Conditionally Immortalized Long-Term Stem Cells and Methods of Making and Using Such Cells

Field of the Invention

The present invention generally relates to conditionally immortalized long term stem cells, to methods of producing such cells, and to methods of using such cells, including therapeutic methods and drug discovery methods.

Background of the Invention

The ability to manipulate the bone marrow output of various blood cells has become an important tool in the management of several diseases. Some of the best new therapies for hematological malignancies are based on the development of compounds that push leukemic cells to differentiate into lineages to which they are committed prior to the transforming event. One such example is the case of acute promyelocytic leukemia. Upon treatment of patients with Arsenic Trioxide, the malignant cells are pushed along the myelomonocytic pathway leading to remission of those tumors. Another example lies in promotion of successful engraftment of transplanted bone marrow stem cells (long term reconstituting hematopoietic stem cells, or lt-HSC) in irradiated individuals. The appearance of differentiated blood cells can be accelerated by the systemic administration of cytokines that are known to specifically induce red blood cell development (erythropoietin, or Epo), or myeloid cell development (granulocyte-macrophage colony-stimulating factor, or GM-CSF). Finally, harvesting of lt-HSC from donors has been greatly simplified by the process of "mobilization" wherein these cells are induced to move from the bone marrow sites where they normally reside into peripheral blood by systemic administration of a cytokine called G-CSF. Stem cells can then by harvested from peripheral blood obviating the painful and elaborate collection of bone marrow biopsies. All of these processes rely on the ability to program and control the biological behavior of lt-HSC.

Accordingly, bone marrow (stem cell) transplantation is an invaluable therapeutic tool for hematologic and immune reconstitution of individuals who have undergone radiation and/or chemotherapy (*e.g.* cancer patients, or have been exposed to high-level radiation), and is also a critical modality for treatment of immune deficiency and hematological malignancies. In addition, bone marrow transplantation would be a highly useful therapy to combat the negative effects of aging on the immune system, as well as on other cells and

tissues. It is estimated that stem cell transplantation could benefit more than 35,000 children and adults per year.

The operative principle behind bone marrow transplantation is replacement of radiation sensitive lt-HSC that give rise to all blood cell types. Recent studies indicate that bone marrow transplantation may have value in the treatment of heart disease. Although the basis of this affect is unknown, it, and other findings, raise the possibility that hematopoietic stem cells (lt-HSC) may be reprogrammed to give rise to other tissues. If this is true, lt-HSC may have much broader utility and provide an alternative to controversial embryonic stem cell therapy.

The major obstacles confronting clinical application of bone marrow transplantation lie first in identification of an appropriately histocompatible marrow donor. This is usually accomplished using registries that have enrolled more than 6 million potential donors. The selected donor must undergo a grueling ordeal of induced mobilization stem cell into the blood followed by 4-5 days of leukapheresis to isolate rare lt-HSC. Transplantation of these cells must be followed by careful monitoring and treatment of the recipient to minimize graft versus host reactions caused by passenger lymphocytes.

Elucidation of the molecular basis of the impairment in hematopoietic lineage development has been complicated historically by the low frequency of relevant cell populations, which prevents biochemical analysis of signaling and downstream responses. In fact, this has been a major limiting factor in all studies of hematopoiesis. In addition, the limited availability of long-term hematopoietic stem cells (LT-HSCs) has also been a major obstacle in the treatment of many types of cancer as well as several kinds of immune deficiencies in humans. To the best of the present inventors' knowledge, there are currently no available cell lines that arose spontaneously that resemble lt-HSCs and can differentiate into normal lineages *in vitro*, or that can reconstitute lethally irradiated mice or sub-lethally irradiated humans, nor have any methods been described to deliberately generate such cell lines. Moreover, there are currently no viable technologies to continuously expand lt-HSCs, such that these cells need to be obtained from a donor every time they are needed.

There is also a dire need for additional modalities to treat hematological malignancies and immune deficiency, and novel cytokines to increase the output of transplanted lt-HSC. In addition, an appropriate platform for target identification and drug discovery does not currently exist. The missing elements are cell lines that represent different developmental stages in hematopoietic lineages. Optimally, such cells should retain

the ability to undergo further differentiation in a specific lineage. Such cell lines are essential for identification of gene products, and thus new drugable targets, involved in regulation of cell development, proliferation and survival. In addition, such cell lines are essential for the screening of small molecule and shRNA libraries for loss-of function studies, as well as cDNA libraries for gain of function studies, in search of novel drugs.

Barriers to current drug discovery in this area include: (a) isolation of a sufficient number of cells from a particular developmental stage; (b) propagation of the cells in vitro for a sufficient length of time; and (c) ability to use conditional oncogenes to screen for drugs that could affect leukemic cells, and not normal HSCs or progenitors.

Therefore, there is a great need in the art for a method to generate lt-HSC cell lines that can be expanded extensively, frozen, and used again whenever they are required, in the absence of subsequent harvests from the donor.

Summary of the Invention

One embodiment of the present invention relates to a method to produce conditionally immortalized adult stem cells. The method includes the steps of: (a) obtaining an expanded population of adult stem cells; (b) transfecting the stem cells with a nucleic acid molecule comprising a protooncogene or biologically active fragment or homologue thereof that promotes cell survival and proliferation, wherein the protooncogene is inducible; (c) transfecting the stem cells with a nucleic acid molecule encoding a protein that inhibits apoptosis of the cell; and (d) expanding the transfected cells in the presence of a combination of stem cell growth factors under conditions whereby the protooncogene is active, to produce conditionally immortalized adult stem cells. In one aspect of this embodiment, the nucleic acid molecule of (b) and/or (c) is contained in an integrating vector. In one aspect, the nucleic acid molecule of (b) and/or (c) is transfected into the cells using a virus or viral vector selected from: retroviral vectors, lentivirus vectors, parvovirus, vaccinia virus, coronavirus, calicivirus, papilloma virus, flavivirus, orthomixovirus, togavirus, picornavirus, adenoviral vectors, modified and attenuated herpesviruses. In one aspect, the nucleic acid molecule of (b) and/or (c) is transfected into the cells using direct electroporation. In one aspect, the nucleic acid molecule or (b) and/or (c) is contained in a vector comprising a nucleic acid sequence encoding a drug-sensitivity protein. In one aspect, the nucleic acid molecule or (b) and/or (c) is contained in a vector comprising nucleic acid sequences

encoding recognition substrate sequences for a recombinase flanking the nucleic acid molecule of (b) or (c).

In one aspect, this embodiment includes the additional steps of: (e) removing the conditions of (d) whereby the protooncogene is active; and (f) culturing the cells of (e) in media comprising growth factors that induce differentiation of the cells. This method can further include: (g) adding to the cells of (f), the conditions of (d) whereby the protooncogene is active, to produce conditionally immortalized cells in an intermediate stage of cell differentiation.

Another embodiment of the present invention relates to a method to produce conditionally immortalized adult stem cells, comprising: (a) obtaining an expanded population of adult stem cells; (b) culturing the stem cells in the presence of: (1) a combination of stem cell growth factors; (2) a first Tat-fusion protein, wherein Tat is fused to a protein encoded by a protooncogene or biologically active fragment or homologue thereof that promotes cell survival and proliferation; and (3) a second Tat-fusion protein, wherein Tat is fused to a protein that inhibits apoptosis in the stem cells.

Yet another embodiment of the present invention relates to method to produce conditionally immortalized embryonic stem cells, comprising: (a) obtaining an expanded population of embryonic stem cells; (b) transfecting the stem cells with a nucleic acid molecule comprising a protooncogene or biologically active fragment or homologue thereof that promotes cell survival and proliferation, wherein the protooncogene is inducible; (c) transfecting the stem cells with a nucleic acid molecule encoding a protein that inhibits apoptosis of the cell; and (d) expanding the transfected cells in the presence of a combination of stem cell growth factors under conditions whereby the protooncogene is active, to produce conditionally immortalized embryonic stem cells.

Another embodiment of the present invention relates to method to produce conditionally immortalized stem cells, comprising: (a) obtaining an expanded population of stem cells; (b) culturing the stem cells in the presence of: (1) a combination of stem cell growth factors; (2) a protein encoded by a protooncogene or biologically active fragment or homologue thereof that promotes cell survival and proliferation; and; (3) a protein that inhibits apoptosis in the stem cells. The protein of (2) and (3) are delivered into the stem cells using any suitable delivery system, including, but not limited to, Tat fusion, aptamers technology, or CHARIOT™ technology.

