



Published in final edited form as:

Biogerontology. 2013 December ; 14(6): . doi:10.1007/s10522-013-9451-6.

Mechanistic Links between Aging and Lung Fibrosis

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Abstract

Our understanding of the biology of aging has advanced significantly in recent years. This has resulted in the recent formulation of the “hallmarks of aging” that include genomic instability, telomere attrition, epigenetic alterations, loss of proteostasis, deregulated nutrient sensing, mitochondrial dysfunction, cellular senescence, stem cell exhaustion, and altered intercellular communication. Idiopathic pulmonary fibrosis (IPF) is a progressive and fatal lung disease that results from the accumulation of scar tissue in the lungs of affected individuals. IPF is a disease of aging that most commonly affects human subjects older than sixty years of age. While progress has been made in elucidating key pathological processes in IPF, the relationship of these processes to those that occur during aging are not well defined. In this review, we explore existing and emerging paradigms in the pathogenesis of IPF in light of the recently defined hallmarks of aging.

Introduction: Idiopathic Pulmonary Fibrosis is a Disease of Aging

There is uncertainty and debate regarding theories of aging (i.e., why it occurs), its mechanisms (i.e., how it occurs) and whether the process can be influenced to extend lifespan, particularly in humans. Significant progress has been made over the past three decades in our understanding of the biology of aging, recently summarized in a review entitled, the “hallmarks of aging” (Lopez-Otin et al. 2013). While the question of whether lifespan of humans can be extended by pharmacologic interventions or regenerative therapies remains controversial (Warner et al. 2005; de Grey 2005), perhaps less controversial is the proposition that the emerging knowledge of the biology of aging will inform novel therapeutics and interventions for age-related diseases. In this short review, we provide evidence for idiopathic pulmonary fibrosis (IPF) as an age-related disease and explore mechanisms for its pathobiology in light of the recently proposed hallmarks of aging (Lopez-Otin et al. 2013).

IPF is a disease of aging (Raghu et al. 2006; Fell et al. 2010; Collard 2010). The incidence and prevalence of IPF increase almost exponentially with each decade of life; two-thirds of IPF patients are older than 60 years at the time of presentation with a mean age of 66 years at the time of diagnosis (Raghu et al. 2006). Thus, similar to other more common age-related diseases such as cardiovascular disease, neurodegenerative diseases, cancer, osteoporosis, and diabetes, IPF is likely to share common pathophysiologic mechanisms with the aging process, itself (Thannickal and Loyd 2008). The hallmarks of aging include genomic instability, telomere attrition, epigenetic alterations, loss of proteostasis, deregulated nutrient sensing, mitochondrial dysfunction, cellular senescence, stem cell exhaustion, and altered intercellular communication (Lopez-Otin et al. 2013). What is the current evidence that these, often overlapping, processes contribute to the pathobiology of IPF?

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Genomic Instability

The accumulation of nuclear and mitochondrial DNA damage commonly accompanies the aging process (Moskalev et al. 2013; Park and Larsson 2011). Increased DNA damage has been linked to accelerated aging in a number of progeroid syndromes (Burtner and Kennedy 2010). There is emerging evidence that augmentation of DNA repair mechanisms may prolong lifespan and protect against aging-related disease (Baker et al. 2013). Microsatellite instability and loss of heterozygosity (LOH) are more frequent in IPF (Vassilakis et al. 2000; Ricci et al. 2013). LOH at the homeodomain-interacting protein kinase 2 (HIPK2) gene, which is typically activated by genotoxic stimuli, was reported to underlie apoptosis resistance, specifically of IPF fibroblasts (Ricci et al. 2013).

Proteomic analyses of IPF lung tissue support the activation of a DNA damage response (Korfei et al. 2011). The expression of p53 and p21 are upregulated in association with chronic DNA damage of IPF lung epithelial cells, mediating either G1 arrest or apoptosis (Kuwano et al. 1996). IPF lung epithelial cells also express deltaN-p63 at sites of abnormal proliferation at bronchiolo-alveolar junctions, characterized by epithelial hyperplasia, squamous metaplasia, bronchiolization, and abnormal p53 nuclear accumulation (Chilosi et al. 2002; Chilosi et al. 2003). Mitochondrial DNA repair enzymes such as 8-oxoguanine DNA glycosylase (Ogg1) appear to be activated in asbestos-induced lung fibrosis, presumably in an attempt to counteract oxidative stress and apoptosis of lung epithelial cells (Liu et al. 2010a). Together, these studies indicate that different cell types of the lung show evidence of chronic DNA damage response. Moreover, the observation that lung fibrosis can develop in pediatric patients harboring deficiencies in DNA-repair pathways (Schroeder et al. 2005; Vece et al. 2012; Kropski et al. 2013), further supports the concept of deficiencies in DNA repair pathways contributing to the pathogenesis of IPF.

