
M E M O R A N D U M

November 20, 2013

From: Alan Trounson, President; Michael Yaffe, Associate Director of Research Activities
To: Independent Citizens Oversight Committee (ICOC)
Subject: hiPSC Derivation Award Supplement

hiPSC Derivation Award Supplement

Proposal

Request ICOC approval for a supplement to the hiPSC Derivation Award (ID1-06557) to support genomic analysis of donor tissue and derived cell lines

Overview

- Purpose: to enable advanced genomics analysis (SNP analysis) on primary tissue samples and derived hiPSC lines
- Funding Mechanism: funds will supplement the hiPSC Derivation Award (ID1-06557) to Cellular Dynamics International (CDI), Thomas Novak, PD.
- Total supplement cost: \$2.0 million

Rationale

The CIRM hiPSC Initiative will generate a high quality collection of disease-specific and control pluripotent stem cell lines that will serve as a unique resource for researchers and drug developers. The Initiative specifically targets 11 prevalent, genetically complex diseases for the generation of hiPSC lines from 3000 individuals. Use of these hiPSC lines should contribute significantly to the elucidation of disease mechanisms and improve treatment options through disease modeling, target discovery and the discovery and development of novel drugs.

Subsequent to design of the RFA, proposal review and ICOC award approval, a group of 7 independent genomics and human genetics experts, convened to address the development of shared controls, as recommended by the Grants Working Group, recommended that all collected tissue samples and derived cell lines be subject to a genomics analysis involving whole genome single nucleotide polymorphism (SNP) analysis. These experts stressed that information from this analysis would greatly increase the value and usefulness of the resulting stem cell lines. In particular, the SNP analysis would facilitate:

- High-precision case-control matching of samples
- Analysis of sample genetic ancestry and genetic diversity of the collection

- Unambiguous identity matching of derived cell lines and differentiated cells with original tissue samples
- Determination of genomic integrity of hiPSC lines
- Identification and analysis of disease-associated SNP markers

The original award did not include adequate funds to support this advanced genomics analysis. The requested supplement will enable SNP analysis of DNA from the 3000 tissue samples and 9000 derived hiPSC lines. The SNP data will significantly increase the importance and utility of the CIRM hiPSC collection.