Yet another embodiment of the present invention relates to a method to produce conditionally immortalized stem cells, comprising: (a) obtaining an expanded population of stem cells; (b) delivering into the cells a protein encoded by a protooncogene or biologically active fragment or homologue thereof that promotes cell survival and proliferation, or a nucleic acid molecule encoding the same, wherein the protooncogene is inducible; (c) inhibiting apoptosis in the stem cells by delivering into the cells a protein that inhibits apoptosis of the cell, a nucleic acid molecule encoding the protein that inhibits apoptosis of the cell, or a nucleic acid molecule or protein that inhibits a proapoptotic protein in the cells; and (d) expanding the cells in the presence of a combination of stem cell growth factors under conditions whereby the protooncogene is active, to produce conditionally immortalized adult stem cells.

In any of the embodiments described above, the protooncogene can be selected from, but is not limited to: MYC-ER and ICN-1-ER. In any of the embodiments described above, the protein that inhibits apoptosis can be selected from, but is not limited to a member of the Bcl-2 family that inhibits apoptosis, such as Bcl-2, Bcl-X, Bcl-w, BclXL, Mcl-1, Dad-1, or hTERT. When the protooncogene is MYC-ER or ICN-1-ER, the conditions under which the protooncogene is active can include the presence of tamoxifen or an agonist thereof. In one aspect the cells are transfected with or are delivered (as a protein) *MYC*-ER and Bcl-2; *MYC*-ER and hTERT; ICN-1-ER and Bcl-2; ICN-1-ER and hTERT; or *MYC*-ER and ICN-1-ER.

In any of the embodiments described above, the step of expanding can be conducted in a medium including, but not limited to, (1) interleukin-6 (IL-6), IL-3 and stem cell factor (SCF); (2) a serum-free medium comprising stem cell factor (SCF), thrombopoietin (TPO), insulin-like Growth Factor 2 (IGF-2) and fibroblast Growth Factor 1 (FGF-1).

In any of the embodiments described above, the adult stem cells can include, but are not limited to: hematopoietic stem cells, intestinal stem cells, osteoblastic stem cells, mesenchymal stem cells, neural stem cells, epithelial stem cells, cardiac myocyte progenitor stem cells, skin stem cells, skeletal muscle stem cells, and liver stem cells. In one aspect, the mesenchymal stem cells are selected from lung mesenchymal stem cells and bone marrow stromal cells. In one aspect, the epithelial stem cells are selected from the group consisting of lung epithelial stem cells, breast epithelial stem cells, vascular epithelial stem cells and intestinal epithelial stem cells. In one aspect, the skin stem cells are selected from the group consisting of epidermal stem cells and follicular stem cells (hair follicle stem cells). In one aspect, the neural cells are selected from neuronal dopaminergic stem cells and motor-

neuronal stem cells. In one aspect, the stem cells are from fresh or cryopreserved cord blood. In one aspect, the stem cells are hematopoietic progenitor cells obtained from the peripheral blood of normal or granulocyte colony-stimulating factor (G-CSF) treated patients.

In any of the embodiments described above, the method can further include genetically modifying the stem cells to correct a genetic defect in the cells, genetically modifying the stem cells to silence the expression of a gene, and/or genetically modifying the stem cells to overexpress a gene.

In any of the embodiments described above, the method can further include storing the cells. In one aspect, the method further includes retrieving the cells from storage and culturing the cells.

Another embodiment of the present invention relates to cells produced by any method described above or elsewhere herein.

Yet another embodiment of the present invention relates to a method to provide adult stem cells, or cells differentiated therefrom, to an individual comprising: (a) providing a source of conditionally immortalized adult stem cells produced by any method described above or elsewhere herein; (b) removing the conditions under which the stem cells of (a) are conditionally immortalized; and (c) administering the stem cells or cells differentiated therefrom to the individual. In one aspect, the cells were previously obtained from the individual in (c). In one aspect, the cells were obtained from a previously frozen stock of said cells. In one aspect, the cells are freshly obtained from the individual and conditionally immortalized by any method described above or elsewhere herein. In one aspect, the individual has cancer. In another aspect, the individual has leukemia. In another aspect, the individual has an immune deficiency disorder. In another aspect, the individual has an anemia disorder. In another aspect, the individual is undergoing reconstructive surgery. In another aspect, the individual is undergoing elective cosmetic surgery. In another aspect, the individual is undergoing transplantation surgery. In one aspect, the individual is in need of stem cells, or cells differentiated therefrom, selected from: hematopoietic stem cells, intestinal stem cells, osteoblastic stem cells, mesenchymal stem cells, neural stem cells, epithelial stem cells, cardiac myocyte progenitor stem cells, skin stem cells, skeletal muscle stem cells, and liver stem cells. In another aspect, the individual is in need of improved immune cell function. In another aspect, the individual has a genetic defect that is corrected by the stem cell.

Yet another embodiment of the present invention relates to a method to identify compounds that regulate lineage commitment and/or cell differentiation and development, comprising: (a) contacting adult stem cells produced by any method described above or elsewhere herein; and (b) detecting at least one genotypic or phenotypic characteristic in the stem cells of (a), as compared to the stem cells in the absence of the compound, wherein detection of a difference in the characteristic in the presence of the compound indicates that the compound affects the characteristic in the stem cell.

Another embodiment of the present invention relates to a method to study lineage commitment and/or cell differentiation and development, comprising evaluating adult stem cells produced by any method described above or elsewhere herein, or cells differentiated therefrom, to detect at least one genotypic or phenotypic characteristic of the cells.

Yet another embodiment of the present invention relates to the use of the cells produced by any method described above or elsewhere herein in a medicament for treating a condition or disease in which transplantation of stem cells is beneficial.

Another embodiment of the present invention relates to a mouse model of acute myeloid leukemia (AML), comprising a mouse produced by a method comprising: (a) lethally irradiating a mouse; (b) transferring conditionally immortalized long-term stem cells produced by any method described above or elsewhere herein and whole bone marrow cells from a $Rag^{-/-}$ mouse into the mouse; and (c) injecting periodic doses of tamoxifen or an agonist thereof into the mouse until the mouse develops clinical signs of AML. In one aspect, the cells are transfected with or are delivered (as a protein) *MYC*-ER and Bcl-2.

Another embodiment of the invention relates to tumor cells obtained from the mouse model of AML described above.

Yet another embodiment of the invention relates to the use of the mouse model of AML for preclinical testing of drug candidates specific for human proteins; to identify, develop, and/or test a compound for use in the diagnosis of, study of, or treatment of AML; or to identify, develop, and/or test a target for use in the diagnosis of, study of, or treatment of AML.

Brief Description of the Drawings of the Invention

Fig. 1 is a graph showing mortality curves following bone marrow transplantation of transduced cells and activation of *MYC* function with 4OHT, *in vivo*.

Fig. 2 is a scatter plot showing scatter characteristics and GFP expression levels of HSCs derived from young and aged mice, following in vitro transduction. The dot plots represent the flow cytometric data for the forward (FSC) and side (SSC) scatter characteristics of the HSCs after three days in culture with IL-3, IL-6 and SCF. These two criteria correlate with cell size (FSC) and granularity (SSC).

Fig. 3 is a scatter plot showing the phenotypic comparison of cell lines derived from irradiated recipients reconstituted using BCL-2, *MYC*-ER and EGFP-transduced hematopoietic stem cells from aged (>60% ID^{-} repertoire) and young 3-83 μδ transgenic mice. Shown is the phenotype of representative clones 3 (young) and 3 (aged) months after initiation of culture.

Fig. 4 is a scatter plot showing the spontaneous differentiation of the aged LT-HSC line (ABM46) in vitro following withdrawal of tamoxifen (stem cell and B lineage marker expression are analyzed by flow cytometry).

Fig. 5 is a scatter plot showing the analysis of hematopoietic cell compartments derived from LT-HSC lines 6 weeks after adoptive transfer into irradiated young recipients. Data from three mice are presented in this figure, one mouse received the aged HSC line ABM42, and two mice received aged HSC line ABM46.

Fig. 6 is a scatter plot showing that the development of the B-cell compartment is compromised in mice reconstituted with ABM42 and ABM46 cell lines. Data from three mice are presented in this figure, one mouse received the aged HSC line ABM42, and two mice received aged HSC line ABM46.

Fig. 7 is a scatter plot showing T-cell development in mice that were reconstituted with ABM42 and ABM46 cell lines. Data from three mice are presented in this figure, one mouse received the aged HSC line ABM42, and two mice received aged HSC line ABM46.

