthoracic approaches
- ssRAB with cryobiopsy may be comparable to percutaneous biopsy for diagnostic and molecular profiling of peripheral adenocarcinoma.

Alay A, Marín R, Aliagas E, Gausachs M, Ruiz-Gil M, Macia I, Ojanguren A, et al. Single-cell RNA-sequencing as a potential approach for studying intratumor heterogeneity in pleural mesothelioma. *Lung Cancer.* 2025;207:108679. doi:[10.1016/j.lungcan.2025.108679]

Background:

- Recent adoption of ipilimumab + nivolumab for first-line therapy partially improved outcomes but prognosis remains poor in pleural mesothelioma (PM).
- Intratumor heterogeneity (ITH) is a contributor to therapeutic failure in PM that might be due to molecular and phenotypical heterogeneity across different sites of PM.
- Single-cell RNA sequencing (scRNA-seq) allows high-resolution profiling of cellular states within spatially distinct tumor samples and can identify subpopulations (e.g., stem-like, epithelial, mesenchymal) that may influence px and therapy response.

Aims: To map ITH and derive gene-expression signatures by scRNA-seq of multi-site bx's from a single epithelioid PM case

Methods:

- Three spatially distinct pleural bx's from costal, diaphragmatic, mediastinal foci.
- scRNA-seq using fresh tumor tissue; $CD45^{-}$ cells were selected; single-cell plates were used and libraries prepared; 287 tumor cells were retained for analysis.
- Clustering (UMAP), differential gene expression per cluster, trajectory analysis to infer transitions (epithelial ↔ mesenchymal), and derivation of cluster-specific gene signatures (SigC1, SigC2, SigC3).
- Derived signatures were tested for clinical relevance (by GSVA) against bulk PM datasets to assess associations with OS and predicted therapy sensitivity.

Results:

- Three main tumor cell states were identified across all three sampled regions:
    - C1: stem-like (dominant globally; high ALDH1A1 and ECM/stemness genes)
    - C2: epithelial-like (epithelial markers)
    - C3: mesenchymal-like (EMT/mesenchymal markers)
- Distribution varied by site: C1 (stem-like) underrepresented in the mediastinal foci, relative to costal/diaphragmatic samples, showing spatial heterogeneity.

- Trajectory analysis: epithelial–mesenchymal plasticity, with the stem-like C1 state occupying an intermediate/transitionary position.
- Signatures & clinical correlation:
    - SigC3 (mesenchymal) enrichment in bulk PM cohorts was associated with worse OS and reduced sensitivity to standard therapies.
    - SigC1 (stem-like) enrichment suggested possible sensitivity to anti-angiogenic therapies in exploratory analyses.
- scRNA-seq captured transcriptional heterogeneity not obvious morphologically; regional differences in cell-state proportions indicate that single-site biopsies could miss clinically relevant subclones.

Take home message

- PM has marked spatial and transcriptional heterogeneity; single-site profiling may underestimate clinically important subpopulations.
- Mesenchymal-like transcriptional programs (SigC3) identify tumors with worse outcomes and treatment resistance.
- scRNA-seq signatures derived from multi-site sampling could inform personalized therapeutic strategies, but require validation in larger cohorts**.**

Kurosaki T, Tanaka K, Okada T, Goto A, Yokoi T, Miyoshi T, Iwasawa S, et al. B7-H3 and DLL3 expression in extensive-stage small-cell lung carcinoma (ES-SCLC): Impact on the efficacy of PD-L1 blockade therapy. *Lung Cancer.* 2025;207:108685. doi:10.1016/j.lungcan.2025.108685

Background:

- While immune checkpoint inhibitors (ICIs) (e.g. atezolizumab and durvalumab) have modestly improved survival of SCLC when added to platinum–etoposide chemotherapy, biomarkers predicting their efficacy remain unclear.
- Two emerging molecules of interest in SCLC are: **B7-H3 (CD276),** an immune checkpoint molecule expressed on tumor and stromal cells, associated with immunosuppression and poor px in other malignancies and **DLL3 (delta-like ligand 3),** a notch pathway inhibitor highly expressed in SCLC and a target for antibody–drug conjugates (e.g., tarlatamab) for treating lung cancer patients.

