

Comparative Analysis of Human iPSC-derived Cardiomyocytes in Diversity and Disease Modeling

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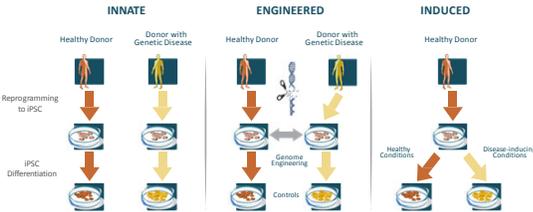
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Abstract

Human cell types differentiated from induced pluripotent stem cells (hiPSC) offer a unique access to human cellular material for safety and toxicity screening. Here, we present data demonstrating the utility of hiPSC-derived cardiomyocytes (hiPSC-CMs) in safety assessment and disease modeling. We include a comparative assessment of cancer therapeutics-related cardiac dysfunction (CTCRD) compounds doxorubicin (type I) and sunitinib (type II) across hiPSC-CMs derived from 6 healthy donors (DIV 14) at three concentrations [0.1, 1.0, and 10 μ M]. Clinically Type I CTCRD may be associated with cellular death, structural changes, and permanent damage while Type II CTCRD may be associated with cellular dysfunction, no structural changes, and reversible damage. Here we were able to identify both type I and type II CTCRD using a selected in-vitro cohort of hiPSC-CMs. These data provide additional insight into

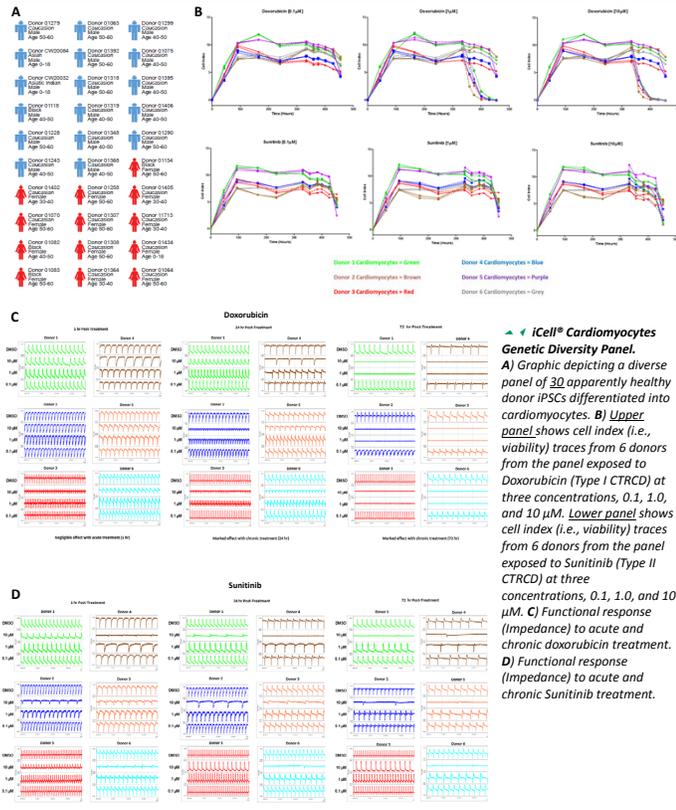
sensitivities to cancer therapeutics across different donors. We then examined basic characterization data from several hiPSC-CM disease models including hypertrophic cardiomyopathy MYH7 (R403Q), LMNA-related dilated cardiomyopathy LMNA (L35P), and Brugada syndrome (BrS) type 3 CACNA1C (G490R) each with its respective isogenic control at DIV 14. We further identify the functional consequences of each mutation and demonstrate that each model recapitulates classical hallmarks of the disease phenotype. These data illustrate how hiPSC-CMs provide an excellent model system for assessing compound effects across multiple donors and disease models. Taken together, these examples should help to create new avenues for safety liability assessment and toxicology studies, as well as serve as a template for future opportunities in disease modeling with hiPSC-CMs.