Fig. 8 is a scatter plot and graph showing the phenotypic comparison of cell lines derived from HSCs obtained from young C57/BL6 mice that were retrovirally transduced with BCL-2 and *MYC*-ER and maintained in continuous *in vitro* culture for >90 days. The panels represent the results of the flow cytometric analysis for expression of the viral expression markers (GFP and Thy1.1), as well as four markers required to define long-term HSCs in mice, Sca-1, c-kit, CD34 and Flk-2. The four cell lines contained subpopulations that retained the phenotypes of lt-HSCs (Sca-1+, c-kit+, CD34-, flk-2-).

Fig. 9 is a scatter plot and graph showing a phenotypic comparison of cell lines derived from HSCs obtained from young C57/BL6 mice that were retrovirally transduced

with *different combinations* of oncogenes and maintained in continuous *in vitro* culture for >90 days (pMIG-*MYC* and pMIT-Bcl-2 (top panels), pMIG-MYC.ER and pMIG-hTERT (middle panels), or pMIG-ICN.1.ER and pMIT-Bcl-2 (bottom panels)).

Fig. 10 is a scatter plot and graph showing a phenotypic comparison of cell lines derived from HSCs obtained from young C57/BL6 mice that were retrovirally transduced with *different combinations* of oncogenes and maintained in continuous in vitro culture for >90 days (pMIG- ICN.1.ER and pMIT-Bcl-2 (top panels), pMIG-ICN.1 and pMIT-Bcl-2 (second row panels), or pMIG-ICN.1 and pMIG-Bcl-2 (third row panels), or pMIG-hTERT and pMIT-Bcl-2 (bottom panels)).

Fig. 11 is a scatter plot and graph showing a phenotypic comparison of cell lines derived from HSCs obtained from young C57/BL6 mice that were retrovirally transduced with *different combinations* of oncogenes and maintained in continuous in vitro culture for >90 days (pMIG-*MYC* and pMIG-ICN.1 (top panels), pMIG-MYC.ER and pMIG-ICN.1 (middle panels), or pMIG-ICN.1.ER and pMIG-MYC (bottom panels)).

Fig. 12 is a scatter plot showing the *in vivo* reconstitution of T cell and B cell compartments from cell lines derived from HSCs obtained from young C57/BL6 mice that were retrovirally transduced with different combinations of oncogenes and maintained in continuous in vitro culture for >90 days.

Fig. 13 is a schematic drawing showing the use of recognition substrate sequences (RSS's) for recombinases in order to ensure the excision of recombinant DNA from conditionally immortalized long-term stem cells of the invention prior to transplantation.

Fig. 14 is a graph showing the detection of cells of the NK and erythroid lineage differentiated from conditionally immortalized long-term stem cells of the invention.

Detailed Description of the Invention

The present invention provides a solution to the problem of being able to generate, maintain and manipulate stable cell lines derived from long-term stem cells, and particularly, long-term hematopoietic stem cells (lt-HSCs), that can give rise to all cell lineages that would normally arise from such cells when placed under the appropriate conditions. The present invention generally relates to methods to produce conditionally immortalized, long-term stem cells, to the stem cells produced by such methods, and to methods of using such stem cells. More specifically, using long-term hematopoietic stem cells as an exemplary stem cell population, the present inventors have established a powerful method to produce stem cells that are conditionally immortalized (*e.g.*, reversibly immortalized or immortalized under specified conditions which is reversible when such conditions are removed), such stem cells being capable differentiating into normal cell lineages *in vitro* and *in vivo*, and being capable of reconstituting subjects in need of such cells. Indeed, the present invention can eliminate the need for a bone marrow donor, since the invention provides for the ability to harvest stem cells from a patient prior to a procedure (*e.g.*, chemotherapy, radiation, etc.), to expand such cells, and return them to the patient. Moreover, such stem cells can be expanded extensively, stored (*e.g.*, frozen), and then retrieved and expanded again, manipulated, and/or used repeatedly as required or desired. Such stem cells can be manipulated, for example, to correct a genetic defect or provide a benefit to a subject (therapeutic or preventative), or differentiated into a desired cell type. Finally, such cells can be used in a variety of assays for the identification of new targets involved in regulation of cell development, proliferation and survival, and the identification and development of drugs useful in ameliorating or treating diseases and conditions that would benefit from the regulation of cell development, proliferation and/or survival.

The present inventors have developed novel technology that allows the conditional immortalization of long-term stem cells, exemplified herein by long-term hematopoietic stem cells (lt-HSCs). The resulting cell lines can be expanded (propagated) indefinitely and exponentially *in vitro* and/or cryopreserved (stored), and have the ability to rescue lethally irradiated mice and to reconstitute all blood cell lineages in such animals. Furthermore, the inventors have been able to generate differentiated blood cells *in vitro* by extinguishing the function of the transforming oncogene. Such cells and the methods of producing them as described herein will allow the generation of transplantable human stem cells that carry no recombinant DNA, and thus pose no long term risk to the recipient. These conditionally

immortalized lt-HSC's of the invention can be stabilized in their mature phenotypes and cell lines established in which the mature phenotype is preserved after reactivation of the oncogene. For example, the inventors have been able to develop $CD4^+$ $\alpha\beta^+$ T cells, as well as dendritic cell lines.

Applied in the clinical setting, this technology has the following advantages over bone marrow transplantation:

1. Very few lt-HSC are needed to establish clones;

2. Clones represent a renewable resource that can be stored indefinitely and accessed quickly;

3. The cost of this therapy should be much less than conventional bone marrow transplantation;

4. Use of lt-HSC clones should mitigate the threat of graft-versus-host disease, and associated costs;

5. This technology can, at least in some cases, mitigate the need for a bone marrow donor.

In addition, the present invention provides for the use of the conditionally transformed long-term stem cells, such as the lt-HSC cells, to generate cells representing differentiated lineages (*e.g.*, differentiated hematopoietic lineages, including intermediate stages of development of hematopoietic lineages). For example, in addition to countless therapeutic and preventative applications, these cell lines will allow the identification of novel compounds that can induce differentiation of malignant cells, arrest their growth, or induce apoptosis. These cells will also permit screening for novel cytokines and growth factors that direct the differentiation of stem cells in a particular pathway. Such cell lines simply do not exist and will be essential for drug discovery.

More specifically, in an effort to overcome the limitations in the art with regard to the provision and use of long term populations of adult-derived stem cells (although the invention is not limited to adult-derived stem cells, as discussed below), the present inventors have developed novel methods of producing of conditionally transformed cell lines representing early hematopoietic stem cell progenitors. In a specific, non-limiting example of the technology described and exemplified herein, the strategy involved the transfection (*e.g.*, by retroviral transduction) of bone marrow stem cells from 5-fluorouracil (5-FU)-treated 3-83μδ mice. The inventors utilized the pMSCV bisistronic retroviral vector with inserts encoding Bcl-2 and green fluorescent protein (GFP) (as a reporter gene), and MYC-

ER and GFP (again as a reporter gene). MYC was selected because of its ability to substitute for cytokine-derived survival and proliferative signals in lymphocytes. By restricting the target cell, the inventors hypothesized that stem cell tumors would form. Importantly, MYC-ER function is tamoxifen dependent in this setting, allowing for the termination of MYC function and transformation by withdrawing tamoxifen from the animal or cultures. In cells transduced with MYC-ER, the fusion protein is produced, but is retained in the cytoplasm until exposed to tamoxifen. Bcl-2 was selected because of its ability to inhibit apoptosis of cells that would normally occur as a result of exposure to the MYC signals and more particularly, when MYC is "inactivated" or removed by withdrawal of the tamoxifen from the cells. This novel combination of gene types (*i.e.,* the invention is not limited to these specific genes, as discussed in more detail below) is partly responsible for the successful production of conditionally immortalized stem cells according to the present invention, and can readily be extended to other similar combinations of genes, as discussed in detail below.

Recipients of the transduced stem cells described above produced tumors (in the presence of 4OHT), and tumor cells from the bone marrow, spleen and lymph node were harvested and placed in culture with tamoxifen and a stem cell growth factor cocktail. The present inventors have discovered that, in the absence of an appropriate combination of stem cell growth factors, the stem cells produced by the present method will stop growing and die within a short period of time. Therefore, the use of a stem cell growth factor "cocktail" (*i.e.,* combination of appropriate or suitable growth factors for stem cells) after transfection of the cells with the combination of genes discussed above is a second important aspect of the method of the present invention. This cocktail, while having the general characteristic of promoting and maintaining the growth of the stem cells, is not limited to a particular combination of growth factors, and parameters for selection of such factors are discussed in detail below.