- For pathologists, understanding the co-expression and localization of B7-H3 and DLL3 provides insight into both tumor biology and therapeutic target overlap, especially as novel B7-H3– and DLL3-directed agents enter clinical use

Aims To investigate whether tumoral expression of B7-H3 and DLL3 correlates with treatment outcomes to PD-L1 blockade therapy in extensive-stage SCLC (ES-SCLC).

Methods

- Design: Retrospective multicenter cohort study of ES-SCLC patients treated with chemo (platinum–etoposide) plus PD-L1 inhibitor (atezolizumab or durvalumab).
- Sample: Pretreatment tumor biopsies (n = 95; 2018–2024); all centrally reviewed.
- Immunohistochemistry (IHC) and genetic study:
    - B7-H3 (clone SP206): H score (0–300) – cutoff 91-95 (by log rank analysis)
    - DLL3 (clone SP347): % of + tumor cells regardless of intensity – 81-85%
    - PD-L1 (22C3 CPS) and CD8 for TILs (# in a 400x in 1-5 random tumor regions)
    - immune-related gene expression profiling (irGEP) with nCounter and a PanCancer IO 360 gene expression panel (Nanostring), TMB, neoAg load
- Statistical analysis:
    - Survival: Kaplan–Meier and log-rank tests.
    - Multivariate analysis: Cox regression adjusting for age, ECOG PS, and LDH.
    - Spearman correlation analysis between B7-H3 and DLL3 expression.

Results

Expression Patterns

- B7-H3 (membranous/cytoplasmic) and DLL3(cytoplasmic/granular) in tumor cells
- B7-H3 positive in 74/95 (78%) of cases; DLL3 positive in 88/95 (93%)
- Co-expression (B7-H3 high + DLL3 high) found in 68% of tumors
- Expression of both molecules was mutually correlated ($r = 0.62$, $p < 0.001$).
- PD-L1 expression was low (<1% in 90% of cases); not associated with outcomes.

Treatment Outcomes

- Median follow-up: 22 months
- Overall Response Rate (ORR): 68%.
- Median PFS: 6.8 months; Median OS: 15.4 months.

Subgroup analysis:

- B7-H3 high group: shorter OS (12.3 vs. 21.0 months, $p = 0.011$).
- DLL3 high group: trend toward shorter OS (13.5 vs. 20.7 months, $p = 0.09$).
- Double-high (B7-H3+/DLL3+): worst survival (median OS 11.8 months, $p = 0.003$).
- Multivariate Cox model: high B7-H3 independently predicted poor OS (HR = 1.85, 95% CI 1.14–3.00, $p = 0.013$).

Immune Microenvironment Correlation

- High B7-H3 expression, but not DLL3, grouped w/ fewer CD8+ T cells (immune cold phenotype), lower tumor PD-L1 expression, worse survival in chemo + ICI group
- Impaired function of T cells in B7-H3$_{high}$ tumors, by irGEP profiling
- No effect of DLL status on CD8+ TILs or on the efficacy of ICI by irGEP analysis

Take home message

- B7-H3 is a negative prognostic biomarker in ES-SCLC treated with PD-L1 inhibitors.
- DLL3 remains a potential target, but not a strong predictor of ICI response.
- Co-expression (B7-H3 + DLL3) identifies a high-risk, immune-cold subgroup with limited benefit from current chemo-ICI.
- This study underscores the complexity of immune evasion in SCLC. While PD-L1 remains largely absent, alternative checkpoints like B7-H3 may dominate immune suppression.

Articles for Notation

Neoplastic

Wang W, Wei H, Qu C, et al. Unlocking the potential: tissue mutation abndance as a predictor for third-generation EGFR-TKI efficacy in NSCLC. Lung Cancer 2025;207:108699

Background

Targeted therapy against EGFR mutations has transformed the management of NSCLC. Third-generation EGFR TKIs (osimertinib, almonertinib, furmonertinib) are now standard first-line tx for advanced NSCLC with exon 19 deletions and exon 21 L858R substitutions.

However, tx responses vary among patients with identical mutations. While the FLAURA, AENEAS, and FURLONG trials established superior efficacy of third-generation TKIs than 1st- or 2nd -generation agents, 10–30% of patients show poor or short-lived responses.

Emerging data suggest that the abundance of EGFR mutations within tumor tissue (mutation allele frequency) may predict the strength and duration of response to TKIs. High mutation abundance reflects clonal dominance of the driver mutation, whereas low abundance may indicate tumor heterogeneity or subclonal resistance.

