Editorial

Forever Young
Induced Pluripotent Stem Cells as Models of Inherited Arrhythmias

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Mutations in the α subunit of the cardiac sodium channel, encoded by SCN5A, have been identified in a broad range of cardiac rhythm disorders that include long QT3 (LQT3), Brugada syndrome, progressive cardiac conduction disease, sick sinus syndrome, atrial fibrillation, and dilated cardiomyopathy. Since the identification of the first SCN5A mutation in long QT syndrome in 1995, >200 mutations have now been reported.1 Initially, it was assumed that each arrhythmic phenotype was attributable to a specific SCN5A mutation; however, overlap syndromes, in which single individuals exhibit clinical features of Brugada syndrome and LQT3, are now well characterized.2 The broad phenotypic range of SCN5A mutations underscores the importance of tight sodium channel regulation in maintaining normal rhythmicity.

Characterization of sodium channel mutations using heterologous expression systems in nonexcitable cells can produce inconsistent and even confounding results.4,6,7 A striking example was reported by Roden and colleagues,6 who showed that D1275N SCN5A expressed in knock-in mice demonstrated slowed conduction, heart block, atrial and ventricular arrhythmias, and dilated cardiomyopathy, faithfully phenocopying the human disease. Isolated ventricular myocytes from D1275N mutant mice displayed reduced sodium channel abundance and reduced peak sodium current. In contrast, the same mutation heterologously expressed in Chinese hamster ovary cells or tsA201, with or without the β1 subunit, showed near-normal sodium channel function.6 Similarly, overexpression of the Ankyrin-G binding mutant, E1053K SCN5A, in human embryonic kidney 293 cells showed normal membrane targeting, whereas expression of the mutant channel in ventricular myocytes abolished proper membrane trafficking.4

Harnessing the power of induced pluripotent stem cells (iPSC) would obviate the need for heterologous expression systems, because potentially limitless supplies of personalized cardiomyocytes could be generated. This approach would, in theory, circumvent species-specific and interpersonal variations, allowing unprecedented resolution of channel behavior from patient-derived cells. For this reason, momentum has grown, both in bio-banking patient specimens and in generating cardiomyocytes from iPSCs (iPSC-CM), to recapitulate human channelopathies in a dish.8,9 However, tempering this enthusiasm for iPSC-CMs to model adult channelopathies is the well-described phenotypic immaturity of iPSC-CMs.10 Electrophysiologically, cardiomyocytes derived from human embryonic stem cells (ESCs) and human iPSCs have significantly reduced upstroke velocities and have relatively depolarized resting membrane potentials, mimicking fetal cardiomyocytes.5,8,11,12 Similarly, mouse iPSC-CMs exhibit delayed maturation, even after prolonged differentiation, when compared with mouse ESC-derived cardiomyocytes and fetal myocytes, possibly as a result of epigenetic memory.10 Therefore, the feasibility of using iPSC-CMs in studying sodium channel physiology, in particular, has been questioned.

In this issue of Circulation, Mummery and colleagues13 specifically address the issue of whether cardiomyocytes derived from several pluripotent stem cell lines (mouse ESC, mouse iPSC, and human iPSC) can serve as a suitable model for studying complex sodium channel mutations. To that end, electrophysiological analyses were performed on derived cardiomyocytes bearing the murine equivalent of the human 1795insD SCN5A mutation, the first characterized overlap mutation exhibiting features of both Brugada syndrome and LQT3.2 Cardiomyocytes were generated from mouse iPSCs derived from Scn5a<sup>1795insD</sup> tail tip fibroblasts or mouse

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embryonic fibroblasts and from mouse ESCs used to create the Scn5a<sup>1798insD/H11001</sup> mouse. Biophysical analysis demonstrated features of both loss-of-function (reduced sodium current density) and gain-of-function (larger persistent <i>I<sub>Na</sub></i>), mirroring the defects noted in primary Scn5a<sup>1798insD/H11001</sup>-adult cardiomyocytes. Corresponding changes in action potential recordings such as reduced upstroke velocity and prolonged action potential duration were noted in mutant myocytes. Furthermore, human iPSC-CMs generated from an affected individual recapitulated the biophysical abnormalities noted in mPSC-derived cardiomyocytes. Therefore, although the phenotypic immaturity of cardiomyocytes derived from mouse ESCs and mouse/human iPSCs has served as a significant hurdle for regenerative applications, their tendency to remain forever young does not preclude their use in studying complex sodium channel mutations exhibiting both loss- and gain-of-function mutations.

The concept of using iPSC-CMs for studying sodium channel mutations has significant implications. The ability to perform expression profiling between family members or, ideally, identical twins who manifest significant phenotypic variability, can help to identify critical genetic modifiers of disease severity. iPSC-CMs can also move us closer to personalized medicine for Brugada syndrome and LQT3, where drug regimens can be tested in vitro before being administered to patients. For example, mexiltine has been found to have a beneficial effect on shortening the QT interval in LQT3, but not in all patients. After a systematic biophysical characterization of mutant channels, Priori and colleagues<sup>14</sup> concluded that a hyperpolarizing shift of inactivation may predict a positive response to mexiltine. Furthermore, sodium channel blockade may be detrimental for patients with overlap syndromes. Therefore, the ability to screen patient’s iPSC-CMs for response to drug therapy while avoiding untoward effects may move us closer to tailored therapy for inherited channelopathies.

Another potential area of growth for iPSC-CMs will likely be in high throughput/high content screens to rapidly identify novel short-interfering RNAs, small molecules, or drugs that can correct trafficking defects, alter sodium channel activity, or enhance translational readthrough of nonsense mutations. Nonsense mutations, which introduce a premature termination codon in the open reading frame of an allele, have been identified in <i(SCN5A)</i>. Enhancing translational readthrough is an emerging technology that enables ribosomes to bypass premature termination codons, allowing full-length proteins to be made.<sup>15</sup> Two strategies to improve readthrough have been reported in an <i(SCN5A)</i> nonsense mutation (W822X): (1) reduction of translational fidelity using aminoacyl-synthetases and (2) decreased translation termination efficiency using short-interfering RNA targeting the eukaryotic release factor, eRF3a.<sup>15</sup> Either approach restored <i>I<sub>Na</sub></i> to ~30% from <3% of wild-type levels by increasing full-length protein expression. Translational readthrough-corrected channels behaved similarly to wild-type channels with regard to kinetics and voltage dependency. Furthermore, there was no evidence of abnormal readthrough of natural stop codons. A major limitation of this work was the use of heterologous expression of W822X Scn5a in human embryonic kidney 293 cells.<sup>15</sup> Recapitulation of this work in iPSC-CMs is warranted and would provide a more accurate readout of enhanced readthrough on full-length sodium channel expression and function in the endogenous cardiomyocyte.

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**References**


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