The stem cells generated by the method of the present invention could be expanded in culture and were homogeneously positive for, *e.g.,* Sca1, positive for Endoglin and ckit, and negative for CD34, Flt3, B220, CD19 and mIgM, which are indicative of the phenotype of lt-HSC, which is well-characterized in the art. These cells could be frozen (cryopreserved, or stored), and then easily recovered and cultured after freezing. Importantly, the recovered cells were homogenous in phenotype and exhibited the phenotype of lt-HSC (*e.g.,* again, uniformly GFP bright cells were positive for Sca1, Endoglin and ckit,

and negative for CD34, Flt3, B220, CD19 and mIgM). This phenotype corresponds perfectly with the published characteristics of long term repopulating pluripotent stem cells (Reya et al., 2003, *Nature* 423:409-14) that provide all long-term reconstitution in mice.

The inventors have further developed this method so that it can be performed completely *in vitro* (*i.e.,* the initial procedure was conducted partly *in vivo* as described above). The inventors have also demonstrated that other combinations of genes having similar characteristics as those described above also result in the conditional immortalization of lt-HSCs. Furthermore, the cell lines can be differentiated *in vitro* into hematopoietic lineages by removing the tamoxifen and providing the appropriate growth factors, and will differentiate *in vivo* into all hematopoietic lineages in recipient animals in which tamoxifen is withheld. In addition, the cells can be differentiated into intermediate levels of development that have a stable phenotype and retain their ability to further differentiate along their committed pathway upon application or removal of the appropriate signal (described herein). Such cells are invaluable for various therapeutic applications. All of these experiments are described in detail below and in the Examples.

The methods and cell lines of the present invention provide a unique opportunity not only to study in detail the molecular, biochemical and cellular events that are associated with the commitment of adult stem cells toward various cell lineages and to study the differentiation and development of stem cells into various cell lineages, but also provide unique therapeutic and drug discovery tools.

For example, the stem cell lines of the present invention provide a unique source of expandable stem cells for use in a variety of transplantation, therapeutic and preventative strategies, including the treatment of cancer, and particularly, cancer that is treated by radiation. In current therapy for leukemia, for example, limited access to bone marrow donors and finite supplies of stem cells from such donors severely limit the options for reconstitution of a patient after radiation therapy. The present invention solves this problem by providing a means to generate a continuously expandable and renewable supply of autologous stem cells or histocompatible stem cells that can be stored and recovered as needed. Such technology could ultimately ablate the need for bone marrow donors altogether. In addition, a variety of immune deficiency disorders and anemia disorders (*e.g.,* aplastic anemia or hemolytic anemia) will also benefit greatly from this technology, since the present invention provides the ability to repopulate hematopoietic cells of an individual as needed by the individual. Furthermore, the aging process is associated with several

important changes in the hematopoietic compartment, including the increasing inability to mount a productive immune response, among others. Hematopoietic stem cells from aged mice have been shown to contain a higher level of mRNAs for DNA-repair problems. This may ultimately affect their ability to self-renew, undergo differentiation, undergo proliferation, and survive in response to bone marrow cytokines. Therefore, an aging individual can also benefit from the present invention in that a continuous supply of healthy hematopoietic cells can be provided to correct or ameliorate such deficiencies.

The technology of the present invention is not limited to bone marrow stem cells, but can be applied to virtually any type of stem cell, and can be extended beyond adult-derived cells to embryonic stem cells.

In one example, another application of the present invention relates to the generation of continuously expandable and renewable hair follicle stem cells. The development of conditionally immortalized stem cells from this lineage can be use in the context of reconstructive surgery for burn victims, for any individual that undergoes chemotherapy and/or radiation therapy resulting in the irreversible loss of hair growth, as well as patients following any surgical procedure affecting the skull. Furthermore, such cells could be used for elective procedures that involve the induction of hair growth in individuals affected by hereditary pattern baldness. Similarly, application of the present invention to stem cells of the skin will be invaluable for use in wound healing and treatment of burn victims, as well as plastic reconstructive surgery for trauma and other patients, as well as elective surgeries, including, but not limited to, cosmetic surgery. Such cells can be additionally genetically manipulated to correct inborn or acquired genetic defects in young and aged individuals. One of skill in the art will understand based on this disclosure that benefits can be derived from the use of the present invention on various other stem cell populations, including, but not limited to, stem cells derived from lung, breast, and intestinal epithelium and stem cells derived from neural and cardiac tissue, to name just a few. Other stem cell types are referenced elsewhere herein.

In addition, the present invention provides the unique opportunity for an individual to have access to expandable supplies of autologous stem cells and cells differentiated therefrom as needed throughout the life of the individual. For example, as the body ages, it is known that immune function and immune memory deteriorates. However, using the technology provided by the present invention, it will be possible to repopulate an individual with new, autologous stem cells that are capable of differentiation into all of the cells of the

hematopoietic lineage, thus providing the aged individual with a "young" immune system. In addition, stem cells generated by the present method can be stored and used as part of therapeutic protocols during the lifetime of the individual, should they be needed (*e.g.*, in the event the individual develops a cancer or immune deficiency disease or has another need for newly generated, autologous cells of virtually any type).

The present invention also provides unique opportunities for gene therapy. Specifically, genetic defects can now be corrected or beneficial gene modifications can be introduced into somatic cells by manipulating autologous stem cells obtained from an individual that have been conditionally immortalized and expanded using the method of the present invention. The stem cells can then be reintroduced into the individual from which they were obtained.

The stem cells produced by the method of the invention can also be used in a variety of drug discovery assays. Since one can now produce virtually unlimited supplies of homogeneous stem cells that can readily be stored, recovered, expanded and manipulated, such stem cells can be used as stem cells or differentiated into various cell lineages and used in assays to test various compounds for effects on cell differentiation, gene expression, and cell processes. The cells can be manipulated prior to contact with the compounds, such as by genetic manipulation. Stem cells from individuals with genetic defects can be evaluated in such assays in order to identify therapeutic compounds (*e.g.*, cancer therapeutics) and evaluate gene replacement therapies. Indeed, the technology of the present invention provides an opportunity to target the cells of a specific individual to identify drug candidates and therapeutic candidates and strategies that are "tailored" to the cells of an individual. An example of such an assay is described in detail below.

With regard to research and discovery in the area of lineage commitment and cell differentiation and development, prior to the present invention, such studies were severely hampered by the lack of access to and the inability to generate sufficient numbers of the desired cell population to perform desired experiments. For example, in order to identify or screen for intermediates in the differentiation of a particular progenitor cell line, a sufficient number of cells must be obtained to provide meaningful and reproducible results. The progenitor cell line should also retain the ability to further differentiate in the lineage to which it has already committed, hence making these novel tools that do not currently exits, nor are there other descriptions of technology needed to generate those cells. Using technologies available at the time of the invention, this was not possible. The present

invention solves the problem by providing expandable and essentially unlimited supplies of homogeneous stem cells that can be used in a variety of experiments. This technology will greatly enhance research capabilities in the area of cell differentiation and discovery.

As discussed above, the method for conditionally immortalizing lt-HSCs of the present invention can be adapted for additional stem cells derived from other tissues. For example, by adapting the gene delivery and growth factors, if needed, the present invention can be applied to a variety of different stem cells as described below. Such cells can also be expanded *in vitro*, and proceed to differentiate upon inactivation of the oncogenes, as described herein for hematopoietic stem cells. These cells can then be used for therapeutic applications that include tissue repair and tissue regeneration/engineering. Accordingly, the MYC-ER and Bcl-2 combination of genes, or any of the other combinations described herein, can be transfected by any method described herein or deemed suitable by one of skill in the art given this disclosure (including by a variety of viral-mediated methods), into cells including, but not limited to, mesenchymal stem cells (including, but not limited to, lung mesenchymal stem cells, bone marrow stromal cells), neural stem cells (including, but not limited to, neuronal dopaminergic stem cells and motor-neuronal stem cells), epithelial stem cells (including, but not limited to, lung epithelial stem cells, breast epithelial stem cells, and intestinal epithelial stem cells), cardiac myocyte progenitor stem cells, skin stem cells (including, but not limited to, epidermal stem cells and follicular stem cells), skeletal muscle stem cells, endothelial stem cells (*e.g.,* lung endothelial stem cells), and liver stem cells, to generate conditionally immortalized cell lines that can be expanded *in vitro* and proceed to differentiate upon inactivation of the oncogenes. In addition to the therapeutic potential of such cell lines, these lines can be further modified *in vitro* (or *ex vivo*) in order to correct inborn genetic defects, and used for studying the molecular basis of early lineage commitment and differentiation. While these cells may be a novel source of potentially relevant therapeutic targets, these cell lines will also be useful for the screening of small molecules that either prevent or induce differentiation, and for the identification of novel compounds and molecular targets for various therapies, including, but not limited to, cancer therapy and immune deficiency therapy.