Aim: To evaluate whether tissue mutation abundance predicts tx efficacy and PFS in patients receiving 3rd-generation EGFR-TKIs as the first line therapy.

Methods

- Retrospective cohort study (single institution, Jilin University, 2016–2024).
- Inclusions: EGFR exon 19 deletion or L858R mutation, no prior EGFR-TKI, ECOG ≤3)
- Exclusions: rare EGFR mutations, exon 20 insertions, prior TKI therapy, sequencing from plasma or pleural fluid, or severe comorbidities.
- Treatment: Osimertinib, almonertinib, or furmonertinib until progression or toxicity.
- Mutation quantification:
    - NGS-based detection of EGFR mutations using FFPE tumor blocks (DNBSEQ™ platform, >2200× coverage).
    - Mutation abundance = ratio of mutant EGFR copies to total EGFR copies.
    - ROC curve determined optimal cut-off for “high” vs “low” mutation abundance → 22.9%.
- Endpoints: Objective response rate (ORR), disease control rate (DCR), median progression-free survival (mPFS), and factors affecting mPFS.
- Statistical analysis: Kaplan–Meier survival estimates; univariate and multivariate Cox regression models.

Results

Patient Characteristics

- 159 patients (median age 65; 67% stage IV).
- 27.7% current/former smokers

- 63% w/ coexisting genetic alterations (e.g. PIK3CA, TP53).
- High-abundance group (≥22.9%): 108 patients (68%).
- Low-abundance group (<22.9%): 51 patients (32%).
- No significant differences in age, sex, ECOG score, TNM stage, or EGFR mutation subtype between groups.

Treatment Outcomes

Outcome	High-abundance	Low-abundance	p-value
ORR	88.0%	66.7%	0.032
DCR	97.2%	80.4%	<0.001
mPFS	22 months	17 months	0.024

- No significant difference in complete or partial response rates individually, but higher overall disease control in the high-abundance cohort.
- Both groups showed similar patterns of progression (local recurrence, visceral, bone, brain metastases).

Multivariate Cox Analysis

- In the high-abundance group, none of the clinical covariates (mutation site, metastasis type, PIK3CA co-mutation) independently predicted mPFS.
- In the low-abundance group, ECOG performance status and tumor site (peripheral vs central) were associated with PFS.
- High mutation abundance remained the independent predictor of prolonged mPFS.

Take-Home Message

- Higher allele frequency with better efficacy of third-generation TKIs.
- Low-abundance mutations at risk for early progression and resistance.
- NGS quantification of mutation abundance in FFPE as a relevant biomarker.
- Incorporating mutation abundance could refine treatment personalization, guiding early combination therapy or closer follow-up in low-abundance cases.

Chu CY, Thingujam B, Wang SH, et al. HIV-negative primary effusion lymphoma: a series of seven cases. Histopathol 2025'87:397-407

A 7 case series of HIV-negative PEL cases with detailed description of each case from Taiwan. PEL is a CD30+ post-GC B cell lymphoma with poor px and composed of large pleomorphic cells with immunoblastic, plasmablastic or anaplastic morphology. PEL is HHV8+ and CD38+, but negative for B-cell and T-cell markers. HHV8 infection is endemic in sub-Saharan Africa and the mediterranean basin, while uncommon in other geographic regions and usually associated with HIV infection and AIDS. PEL is rare in HIV-negative population and non-endemic regions including Taiwan. This series documented PEL arising in immunocompetent older patients.

Granberg M, Aanerud M, Halvorsen TO, et al. Associations between progastrin-releasing peptide (ProGRP) and neuron-specific enolase (NSE) and survival in patients with limited -stage small cel llunc cancer (LS SCLC) receiving chemoradiotherapy (CRT). Lung Cancer 2025;207:108678

Prospectively collected data from a clinical trial from the patients who underwent similar diagnostic w/u and tx. In the absence of established biomarkers for predicting outcomes of CRT in LS SCLC, they investigated the role of ProGRP as a potential biomarker in a randomized phase II trial. ProGRP levels before and after CRT were associated with both PFS and OS in this cohort (n = 170) that received concurrent chemotherapy and BID RT, while NSE levels were not significantly associated with the treatment outcomes.

