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⊕ Fibroblast Activating Protein: Skimming the Surface of Molecular Imaging to Assess Fibrotic Disease Activity

Noninvasive studies to assist with the diagnosis of pulmonary fibrosis and individual prognostication represent a “holy grail” for idiopathic

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pulmonary fibrosis (IPF) and other interstitial lung diseases (ILDs). Multiple studies have investigated the ability of physiologic measurements, molecular profiling, circulating cellular markers (i.e., monocytes), and imaging biomarkers to predict disease progression. However, there remains no clinically used disease activity marker for single-time point assessment to assist with treatment decisions. In this issue of the *Journal*, Yang and colleagues (pp. 160–172) evaluate “fibroblast activating protein” (FAP) as a molecular marker of disease activity with the potential to be leveraged for prognostic purposes (1).

FAP is a transmembrane serine protease that was initially found to be expressed by cancer-associated stromal cells and subsequently

shown to be expressed on other cell types, including macrophages (2). While associated with fibrosis, FAP has been shown to have antifibrotic actions linked to its role in the proteolytic degradation and processing of collagen. Indeed, FAP-deficient mice have increased collagen accumulation in lungs after radiation- or bleomycin-induced injury (3). However, FAP is also reported to enhance α_2 -antiplasmin function, which would be expected to stabilize fibrinogen and fibronectin and contribute to lung fibrosis (4, 5).

FAP expression is increased by the profibrotic cytokine TGF- β (transforming growth factor- β), and expression is increased in murine models of lung fibrosis. Within the lungs of patients with IPF, FAP was upregulated within fibroblastic foci, but not in the adjacent alveolar epithelium or in normal lung tissues (6). However, increased expression may not be detrimental; a recent study showed that depletion of FAP⁺ cells or genetic deletion of FAP exacerbated fibrosis in a murine model of repetitive bleomycin injury and had no impact on fibrosis induced by adenoviral overexpression of TGF- β (7). Regardless of its role in pathogenesis, recent studies have used FAP to direct delivery of approved and emerging antifibrotic drugs, supporting its potential as an indicator of active wound repair and fibrosis (8, 9).

Here Yang and colleagues (1) evaluate FAP expression using human lung fibroblasts, a murine model of pulmonary fibrosis, single-cell sequencing, and a radiolabeled FAP inhibitor administered to patients with ILD. This study has several major findings. Fibroblast expression of FAP is induced by TGF- β . Similar findings have been shown in fibroblasts from several sources and disease states (2, 6). *In vivo*, increased FAP expression was detected 1 week after bleomycin-induced lung injury. FAP expression was increased in fibrotic human lung tissue, with half of explanted IPF samples and almost all of silicosis lung tissue samples showing elevations, demonstrating that increased FAP expression is not specific for IPF. Single-cell transcriptomic analysis indicated that FAP was highly expressed in mesenchymal cells and that there was moderate correlation with other mesenchymal cell markers associated with fibrosis (α -SMA [α -smooth muscle actin], fibronectin, and collagen I).

In a small group of healthy volunteers and a larger group of subjects with ILD (IPF and non-IPF), ⁶⁸Ga-FAPI-04 positron emission technology (PET) uptake was increased in the lungs of subjects with ILD compared with healthy volunteers. Differences in total standardized uptake value (SUV_{total}) but not mean standardized uptake value were seen between the IPF and non-IPF ILD groups, with the IPF group having a higher SUV_{total}. As SUV_{total}, a measurement defined by the authors, captures the extent of probe uptake above a threshold, this finding hints at underlying biologic heterogeneity among ILD subtypes. SUV_{total} correlated moderately with subsequent changes in FVC and DL_{CO}; however, the follow-up times for pulmonary function testing were nonuniform, ranging from 4 to 24 months.

A major strength of this study lies in the application of molecular imaging to establish a link between FAP expression as a biologic indicator of fibroblast activation and a noninvasive indicator of disease activity. PET probes targeting type I collagen, CCR2 (C-C chemokine receptor 2), α v β 6 integrin, and CXCR4 (C-X-C motif chemokine receptor 4) have been recently applied to patients with IPF to detect disease or to assess treatment effects (10–13).