General Definitions

In accordance with the present invention, reference to an isolated nucleic acid molecule herein is a nucleic acid molecule that has been removed from its natural milieu (i.e., that has been subject to human manipulation), its natural milieu being the genome or

chromosome in which the nucleic acid molecule is found in nature. As such, "isolated" does not necessarily reflect the extent to which the nucleic acid molecule has been purified, but indicates that the molecule does not include an entire genome or an entire chromosome in which the nucleic acid molecule is found in nature. An isolated nucleic acid molecule can include a gene. An isolated nucleic acid molecule that includes a gene is not a fragment of a chromosome that includes such gene, but rather includes the coding region and regulatory regions associated with the gene, but no additional genes that are naturally found on the same chromosome. An isolated nucleic acid molecule can also include a specified nucleic acid sequence flanked by (i.e., at the 5' and/or the 3' end of the sequence) additional nucleic acids that do not normally flank the specified nucleic acid sequence in nature (i.e., heterologous sequences). Isolated nucleic acid molecule can include DNA, RNA (e.g., mRNA), or derivatives of either DNA or RNA (e.g., cDNA, siRNA, shRNA). Although the phrase "nucleic acid molecule" primarily refers to the physical nucleic acid molecule and the phrase "nucleic acid sequence" primarily refers to the sequence of nucleotides on the nucleic acid molecule, the two phrases can be used interchangeably, especially with respect to a nucleic acid molecule, or a nucleic acid sequence, being capable of encoding a protein or domain of a protein.

Preferably, an isolated nucleic acid molecule of the present invention is produced using recombinant DNA technology (e.g., polymerase chain reaction (PCR) amplification, cloning) or chemical synthesis. Isolated nucleic acid molecules include natural nucleic acid molecules and homologues thereof, including, but not limited to, natural allelic variants and modified nucleic acid molecules in which nucleotides have been inserted, deleted, substituted, and/or inverted in such a manner that such modifications provide the desired effect (e.g., provision of an inducible protooncogene, as described herein).

A nucleic acid molecule homologue can be produced using a number of methods known to those skilled in the art (see, for example, Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Labs Press (1989)). For example, nucleic acid molecules can be modified using a variety of techniques including, but not limited to, classic mutagenesis techniques and recombinant DNA techniques, such as site-directed mutagenesis, chemical treatment of a nucleic acid molecule to induce mutations, restriction enzyme cleavage of a nucleic acid fragment, ligation of nucleic acid fragments, PCR amplification and/or mutagenesis of selected regions of a nucleic acid sequence, synthesis of oligonucleotide mixtures and ligation of mixture groups to "build" a mixture of nucleic acid

molecules and combinations thereof. Nucleic acid molecule homologues can be selected from a mixture of modified nucleic acids by screening for the function of the protein encoded by the nucleic acid and/or by hybridization with a wild-type gene.

The minimum size of a nucleic acid molecule or polynucleotide of the present invention is a size sufficient to encode a protein useful in the present invention, such as a protein encoded by a protooncogene or functional portion thereof (*i.e.,* a portion that has the biological activity of the full-length protein and that is sufficient for use in the method of the invention), or an anti-apoptotic protein or a functional portion thereof (*i.e.,* a portion that has the biological activity of the full-length protein and that is sufficient for use in the method of the invention). Other nucleic acid molecules that may be useful in the present invention can include nucleic acid molecules of a minimum size sufficient to form a probe or oligonucleotide primer that is capable of forming a stable hybrid with the complementary sequence of a nucleic acid molecule encoding the natural protein (e.g., under moderate, high or very high stringency conditions), which is typically at least 5 nucleotides in length, and preferably ranges from about 5 to about 50 or about 500 nucleotides or greater, including any length in between, in whole number increments (i.e., 5, 6, 7, 8, 9, 10,...33, 34,...256, 257,...500). There is no limit, other than a practical limit, on the maximal size of a nucleic acid molecule of the present invention, in that the nucleic acid molecule can include a sequence or sequences sufficient to be useful in any of the embodiments of the invention described herein.

As used herein, stringent hybridization conditions refer to standard hybridization conditions under which nucleic acid molecules are used to identify similar nucleic acid molecules. Such standard conditions are disclosed, for example, in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Labs Press, 1989. Sambrook et al., *ibid.*, is incorporated by reference herein in its entirety (see specifically, pages 9.31-9.62). In addition, formulae to calculate the appropriate hybridization and wash conditions to achieve hybridization permitting varying degrees of mismatch of nucleotides are disclosed, for example, in Meinkoth et al., 1984, *Anal. Biochem.* 138, 267-284; Meinkoth et al., *ibid.*, is incorporated by reference herein in its entirety.

More particularly, moderate stringency hybridization and washing conditions, as referred to herein, refer to conditions which permit isolation of nucleic acid molecules having at least about 70% nucleic acid sequence identity with the nucleic acid molecule being used to probe in the hybridization reaction (i.e., conditions permitting about 30% or

less mismatch of nucleotides). High stringency hybridization and washing conditions, as referred to herein, refer to conditions which permit isolation of nucleic acid molecules having at least about 80% nucleic acid sequence identity with the nucleic acid molecule being used to probe in the hybridization reaction (i.e., conditions permitting about 20% or less mismatch of nucleotides). Very high stringency hybridization and washing conditions, as referred to herein, refer to conditions which permit isolation of nucleic acid molecules having at least about 90% nucleic acid sequence identity with the nucleic acid molecule being used to probe in the hybridization reaction (i.e., conditions permitting about 10% or less mismatch of nucleotides). As discussed above, one of skill in the art can use the formulae in Meinkoth et al., *ibid.* to calculate the appropriate hybridization and wash conditions to achieve these particular levels of nucleotide mismatch. Such conditions will vary, depending on whether DNA:RNA or DNA:DNA hybrids are being formed. Calculated melting temperatures for DNA:DNA hybrids are 10°C less than for DNA:RNA hybrids. In particular embodiments, stringent hybridization conditions for DNA:DNA hybrids include hybridization at an ionic strength of 6X SSC (0.9 M Na^+) at a temperature of between about 20°C and about 35°C (lower stringency), more preferably, between about 28°C and about 40°C (more stringent), and even more preferably, between about 35°C and about 45°C (even more stringent), with appropriate wash conditions. In particular embodiments, stringent hybridization conditions for DNA:RNA hybrids include hybridization at an ionic strength of 6X SSC (0.9 M Na^+) at a temperature of between about 30°C and about 45°C, more preferably, between about 38°C and about 50°C, and even more preferably, between about 45°C and about 55°C, with similarly stringent wash conditions. These values are based on calculations of a melting temperature for molecules larger than about 100 nucleotides, 0% formamide and a G + C content of about 40%. Alternatively, T_m can be calculated empirically as set forth in Sambrook et al., *supra*, pages 9.31 to 9.62. In general, the wash conditions should be as stringent as possible, and should be appropriate for the chosen hybridization conditions. For example, hybridization conditions can include a combination of salt and temperature conditions that are approximately 20-25°C below the calculated T_m of a particular hybrid, and wash conditions typically include a combination of salt and temperature conditions that are approximately 12-20°C below the calculated T_m of the particular hybrid. One example of hybridization conditions suitable for use with DNA:DNA hybrids includes a 2-24 hour hybridization in 6X SSC (50% formamide) at about 42°C, followed by washing steps that include one or more washes at room temperature in about 2X

SSC, followed by additional washes at higher temperatures and lower ionic strength (e.g., at least one wash as about 37°C in about 0.1X-0.5X SSC, followed by at least one wash at about 68°C in about 0.1X-0.5X SSC).