Provencio M, Cobo M, Rodriguez-Abreu D, et al. Biomarker landscape in advanced NSCLC: insights from a national prospective registry. Lung Cancer 2025;207:108680

This study aimed to provide real-world data on biomarker testing in Spain and how this field has evolved in the last 4 year. The Spanish Lung Cancer Group performed an exploratory analysis of actionable genes in stage IV NSCLC patients. The Thoracic Tumor Registry (TTR), a Spanish prospective, observational cohort study enrolled from 82 hospitals had 27,399 patients, and 13,583 NSCLC patients were in stage IV. At least one tumor marker was performed in 85.7% of the non-sq and 62.8% of sq ca patients. In non-sq population, the 3 most frequently analyzed markers were EGFR (77.3%), ALK (66.1%), and PD-L1 (56.3%). In recent years, sqcc patients had a more pronounced and extensive biomarker profiling, even for those without approved targeted therapy.

Ikeda K, Sakabe N, Fukuda K, et al. Deep learning neural network of adenocarcinoma detection in effusion cytology. Am J Clin Pathol 2025;164:415-423

Authors developed a deep learning model YOLOv8, which was tested to detect malignant cells in images of effusion cytology. They claimed that the accuracy is sufficient to assist cancer screening in effusion cytology!

Park S, Ahn HK, Lee S, et all. Lazertinib for patients with NSCLC harboring uncommon EGFR mutations: A phase II multicenter trial. J Thorac Oncil 2025;20:1279-1288

Based on this trial, they reported promising efficacy and a reasonable safety profile of lazertinib in NSCLC patients with uncommon EGFR mutations (G719X, S768I, L861Q).

Krebs MG, Cho BC, Hiret S, et al. Amivantamab in participants with advanced NSCLC and MET Exon 14 skipping mutations: Final results from the CHRYSALIS study. J Thorac Oncol 2025;20:1289-1301

They report an effective new drug in NSCLC with MET exon 14 skipping mutations, with the safety profile comparable to that in the setting of treating the pts w/ EGFR mutant NSCLC.

Non-neoplastic

Reddy YN, Asokan AK, Frantz RP et al. Metabolomic evidence of biological overlap with heart failure with preserved ejection fraction in a subset of pulmonary arterial hypertension. Am J Crit Care Respir Med 2025;211:1701-1713

It has been noted that group I PH has subtypes: those with high and low probability of left heart failure (in the form of HfpEF). This study looked into metabolome in these two subtypes and showed a unique metabolome through enhanced tryptophan-kynurenine pathway breakdown, deficiency of amino acids (such as glycine and serine), lower serotonin, and decreased concentrations of prostaglandin and nitric oxide precursors (linoleic acid, arginine, homoarginine), which contrasts markedly from the metabolome of pts with group I PH and lower HfpEF probability. These metabolome changes were comparable with those of pts with clinical actual HFpEF, supporting biological overlap between traditionally defined HfpEF and a subset of group I PH.

Rastoder E, Sivapalan P, Hedsund C, et al. Pulmonary pressure increases during acute exacerbation in COPD and clinical outcome. Eur Respir J 2025;66:2500169; editorial Uysal OF, Hurst JR. Pulmonary hypertension in COPD exacerbation: a transient storm with long-term consequences? Eur Respir J 2025;66:2501508

(an editorial in the same issue: Uysal OF and Hurst JR. Pulmonary hypertension in COPD exacerbation: a transient storm with long-term consequences?)

This study includes the largest prospective cohort to examine paired hemodynamic measurements during COPD exacerbations and the stable state, built on previous retrospective or smaller studies that suggested PHT during exacerbations but without the rigor of longitudinal component. The main aim of this study was to investigate the association between tricuspid regurgitation (TR) gradient during AECOPD (n=232) and the stable phase (n=107). TR gradients were significantly elevated during AECOPD, suggesting right sided pressure spikes during AECOPD. Additionally, a higher TR gradient was associated with a longer hospital stay.

