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Title: Gene expression profiles of idiopathic interstitial pneumonias: Identification of disease-specific diagnostic markers and molecular therapeutic targets

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Body: Introduction: Idiopathic pulmonary fibrosis (IPF) and nonspecific interstitial pneumonia (NSIP) are characterized by alveolar epithelial damage and inflammatory responses that lead to fibroblast proliferation and, ultimately, to loss of normal pulmonary architecture and function. Differential diagnosis between IPF and NSIP may be difficult. The molecular mechanisms underlying idiopathic interstitial pneumonias (IIPs) remain unclear. Aims: This study aimed to elucidate the mechanisms underlying IIPs and identify disease-specific diagnostic markers and molecular therapeutic targets. Methods: The study included 12 patients with IIPs (IPF, 7 patients; NSIP, 5 patients). RNA was extracted from frozen lung specimens from the study population and was profiled using Illumina Human WG-6 v3 BeadChips. Gene ontology functional annotations were investigated in the genes upregulated in IIPs. Results: Evaluation of 48,000 transcripts in the expression profiles helped identify 1594 transcripts that were commonly upregulated in lung tissues from IIP patients compared to those from normal control subjects. The transcriptional profiles of IPF and NSIP were unexpectedly similar. Lungs with IIP were characterized by increased expression of transcripts associated with cell cycle, ABC transpoters and p53 signaling pathways, such as MDM2, RBL1, RAD21, CFTR and BAX. Conclusion: The current data provide valuable information on the molecular mechanism underlying pulmonary fibrosis in IIP patients. Additionally, several potentially promising and novel diagnostic biomarkers as well as therapeutic targets have been identified for IIPs.