In one embodiment of the present invention, any amino acid sequence described herein, including truncated forms (fragments or portions) and homologues of such sequences, can be produced with from at least one, and up to about 20, additional heterologous amino acids flanking each of the C- and/or N-terminal end of the given amino acid sequence. The resulting protein or polypeptide can be referred to as "consisting essentially of" a given amino acid sequence. According to the present invention, the heterologous amino acids are a sequence of amino acids that are not naturally found (i.e., not found in nature, *in vivo*) flanking the given amino acid sequence or which would not be encoded by the nucleotides that flank the naturally occurring nucleic acid sequence encoding the given amino acid sequence as it occurs in the gene, if such nucleotides in the naturally occurring sequence were translated using standard codon usage for the organism from which the given amino acid sequence is derived. Similarly, the phrase "consisting essentially of", when used with reference to a nucleic acid sequence herein, refers to a nucleic acid sequence encoding a given amino acid sequence that can be flanked by from at least one, and up to as many as about 60, additional heterologous nucleotides at each of the 5' and/or the 3' end of the nucleic acid sequence encoding the given amino acid sequence. The heterologous nucleotides are not naturally found (i.e., not found in nature, *in vivo*) flanking the nucleic acid sequence encoding the given amino acid sequence as it occurs in the natural gene.

According to the present invention, a recombinant vector (also referred to generally as a recombinant nucleic acid molecule, particularly when it contains a nucleic acid sequence of interest according to the invention) is an engineered (i.e., artificially produced) nucleic acid molecule that is used as a tool for manipulating a nucleic acid sequence of choice and for introducing such a nucleic acid sequence into a host cell. The recombinant vector is therefore suitable for use in cloning, sequencing, and/or otherwise manipulating the nucleic acid sequence of choice, such as by expressing and/or delivering the nucleic acid sequence of choice into a host cell. Such a vector typically contains heterologous nucleic acid sequences, *i.e.*, nucleic acid sequences that are not naturally or usually found adjacent to a nucleic acid sequence to be cloned or delivered, although the vector can also contain regulatory nucleic acid sequences (e.g., promoters, untranslated regions) which are naturally found adjacent to nucleic acid molecules of the present invention, or which are useful for

expression of the nucleic acid molecules of the present invention (discussed in detail below). A vector can be either RNA or DNA, either prokaryotic or eukaryotic, and typically is a plasmid or a viral vector. The vector can be maintained as an extrachromosomal element (e.g., a plasmid) or it can be integrated into the chromosome of a host cell. The entire vector can remain in place within a host cell, or under certain conditions, the plasmid DNA can be deleted, leaving behind the nucleic acid molecule of the present invention. Under other conditions, the vector is designed to be excised (removed) from the genome of the host cell at a selected time (described in more detail below). The integrated nucleic acid molecule can be under chromosomal promoter control, under native or plasmid promoter control, or under a combination of several promoter controls. Single or multiple copies of the nucleic acid molecule can be integrated into the chromosome. A recombinant vector of the present invention can contain at least one selectable marker.

According to the present invention, the phrase "operatively linked" refers to linking a nucleic acid molecule to an expression control sequence (e.g., a transcription control sequence and/or a translation control sequence) in a manner such that the molecule can be expressed when transfected (i.e., transformed, transduced, transfected, conjugated or conduced) into a host cell. Transcription control sequences are sequences that control the initiation, elongation, or termination of transcription. Particularly important transcription control sequences are those that control transcription initiation, such as promoter, enhancer, operator and repressor sequences. Suitable transcription control sequences include any transcription control sequence that can function in a host cell or organism into which the recombinant nucleic acid molecule is to be introduced.

According to the present invention, the term "transfection" is used to refer to any method by which an exogenous nucleic acid molecule (i.e., a recombinant nucleic acid molecule) can be inserted into a cell. The term "transduction" is a specific type of transfection in which genetic material is transferred from one source to another, such as by a virus (*e.g.*, a retrovirus) or a transducing bacteriophage. The term "transformation" can be used interchangeably with the term "transfection" when such term is used to refer to the introduction of nucleic acid molecules into microbial cells, such as bacteria and yeast. In microbial systems, the term "transformation" is used to describe an inherited change due to the acquisition of exogenous nucleic acids by the microorganism and is essentially synonymous with the term "transfection." However, in animal cells, transformation has acquired a second meaning that can refer to changes in the growth properties of cells in

culture after they become cancerous, for example. Therefore, to avoid confusion, the term "transfection" is preferably used herein with regard to the introduction of exogenous nucleic acids into animal cells. Therefore, the term "transfection" will be used herein to generally encompass transfection or transduction of animal cells, and transformation or transduction of microbial cells, to the extent that the terms pertain to the introduction of exogenous nucleic acids into a cell. Transfection techniques include, but are not limited to, transformation, transduction, particle bombardment, diffusion, active transport, bath sonication, electroporation, microinjection, lipofection, adsorption, infection and protoplast fusion.

As used herein, reference to an isolated protein or polypeptide in the present invention includes full-length proteins, fusion proteins, chimeric proteins, or any fragment (truncated form, portion) or homologue of such a protein. More specifically, an isolated protein according to the present invention, is a protein (including a polypeptide or peptide) that has been removed from its natural milieu (*i.e.,* that has been subject to human manipulation), and can include, but is not limited to, purified proteins, partially purified proteins, recombinantly produced proteins, membrane bound proteins, proteins complexed with lipids, soluble proteins, synthetically produced proteins, and isolated proteins associated with other proteins. As such, "isolated" does not reflect the extent to which the protein has been purified. Preferably, an isolated protein of the present invention is produced recombinantly. In addition, and again by way of example with respect to the naming of a particular protein (Bcl-2), a "human Bcl-2 protein" or a protein "derived from" a human Bcl-2 protein refers to a Bcl-2 protein (including a homologue or portion of a naturally occurring Bcl-2 protein) from a human (*Homo sapiens*) or to a Bcl-2 protein that has been otherwise produced from the knowledge of the structure (*e.g.*, sequence) and perhaps the function of a naturally occurring Bcl-2 protein from *Homo sapiens*. In other words, a human Bcl-2 protein includes any Bcl-2 protein that has substantially similar structure and function of a naturally occurring Bcl-2 protein from *Homo sapiens* or that is a biologically active (*i.e.,* has biological activity) homologue of a naturally occurring Bcl-2 protein from *Homo sapiens* as described in detail herein. As such, a human Bcl-2 protein can include purified, partially purified, recombinant, mutated/modified and synthetic proteins. According to the present invention, the terms "modification" and "mutation" can be used interchangeably, particularly with regard to the modifications/mutations to the amino acid sequence of a protein (or nucleic acid sequences) described herein.

As used herein, the term "homologue" is used to refer to a protein or peptide which differs from a naturally occurring protein or peptide (i.e., the "prototype" or "wild-type" protein) by modifications, including minor modifications, to the naturally occurring protein or peptide, but which maintains the basic protein and side chain structure of the naturally occurring form. Such changes include, but are not limited to: changes in one or a few (*i.e.*, 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10) amino acid side chains; changes one or a few amino acids, including deletions (e.g., a protein or truncated form of the protein or peptide), insertions and/or substitutions; changes in stereochemistry of one or a few atoms; and/or minor derivatizations, including but not limited to: methylation, glycosylation, phosphorylation, acetylation, myristoylation, prenylation, palmitation, amidation and/or addition of glycosylphosphatidyl inositol. A homologue can have either enhanced, decreased, or substantially similar properties as compared to the naturally occurring protein or peptide. A homologue can include an agonist of a protein or an antagonist of a protein.

Homologues can be the result of natural allelic variation or natural mutation. A naturally occurring allelic variant of a nucleic acid encoding a protein is a gene that occurs at essentially the same locus (or loci) in the genome as the gene which encodes such protein, but which, due to natural variations caused by, for example, mutation or recombination, has a similar but not identical sequence. Allelic variants typically encode proteins having similar activity to that of the protein encoded by the gene to which they are being compared. One class of allelic variants can encode the same protein but have different nucleic acid sequences due to the degeneracy of the genetic code. Allelic variants can also comprise alterations in the 5' or 3' untranslated regions of the gene (e.g., in regulatory control regions). Allelic variants are well known to those skilled in the art.

Homologues can be produced using techniques known in the art for the production of proteins including, but not limited to, direct modifications to the isolated, naturally occurring protein, direct protein synthesis, or modifications to the nucleic acid sequence encoding the protein using, for example, classic or recombinant DNA techniques to effect random or targeted mutagenesis.