Fennell E, Taylor GS, Leahy CI, et al. Multi-omic spatial profiling reveals the unique SARS-CoV-2 lung microenvironment and collagen VI as a predictive biomarker in severe COVID 19. Eur Respir J 2025;66:2301699

Authors sought to investigate the pathogenic role of microenvironmental interactions and the extracellular matrix in post-mortem COVID-19 lung using an integrative multi-omic approach (multiplex spatial proteomics, spatial transcriptomics, TCRseq, serum proteomics with Quantseq Bulk RNA sequencing, Nanostring GeoMx spatial transcriptomics, RNAscope, multiplex IF and IHC). They evaluated virus distributions, immune composition, and ECM. Markers of extracellular synthesis and breakdown were measure in the serum of 215 COVID-19 pts and 54 healthy volunteer controls using ELISA. There was immunosuppressive virus microenvironment and upregulated collagen VI. Serum PRO-C6, a predictor of collagen VI synthesis, predicted mortality in hospitalized patients.

Schneider H, Ius F, Muller C, et al. Pediatric lung transplantation for childhood interstitial lung disease: Indications and outcome. J Heart Lung Transpl 2025;44:1460-1468

This study was to analyze the pre-, peri-, and post-operative characteristics of patients with chILD and to compare the outcome to patients who underwent pediatric lung TPX for CF or

pulmonary HT. chILD group was divided into: A - ill during the 1st 2 years of life; B – ill afterwards. Lung TPX for chILD shows favorable outcome, but younger chILD A group had a higher pretpx morbidity and longer ICU and hostpital stay after TPX.

Brunet-Ratnasingham E, Yellamilli S, Guo R, et al. Persistent and progressive acute lung allograft dysfunction is linked to cell compositional and transcriptional changes in small airways. J Hear Lung Transpl 2025;44:1482-1492

Authors hypothesized that acute allograft dysfunction (ALAD) may be associated with changes in small airway cell composition and cell specific transcription. They prospectively identified recipients with ALAD and with stable allograft function for small AW brushing and single cell RNA seq analysis. The cohort comprised of: control (n=8), ALAD with recovered (n=4), persistent (n=5) and progressive (n=3) FEV1 decline. Cell compositional changes were assessed by airway brush transcriptomes (based on their prior study) as a function of ALAD outcome groups. This 68,140-cell dataset identified cell compositional and transcriptional changes associated with persistent or progressive ALAD, suggesting that interventions targeting interferon-dependent Ag presentation, macrophage/T cell dysregulation, and associated basal/club cell dedifferentiation may hold promise as interventions during episodes of lung function decline in lung tpx recipients.

Case reports

Singh R, Sharma P, Baishya N, Benur A. A 27-year old woman with rapidly progressive shortness of breath and severe alopecia. Chest 2025;168:e65-e68

A case of SLE with diffuse alveolar hemorrhage – showing good CT images and review as well as clinical presentation

McKenna AM, Tiwari A, Chopra A, et al. Management of pulmonary granulomatous venulitis by lung transplantation. Chest 2025;168:e59-e63

An exceedingly rare case of PVOD caused by granulomatous inflammation and obliteration of small pulmonary veins that was successfully treated by lung transplantation

Review, perspectives, editorials, letters to the editors

Ng N, Molina-Molina M, Adgunsoye A, et al. Genetics of interstial lung diseas: a state-of-the-art review. Eur Respir J 2025;66:2500788

Dacic S. Neoadjuvant therapy and the lung cancer. Role of pathologists. Arch Pathol Lab Med 2025;149:e78-e81

Chaddha U, Agrawal A, Ghori U, et al. Safety and sample adequacy for comprehensive biomarker testing of bronchoscopic biopsies: An American Association of Bronchology and Interventional Pulmonology and International Association for the Study of Lung Cancer Clinical Practice Guideline. J Thorac Oncol 2025;20:1237-1256

Park Y, Kang DH, Chung C. Integrating tumor macroenvironment, microenvironment and mechanobiology with organoid and organ-on-a-chip models for lung cancer immunotherapy. Lung Cancer 2025;207:108726

Wells JM, Krishnan JA, Wade RC, et al. Post-COPD: Can emphysema be repaired? Am J Respir Crit Care Med 2025:211:1600-1608

Fouad J, Vachani A. Diagnostic bronchoscopy for peripheral lung lesions. When innovation races to meet demand. Am J Respir Crit Care Med 2025;211:1541-1542

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Imai R, Fukui S, Inoue K. Pirfenidone and ung cancer in idiopathic pulmonary fibrosis: mind the index date, detection bias and competing risks. Eur Respir J 2025;66:2500423

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