Healthy and Diseased Cardiomyocytes for Basic Research and Toxicity Testing

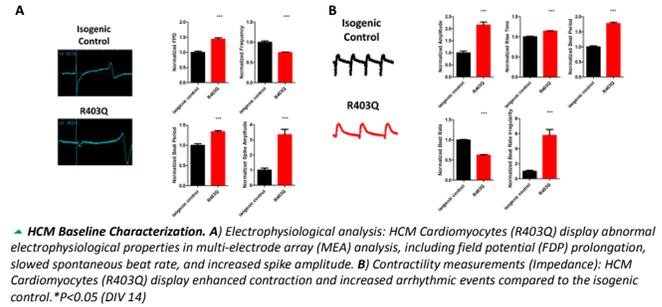


Diversity and Disease Modeling Approaches. Graphic depicting three primary disease modeling approaches: i) Innate modeling where a sample is taken from a healthy or diseased donor; ii) Engineered modeling using genome engineering strategies to introduce or correct a mutation; and iii) Induced modeling where cells are exposed to disease causing conditions (e.g., ET-1).

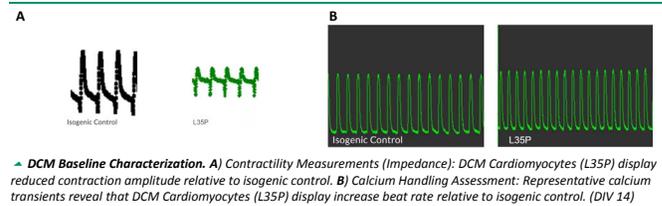
iPSC-derived Genetic Diversity Cardiomyocyte Panel



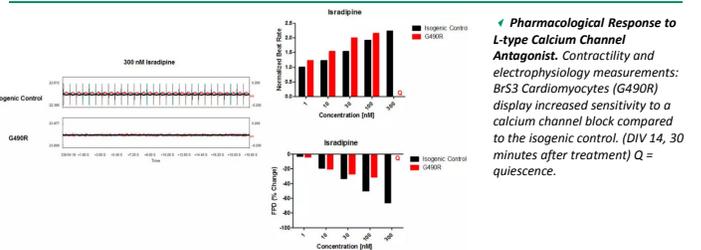
HCM MYH7 R403Q iPSC-derived Cardiomyocytes Display Increased Contractile Properties



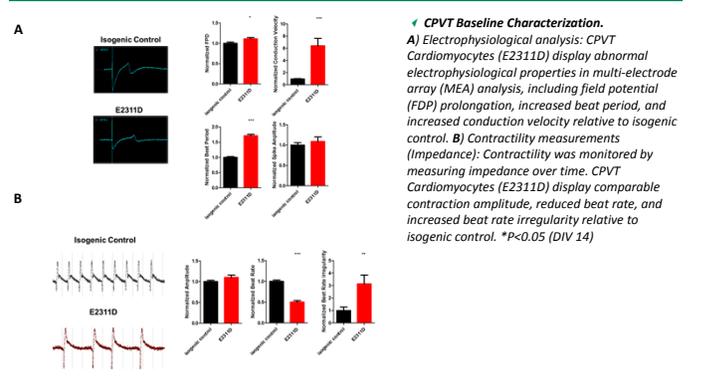
DCM LMNA L35P iPSC-derived Cardiomyocytes Exhibit Reduced Contractile Properties



BrS CACNA1C G490R iPSC-derived Cardiomyocytes Exhibit Increased Sensitivity to Calcium Block



CPVT RYR2 E2311D iPSC-derived Cardiomyocytes Display Reduced Beat Rate in vitro



Conclusion

Human iPSC-CMs from apparently normal and disease donor backgrounds can be used to develop models for clinical trials-in-a-dish and disease-in-a-dish enabling researchers to investigate novel mechanisms and therapies. Here we demonstrate:

- Patient-derived hiPSC-CMs recapitulate innate disease pathophysiology.
- Genome engineering strategies in hiPSCs enable the correction of the disease specific

mutations, thus creating an isogenic control.

- Induced and inherited diseased models display clinically relevant structural and functional features in the dish.

These results demonstrate convenient, novel human cell models for cardiovascular research supporting hiPSC technology as a platform capable of generating cardiomyocytes from healthy and disease relevant genetic backgrounds.