Telomere Attrition

IPF is now recognized as the most common manifestation of telomere-mediated disorders (Alder et al. 2008; Armanios 2012). Telomerase mutations also are the most frequent cause of familial IPF (Armanios et al. 2007; Armanios 2012, 2013). Shortening of telomeres, in the absence of telomerase mutations, is observed in sporadic cases (Alder et al. 2008; Cronkhite et al. 2008), suggesting that this may be common pathophysiological mechanism resulting from a combination of genetic, environmental, and age-related causes (Thannickal and Loyd 2008).

Pathophysiological mechanisms relating short telomeres to specific cellular phenotypes and fibrogenesis remain to be elucidated. Animal models of injury and fibrosis in mice with telomerase deficiency reveal contradictory findings (Liu et al. 2007; Degryse et al. 2012). Further studies of the role of telomerases and telomere length and their role in specific cell types that participate in lung fibrosis are warranted.

Epigenetic Alterations

A number of epigenetic mechanisms involving histone modifications, DNA methylation, and microRNAs (miRNAs) have been implicated in aging (Rando and Chang 2012). Studies that link epigenetic silencing of anti-fibrotic genes and activation of pro-fibrotic genes have begun to emerge. Epigenetic silencing of the putative “fibrosis suppressor” protein, Thy-1, involves both promoter hypermethylation (Sanders et al. 2008; Robinson et al. 2012) and histone modifications (Sanders et al. 2011). The cyclooxygenase-2 (COX-2) gene that is responsible for production of the anti-fibrotic mediator, prostaglandin E₂ (PGE₂), has been linked to reduced histone H3 and H4 acetylation due to decreased recruitment of histone acetyltransferases (HATs) and increased recruitment of transcriptional corepressor

complexes to the COX-2 promoter (Robinson et al. 2012). The same group subsequently demonstrated that repression of another anti-fibrotic chemokine, interferon-inducible protein of 10 kDa (IP-10), is mediated by histone deacetylation and hypermethylation (Coward et al. 2010). The tumor suppressor gene, p14^{ARF}, which mediates anti-apoptotic effects of IPF lung fibroblasts, is silenced by promoter hypermethylation (Cisneros et al. 2012). Since p14^{ARF} induction, as opposed to silencing, is implicated in cellular senescence and aging, the potential cell-specific effects of such epigenetic alterations need to be uncovered. Our group has recently demonstrated that senescent fibroblasts which acquire an apoptosis-resistant phenotype express constitutively high levels of the anti-apoptotic gene, Bcl2, and reduced levels of the anti-apoptotic Bax gene; this altered Bcl-2:Bax ratio is mediated by global and locus-specific histone modifications in senescent fibroblasts (Sanders et al. 2012b). Histone modifications also appear to account for the decreases in Fas expression that confers apoptosis resistance to fibrotic lung fibroblasts (Huang et al. 2013).

DNA methylation patterns are altered in IPF (Sanders et al. 2012a; Rabinovich et al. 2012); however, how these changes relate to the process of aging *per se* is unclear. Similarly, recent studies implicate alterations in the regulation of miRNAs in fibrogenic processes and IPF (Liu et al. 2010b; Cushing et al. 2010; Yang et al. 2012; Dakhlallah et al. 2013). Although miRNAs are increasingly being implicated in age-related diseases (Dimmeler and Nicotera 2013), the interactions between miRNAs and other epigenetic mechanisms that occur in “normal” aging and in specific diseases associated with aging need to be elucidated.

Loss of Proteostasis

The accumulation of unfolded, misfolded or aggregated proteins is a hallmark of many age-related diseases (Powers et al. 2009). Protein quality control is maintained by two major proteolytic systems, the autophagy-lysosomal system and the ubiquitin-proteasomal system, both of which decline with age (Rubinsztein et al. 2011; Koga et al. 2011). There is evidence for unfolded protein response (UPR) and endoplasmic reticulum (ER) stress in alveolar epithelial cells in lungs of patients with familial IPF (Thomas et al. 2002) and sporadic cases (Korfei et al. 2008; Lawson et al. 2008; Korfei et al. 2011). Activation of ER stress in epithelial cells may be mediated by intrinsic abnormalities in protein folding or by extrinsic stress such as viral infections; subsequent apoptosis of epithelial cells may be sufficient to initiate fibrotic remodeling (Sisson et al. 2010). Alternatively, activation of the UPR may induce secretion of the potent pro-fibrotic mediator, transforming growth factor- β 1 (TGF- β 1) (Maitra et al. 2012).

Recent studies indicate that autophagy is diminished in IPF (Patel et al. 2012; Araya et al. 2013). The mechanisms that lead to deficient autophagy are not well understood, as well as how this leads to the aberrant remodeling response in IPF. Interestingly, while many of the “upstream” reparative pathways, including cellular senescence, are activated in another age-related lung disease, chronic obstructive pulmonary disease (COPD), autophagy is reported to be enhanced in COPD (Chen et al. 2008; Hwang et al. 2010). This suggests that autophagy may function as a critical “switch” in the different tissue remodeling responses to lung injury. One suggested mechanism for decreased autophagy is reduced beclin-1, which is combination with reduced expression of the anti-apoptotic Bcl-2 gene, promotes apoptosis-resistance of fibroblasts (Ricci et al. 2012), implicated in the persistence and progression of IPF (Thannickal and Horowitz 2006). In contrast to the notion that it may be protective in IPF, autophagy has also been suggested as a core pathway driving fibrogenesis (Hernandez-Gea and Friedman 2012). It remains to be determined whether such differences relate to the model system utilized or inter-organ differences.

