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Induced Pluripotent Stem Cells in Pulmonary Arterial Hypertension

Pioneering work by Yamanaka's group showed that overexpression of four transcription factors, octamer-binding protein 4 (*OCT4*), Krüppel-like factor 4 (*KLF4*), sex determining region Y-box 2 (*SOX2*), and c-myc avian myelocytomatosis viral oncogene homolog (*c-MYC*), could reprogram somatic cells into induced pluripotent stem cells (iPSCs), which could then be differentiated into all cell types (1). Since that finding, it has become clear that iPSCs hold great promise as models for diseases, drug discovery, and testing of cell-based therapeutic strategies.

Pulmonary diseases are one leading cause of morbidity and mortality worldwide. Currently available treatments can only alleviate symptoms or delay disease progression within a limited time range for patients with end-stage pulmonary diseases. Pulmonary arterial hypertension (PAH) is a complex disorder of pulmonary microvasculature, circulating cells, and right heart, with poor prognosis (2, 3). Animal models of PAH have existed for some time and have provided key insights into disease pathogenesis. Attempts to translate these findings into treatment for patients, however, have been imperfect at best, because at a molecular level animal lungs and lung tissues are different from human lungs and tissues, and thus it has been difficult to recapitulate the disease process in vitro. Use of human lung cells could address some of the deficiencies. However, it is technically difficult to isolate and characterize human cells in enough number to be useful in laboratory studies. iPSCs provide one potential solution to this problem. iPSCs have been used to derive respiratory epithelial cells, vascular endothelial cells, and vascular smooth muscle cells (4-6) and have also been used to study lung development and vascular modeling (4, 7-9). However, whether they can serve as tools to investigate the potential for new therapeutic agents in PAH is unknown.

In this issue of the *Journal*, Sa and colleagues (pp. 930–941) present data from proof-of-principle studies that address an important question: whether iPSCs derived from patients with PAH have potential as tools for drug discovery and testing (10). They compared the pulmonary artery endothelial cells isolated from patients with idiopathic or heritable PAH to endothelial cells (ECs) derived from fibroblast-derived iPSCs from the same patients. The authors show that there are many similarities between the iPSC-ECs and native pulmonary artery endothelial cells, including morphology, functional deficits, reduction of bone morphogenetic protein receptor (BMPR)-II signaling, and, importantly, response to bone morphogenetic protein 9 stimulation

and drug treatment, as well as some differences. Using RNA-seq analyses, they further identified molecular signatures responsible for the observed functional and drug response differences between native ECs and iPSC-ECs. In summary, their data show that iPSCderived ECs can serve as surrogates for native ECs in both functional and drug discovery studies.

Their work suggests that the iPSC-ECs model has the potential to serve as a precision/personalized medicine tool-to determine which one of the many drugs would be effective in a particular patient-because the cells are derived from the same patient who would, in the end, receive the drug. Although this concept maybe exciting, their data also show that the use of these cells is not straightforward, and additional data are needed before broadly generalizable conclusions can be made. For example, they found that only one of two IPSC-ECs derived from patients with heritable PAH (with the same BMPR2 mutation) and only two of six iPSC-ECs derived from patients with idiopathic PAH showed a functional response to Elafin or FK506. Why the treatments did not have a universal effect is currently unknown. One potential mechanism could be preserved fibroblast-specific epigenetic signatures; it is well known that iPSCs can retain some of the epigenetic signatures of the parent cell. Another could be that patient-specific molecular modifiers, such as BMPR2 expression and alternative splicing and estrogen metabolism (11-13), retain their effect regardless of programming. One way to address this question would be to compare iPSC-ECs derived from different originating tissues from the same patient and with each and with other types of endothelial cells, such as circulating ECs, also from the same patient. Another possibility could be that because both Elafin and FK506 specifically affect BMPR-II signaling (14, 15), they might not be effective if BMPR-II signaling is not the primary disease driver in a particular cell line. It may thus be useful to determine if iPSC-ECs and native ECs show similar responses to a wider variety of potential therapeutic agents.

It is important to note that this work involved a small number of cell lines derived from a limited number of patients from a particular pulmonary hypertension (PH) category (Group 1). A larger number of iPSCs from a larger cohort of patients with PH, including patients from the other PH groups and subgroups (Groups 2–5), will need to be analyzed to more conclusively determine the usefulness of this approach to the PH field as a whole.

Given the paucity of treatment options in PAH, there is an urgent need for improved understanding of the molecular

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mechanisms of PAH in human tissues—a vital prerequisite for developing disease models and eventually therapies for PAH. Directed differentiation of iPSCs and generation of pulmonary vascular cell lines and tissues could be an important tool for such studies. This promising work from Sa and colleagues addresses many of these needs and has the potential to provide unparalleled insight into PAH development and pathogenesis and, importantly, significantly speed up new drug discovery.

Author disclosures are available with the text of this article at www.atsjournals.org.

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