In one embodiment, a homologue of a given protein comprises, consists essentially of, or consists of, an amino acid sequence that is at least about 45%, or at least about 50%, or at least about 55%, or at least about 60%, or at least about 65%, or at least about 70%, or at least about 75%, or at least about 80%, or at least about 85%, or at least about 90%, or at least about 95% identical, or at least about 95% identical, or at least about 96% identical, or

at least about 97% identical, or at least about 98% identical, or at least about 99% identical (or any percent identity between 45% and 99%, in whole integer increments), to the amino acid sequence of the reference protein. In one embodiment, the homologue comprises, consists essentially of, or consists of, an amino acid sequence that is less than 100% identical, less than about 99% identical, less than about 98% identical, less than about 97% identical, less than about 96% identical, less than about 95% identical, and so on, in increments of 1%, to less than about 70% identical to the naturally occurring amino acid sequence of the reference protein.

As used herein, unless otherwise specified, reference to a percent (%) identity refers to an evaluation of homology which is performed using: (1) a BLAST 2.0 Basic BLAST homology search using blastp for amino acid searches and blastn for nucleic acid searches with standard default parameters, wherein the query sequence is filtered for low complexity regions by default (described in Altschul, S.F., Madden, T.L., Schääffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25:3389-3402, incorporated herein by reference in its entirety); (2) a BLAST 2 alignment (using the parameters described below); (3) and/or PSI-BLAST with the standard default parameters (Position-Specific Iterated BLAST. It is noted that due to some differences in the standard parameters between BLAST 2.0 Basic BLAST and BLAST 2, two specific sequences might be recognized as having significant homology using the BLAST 2 program, whereas a search performed in BLAST 2.0 Basic BLAST using one of the sequences as the query sequence may not identify the second sequence in the top matches. In addition, PSI-BLAST provides an automated, easy-to-use version of a "profile" search, which is a sensitive way to look for sequence homologues. The program first performs a gapped BLAST database search. The PSI-BLAST program uses the information from any significant alignments returned to construct a position-specific score matrix, which replaces the query sequence for the next round of database searching. Therefore, it is to be understood that percent identity can be determined by using any one of these programs.

Two specific sequences can be aligned to one another using BLAST 2 sequence as described in Tatusova and Madden, (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", *FEMS Microbiol Lett.* 174:247-250, incorporated herein by reference in its entirety. BLAST 2 sequence alignment is performed in blastp or blastn using the BLAST 2.0 algorithm to perform a Gapped BLAST search (BLAST 2.0) between

the two sequences allowing for the introduction of gaps (deletions and insertions) in the resulting alignment. For purposes of clarity herein, a BLAST 2 sequence alignment is performed using the standard default parameters as follows.

For blastn, using 0 BLOSUM62 matrix:
Reward for match = 1
Penalty for mismatch = -2
Open gap (5) and extension gap (2) penalties
gap x_dropoff (50) expect (10) word size (11) filter (on)

For blastp, using 0 BLOSUM62 matrix:
Open gap (11) and extension gap (1) penalties
gap x_dropoff (50) expect (10) word size (3) filter (on).

According to the present invention, an isolated protein, including a biologically active homologue or fragment thereof, has at least one characteristic of biological activity of activity the wild-type, or natural (native) protein. In general, the biological activity or biological action of a protein refers to any function(s) exhibited or performed by the protein that is ascribed to the naturally occurring form of the protein as measured or observed *in vivo* (*i.e.*, in the natural physiological environment of the protein) or *in vitro* (*i.e.*, under laboratory conditions). Modifications, activities or interactions which result in a decrease in protein expression or a decrease in the activity of the protein, can be referred to as inactivation (complete or partial), down-regulation, reduced action, or decreased action or activity of a protein. Similarly, modifications, activities or interactions that result in an increase in protein expression or an increase in the activity of the protein, can be referred to as amplification, overproduction, activation, enhancement, up-regulation or increased action of a protein.

Method of Conditional Immortalization of the Invention

One embodiment of the present invention relates to a method to produce conditionally immortalized, adult stem cells, and preferably long-term stem cells. The method generally includes the following steps: (a) obtaining an expanded population of adult stem cells; (b) transfecting (transducing) the stem cells with a vector comprising a protooncogene that promotes cell survival and proliferation, wherein the protooncogene is regulatable (inducible, controllable), (c) transfecting (transducing) the stem cells with a vector encoding a protein that inhibits apoptosis of the cell; and (d) expanding the transfected cells in the presence of a combination of stem cell growth factors under conditions whereby the protooncogene is active. In one embodiment, the vector is an

integrating vector. Cells produced by this method can be cultured, expanded, stored, recovered, used in therapeutic methods, used in research and discovery methods, genetically manipulated, induced to differentiate by removing the conditions whereby the protooncogene is active, and/or used in any other method described herein or apparent to one of skill in the art given this disclosure. Steps (b) and (c) can be performed in any order.

According to the present invention, the phrase "conditionally immortalized" refers to cells that are immortalized (*e.g.*, capable of indefinite growth without differentiation in a cytokine dependent fashion, while maintaining their ability and potential to differentiate into a number of different lineages under the appropriate conditions) in a reversible manner, such that the cells are immortalized under a specific set of conditions, and when the conditions are removed or changed (or other conditions added), the cells are no longer immortalized and may differentiate into other cell types. The phrase "conditionally immortalized" can be used interchangeably with the phrase "reversibly immortalized". For example, referring to the method of the present invention, the presence of the regulatable protooncogene that promotes cell survival and proliferation causes the cells to retain an immortalized phenotype when the stem cell is placed under conditions that allow the protooncogene to be activated (*e.g.*, tamoxifen or an agonist thereof in the case of MYC-ER). In other words, the cells grow and expand indefinitely in culture, and are maintained in an undifferentiated state under these specific conditions. When these conditions are removed (*e.g.*, the tamoxifen is removed with respect to MYC-ER), the stem cells are no longer immortalized and can differentiate into various cell lineages given the appropriate environment (*e.g.*, the appropriate combination of growth factors).

Reference to "stem cells", as used herein, refers to the term as it is generally understood in the art. For example, stem cells, regardless of their source, are cells that are capable of dividing and renewing themselves for long periods, are unspecialized (undifferentiated), and can give rise to (differentiate into) specialized cell types (*i.e.*, they are progenitor or precursor cells for a variety of different, specialized cell types). "Long-term", when used in connection with stem cells, refers to the ability of stem cells to renew themselves by dividing into the same non-specialized cell type over long periods (*e.g.*, many months, such as at least 3 months, to years) depending on the specific type of stem cell. As discussed herein, phenotypic characteristics of various long-term stem cells from different animal species, such as long-term hematopoietic stem cells (lt-HSC) are known in the art. For example, murine lt-HSC can be identified by the presence of the following cell surface

marker phenotype: c-kit+, Sca-1+, CD34-, flk2- (see Examples). Adult stem cells include stem cells that can be obtained from any non-embryonic tissue or source, and typically generate the cell types of the tissue in which they reside. The term "adult stem cell" may be used interchangeably with the term "somatic stem cell". Embryonic stem cells are stem cells obtained from any embryonic tissue or source.

In one embodiment of the invention, the stem cells used in the present invention can include any adult stem cells obtained from any source. In another embodiment of the invention, stem cells can include embryonic stem cells. Stem cells useful in the present invention include, but are not limited to, hematopoietic stem cells, mesenchymal stem cells (including, but not limited to, lung mesenchymal stem cells, bone marrow stromal cells), neural stem cells, epithelial stem cells (including, but not limited to, lung epithelial stem cells, breast epithelial stem cells, vascular epithelial stem cells, and intestinal epithelial stem cells), intestinal stem cells, cardiac myocyte progenitor stem cells, skin stem cells (including, but not limited to, epidermal stem cells and follicular stem cells (hair follicle stem cells)), skeletal muscle stem cells, osteoblastic precursor stem cells, and liver stem cells.

Hematopoietic stem cells give rise to all of the types of blood cells, including but not limited to, red blood cells (erythrocytes), B lymphocytes, T lymphocytes, natural killer cells, neutrophils, basophils, eosinophils, monocytes, macrophages, and platelets.

Mesenchymal stem cells (including bone marrow stromal cells) give rise to a variety of cell types, including, but not limited to bone cells (osteocytes), cartilage cells (chondrocytes), fat cells (adipocytes), lung cells, and other kinds of connective tissue cells such as those in tendons.

Neural stem cells in the brain give rise to its three major cell types: nerve cells (neurons) and two categories of non-neuronal cells, astrocytes and oligodendrocytes.

Epithelial stem cells in the lining of various tissues give rise to several cell types that form the epithelium in tissues.