Deregulated Nutrient Sensing

There is now strong evidence that decreased nutrient signaling extends lifespan in multiple species (reviewed in Fontana et al. 2010). There is proof-of-concept that mimicking a state of nutrient deficiency with the pharmacological inhibitor, rapamycin, is effective in a TGF- α -induced model of lung fibrosis in mice (Korfhagen et al. 2009), although this was not observed in the murine bleomycin model (Madala et al. 2011). Similarly, activating AMP-activated protein kinase (AMPK) with 5-aminoimidazole-4-carboxamide-1- β -D-ribofuranoside (AICAR) or metformin mediates protection from airway inflammation and remodeling (Park et al. 2012). In this study, the expression of fibronectin and collagen was diminished by metformin through AMPK- α 1 activation in cultured fibroblasts. Further studies are required to determine precise mechanisms of fibrogenesis by anabolic signaling and potential amelioration of fibrosis by pharmacologic “mimics” of nutrient deficiency.

Mitochondrial dysfunction

The free radical theory of aging is being refined as we gain better understanding of the contextual roles of reactive oxygen species (ROS) in adaptive and maladaptive responses in various tissues (Kirkwood and Kowald 2012). There is evidence for mitochondrial dysfunction in asbestos-related lung fibrosis (Liu et al. 2010a), although less known about the role of mitochondrial function and mitochondria-generated ROS (mtROS) in IPF. However, there is emerging implication of mtROS in TGF- β signaling and expression of pro-fibrotic genes (Jain et al. 2013). Interestingly another ROS-generating enzyme, NADPH oxidase-4 (Nox4) that mediates lung fibrosis (Hecker et al. 2009), has been reported to localize to mitochondria (Block et al. 2009; Crespo et al. 2010). Elucidating the interactions between Nox4 and mitochondrial (dys)function (Kozziel et al. 2013; Wolin 2013) in both physiological and pathological states will shed light on their respective (and potentially combined) roles in regulating mitochondrial dynamics, cellular senescence, and fibrosis.

Cellular Senescence

While there is strong evidence that senescent cells accumulate in tissues with aging (Krishnamurthy et al. 2004), the mechanisms by which they contribute to aging and age-related diseases deserves further study. Fibrosis is generally considered as a fibro-“proliferative”, but benign (non-cancerous) disease process. Consistent with this concept, the emergence of senescent fibrogenic cells in the context of wound healing has been proposed to mediate anti-fibrotic effects (Krizhanovsky et al. 2008; Jun and Lau 2010). Thus, similar to its role in tumor-suppression, cellular senescence may function as a mechanism for fibrosis-suppression (Rodier and Campisi 2011). Such “antagonistically pleiotropic” roles of senescence must be reconciled in specific age-related diseases, including IPF, before effective therapeutics targeting senescence pathways can be designed.

Stem Cell Exhaustion

Stem cell exhaustion has been implicated in a number of age-related diseases, including IPF (Chilosi et al. 2010; Chilosi et al. 2013). The principal cells implicated in “stem cell exhaustion” associated with IPF are alveolar type II epithelial cells (Chilosi et al. 2013); however, a hyperplastic response around fibroblastic foci with abnormal bronchiolarization is often seen, an observation that has not been adequately explained. Whether this hyper-proliferative response reflects differences in the susceptibility of distinct groups of airway epithelial stem cells is currently not known. Additionally, a better understanding of stem cell niches that also under aging is required before the potential beneficial effects of stem cell-based therapies for chronic lung diseases can be realized (Mora and Rojas 2013).

Altered Intercellular Communication

There is general consensus among most investigators that fibrosis results from aberrant epithelial-mesenchymal interactions (Thannickal et al. 2004; Chapman 2011). Alterations in and between resident structural cells, immune cells and microbial pathogens (microbiome) occurs during aging (Lopez-Otin et al. 2013), yet how these changes influence the phenotypic expression of fibrosis involving specific organ systems is not understood. Studies on the secretome of (senescent) cells, phenotypic plasticity (or loss thereof), and “inflammaging” (Franceschi et al. 2000) in IPF will illuminate the potential for therapeutic opportunities for this recalcitrant disease process.

Conclusion

IPF is a disease of aging with a progressive and fatal course, and without effective therapies. An understanding of the biology of aging will provide improved understanding of fibrogenesis and its progression; as well inform the design, discovery and development of more effective therapies for this dreadful disease.

Acknowledgments

This work was funded by National Institutes of Health grants, R01 HL067967, R01 HL094230 and P50 HL107181.

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