⁶⁸Ga-FAPI-04 PET/computed tomography has been performed in systemic sclerosis-associated ILD, and the degree of probe uptake was associated with disease progression (14). This study by Yang and colleagues (1) illustrates several important applications of molecular imaging to ILD. First, it can be used to obtain molecular information otherwise not available and thus advance our understanding of molecular heterogeneity within individuals and ILD subtypes. Second, imaging of molecular pathways involved in fibrogenesis could provide a window into disease activity at a single time point. This study also highlights important considerations in using molecular imaging. PET biomarkers that incorporate both magnitude of uptake and amount of lung involved may better predict disease progression for diffuse lung diseases compared with traditional PET measurements such as mean standardized uptake value.

Several important gaps remain in establishing FAP as a reliable marker of disease activity. This study does not definitively link FAP expression with profibrotic fibroblast activity. Indeed, although FAP correlated with ACTA2 (actin alpha 2, smooth muscle), COL1A1 (collagen type I alpha 1 chain), and FN1 (fibronectin 1) in single-cell analysis, transcriptional expression does not always reflect protein concentration. Given its role in collagen turnover, FAP may have a functional role in controlling the wound-repair response to prevent the excessive collagen accumulation that characterizes fibrosis. Thus, studies will need to determine the ability of molecular imaging for FAP to distinguish between physiologic and fibrotic repair. More definitive studies are needed to determine if ⁶⁸Ga-FAPI-04 PET can reliably predict disease progression in ILD and whether FAP activity can predict responsiveness to antifibrotic therapies. Although the premise of differentiating “active” from “stable” disease by noninvasive FAP assessment as a decision tool to guide pharmacotherapy is appealing, fibrosis progression is not linear and for some individuals may occur in a stepwise manner. In the liver, FAP expression in hepatic stellate cells correlates with fibrosis severity (15), and circulating FAP is increased in patients with increased liver stiffness, supporting a potential role for FAP in the risk stratification of patients for liver fibrosis (16). In the lung, one modality may not provide the sensitivity and specificity needed for risk prediction or guidance of therapy in an individual patient. Nevertheless, the combination of accessible serum or genetic markers with physiologic measurements and molecular imaging may improve our ability to risk stratify individuals with ILD. ■

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⊕ Too Little, Too Late: Adult Lung Disease Cannot Be Prevented by Interventions in Adult Life

Ask a layperson what images heart disease conjures up, and they will probably talk about a relatively young adult suddenly clutching their chest and being rushed off to hospital, defibrillators, intensive care units, and interventions and maybe surgery. The sentiment will be “there but for the Grace of God go I”. Ask the same layperson about lung disease, and it will be an old person coughing and maybe on oxygen, the author of their own misfortunes because of current or previous smoking. This is a totally unfair caricature, but without doubt, the perception exists and accounts in part for the disparities in charity funding for heart and lung disease.

However, it is becoming increasingly clear that many adults with lung disease are actually the victims of early life adverse events, long before they had any control over their own fate. The prime example is chronic obstructive pulmonary disease (COPD). Failure to reach a normal plateau of spirometry at age 20–25 years carries a 26% risk of COPD (1), and peak attained spirometry is largely determined by antenatal and early preschool exposures (reviewed in [2]). If early

lung growth is normal, the risk of COPD reduces to 6%, which relates to an accelerated decline in spirometry (1). There are likely many reasons for an accelerated decline in lung function, and no consistent single cause is reported from the big COPD cohorts recruited in adult life, but early adverse exposures such as maternal smoking in pregnancy and severe respiratory infections are implicated in three large studies (3–5). Adult smoking is a factor, but not one that is consistently reported (6). Asthma in the third and fourth decades of life can be traced back to antenatal adverse exposures (7). Women with so-called late onset asthma in fact had airway disease by six years of age, which they had forgotten (8), reminding us how inaccurate retrospective recall of childhood respiratory disease actually is (9). Early adverse life events also increase the risk of occupational asthma (10); in a study of 13,499 occupational cleaners who were administered the Respiratory Health in Europe (RHINE) III questionnaire, the risk of self-reported wheeze, adult-onset asthma and COPD were greatest in those with early life disadvantage, including maternal smoking and severe respiratory tract infection before five years of age.

In this issue of the *Journal*, He and colleagues (pp. 173–182) add to these concerning studies by relating lung cancer risk to early adverse life events (11). They included nearly 400,000 participants from the UK Biobank study in their analysis, in whom nearly 2,000 lung cancers were recorded. These volunteers were recruited to the Biobank at age

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