Skin stem cells occur in the basal layer of the epidermis and at the base of hair follicles. The epidermal stem cells give rise to keratinocytes, which migrate to the surface of the skin and form a protective layer, and the follicular stem cells can give rise to both the hair follicle and to the epidermis. Other sources of adult stem cells will be known to those of skill in the art.

Embryonic stem cells can give rise to all tissues and cells of the body.

Methods for obtaining such stem cells and providing initial culture conditions, such as a liquid culture or semi-solid culture medium, are known in the art. The cells are initially expanded *in vivo* or *in vitro*, by contacting the source of the stem cells with a suitable reagent that expands or enriches such cells in the tissue source or in culture. For example, in the case of hematopoietic stem cells, the donor individual can be treated with an agent that enriches for hematopoietic stem cells and encourages such cells to proliferate without differentiation, such as 5-fluorouracil. Other suitable agents for expansion of a desired stem cell type will be known to those of skill in the art. Alternatively, and preferably, adult stem cells are isolated from a tissue source and then expanded or enriched *in vitro* by exposure to a suitable agent. For example, with regard to hematopoietic stem cells, a method for producing an expanded culture of adult hematopoietic progenitors is described in Van Parijs et al., (1999; *Immunity*, 11, 763-70). Cells are obtained from an individual by any suitable method for obtaining a cell sample from an animal, including, but not limited, to, collection of bone marrow collection of a bodily fluid (*e.g.*, blood), collection of umbilical cord blood, tissue punch, and tissue dissection, including particularly, but not limited to, any biopsies of skin, intestine, cornea, spinal cord, brain tissue, scalp, stomach, breast, lung (*e.g.*, including lavage and bronchioschopy), fine needle aspirates of the bone marrow, amniotic fluid, placenta and yolk sac.

In one embodiment, cells useful in the invention can also be obtained from fresh, or cryopreserved (stored) cord blood, hematopoietic progenitor populations that can be derived from the directed differentiation of embryonic stem (ES) cells *in vitro*, hematopoietic stem cells (HSCs) obtained from the peripheral blood of normal or granulocyte colony-stimulating factor (G-CSF)-treated patients who have been induced to mobilize their lt-HSCs to the peripheral circulation.

Once an expanded population of stem cells is obtained (made available, provided, or produced), the cells are transfected, either sequentially (in any order) or simultaneously, with: (1) a vector comprising a protooncogene that promotes cell survival and proliferation, wherein the protooncogene is regulatable (inducible, controllable), and (2) a vector encoding a protein that inhibits apoptosis of the cell. Preferably, the vector is an integrating vector, defined herein as any vector that has the ability to integrate into the genome of a cell (*e.g.*, a retroviral vector). Various vectors and methods of transfection are described in detail below. The protooncogene is regulatable (inducible or controllable), so that the protooncogene can be activated and deactivated (*i.e.*, turned on or turned off) as desired to either maintain the

stem cell in an immortalized state or to allow it to differentiate into a desired cell type. Protooncongenes can be selected, or designed, to be regulated by any suitable method, including in response to any condition, such as the presence or absence of a compound or agent, temperature, or any other suitable condition. By way of example, the protooncogenes MYC-ER (the estrogen receptor (ER)-regulated MYC) and ICN-1-ER (the ER-regulated intracellular portion of Notch-1) described herein are both inducible in the presence of tamoxifen. It is noted that such genes can also be engineered to be responsive to other dimerizing drugs, such as FK1012, altered forms of Rapamycin, or could be expressed from vectors that contain a tetracycline responsive element. The latter scenario regulates expression of the protein, not the function of a polypeptide present in the cell. Other similar modifications of this platform technology will be apparent to those of skill in the art.

The protooncogene useful in the method of the present invention is any protooncogene that promotes cell survival and proliferation. Preferred protooncogenes to use in the method of the invention include, but are not limited to MYC, ICN-1, hTERT (reverse transcriptase component of the human telomerase), NMYC, S-MYC, L-MYC, Akt (myrystylated). In addition, other suitable genes to use or methods of the invention or ways to modify genes to achieve the desired result include, but are not limited to use of downstream signaling effectors such as pyruvate dehydrogenase kinase 1 (PDK-1); mammalian target of Rapamycin (mTOR); loss of phosphatase and tensin homologue (PTEN) by shRNA; Bcl-3, Cyclin D1, Cyclin D3, Bcl-10, Bcl-6, BCR-ABL (breakpoint cluster region fusion with ABL) and its various mutant forms, constitutively active forms of Stat5 and Stat3, AML1-ETO (fusion of acute myelogenous leukemia 1 and runt-related transcription factor 1), MLL-ENL (mixed lineage leukemia and eleven nineteen leukemia), Hox genes, activated forms of the interleukin-3 (IL-3) receptor β chain, and other cytokine receptor chains (epidermal growth factor receptor (EGFR), c-kit, platelet-derived growth factor receptor (PDGFR), etc.), as well as wnt (all mammalian forms), ß-catenin, sonic hedgehog (shh-1 and all mammalian forms), bmi-1 and c-jun (all mammalian forms). Also, the present invention includes inducing the loss (or inhibition) of cyclin kinase inhibitors by shRNA, including, but not limited to, p16, p19, p21 and p27. In one embodiment, the present invention includes the use of regulatable homologues of any or such protooncogenes (*e.g.*, MYC-ER or ICN-1-ER) or other genes. The Examples describe the use of both MYC-ER or ICN-1-ER to successfully produce conditionally immortalized lt-HSC using the method of present invention.

The nucleic acid sequence encoding human MYC is represented herein as SEQ ID NO:1, which encodes an amino acid sequence represented herein as SEQ ID NO:2. The nucleic acid sequence encoding hTERT is represented herein as SEQ ID NO:3, which encodes an amino acid sequence represented herein as SEQ ID NO:4. The nucleic acid sequence encoding human ICN-1 is represented herein as SEQ ID NO:11, which encodes an amino acid sequence represented herein as SEQ ID NO:12. ICN-1 a portion of Notch-1, and specifically, amino acids 1757-2555 from Notch-1 (see Aster et al., *Mol Cell Biol.* 2000 Oct;20(20):7505-15, incorporated herein by reference in its entirety). The nucleotide and amino acid sequence for MYC-ER are known in the art and the MYC-ER protein is described in Soloman et al., *Oncogene*. 1995 Nov 2;11(9):1893-7, incorporated herein by reference in its entirety. ICN-1-ER was created by the present inventors and the nucleic acid sequence encoding this protein is represented herein as SEQ ID NO:13, which encodes an amino acid sequence represented by SEQ ID NO:14.

Similarly, a preferred anti-apoptosis gene is Bcl-2, although other genes that encode proteins that inhibit apoptosis and particularly, maintain cell survival when the protooncogene is inactivated in the stem cell, are included in the present invention. The nucleic acid sequence encoding Bcl-2 alpha is represented herein as SEQ ID NO:5, which encodes an amino acid sequence of SEQ ID NO:6. Bcl-2 beta is represented herein as SEQ ID NO:7, which encodes an amino acid sequence of SEQ ID NO:8. An "anti-apoptosis" gene is defined herein as any gene that encodes a protein that can inhibit (reduce, prevent, decrease) a process associated with apoptosis in a cell or promote (enhance, increase, stimulate, allow) cell survival, even in the presence of conditions that could induce apoptosis. Proteins associated with apoptosis, and the genes encoding such proteins, are well-known in the art. Such other genes include, but are not limited to, any genes in the Bcl-2 family that will likely be important in the setting of conditional transformation of adult stem cells (*i.e.,* not just hematopoietic stem cells). These genes include, but are not limited to, other pro-survival members of the Bcl-2 family, such as Bcl-X, Bcl-w, BclXL, Mcl-1, Dad-1, or hTERT (reverse transcriptase component of the human telomerase, which has been shown to inhibit proliferation). Such genes are ectopically overexpressed in the presence of the regulated oncogene, as described with Bcl-2 in the working examples herein. In addition, this aspect of the present invention includes using shRNA mediated gene knockdown (or disruption or inhibition by any other method) for BH3-only members of the bcl-2 family that are proapoptotic (*e.g.,* Bim, PUMA, NOXA, Bax, Bak, BclXS, Bad, Bar,

and others), as well as disruption of Caspases 3, 9, 10, MLL-1 (and all mammalian forms), Enl-1 (Endospermless-1) and all mammalian forms, Apaf-1 and other elements that form part of the apoptosome.

The nucleic acid sequence for each of these genes described above or the coding region thereof is known in the art and is publicly available, including for humans. Similarly, the amino acid sequence for proteins encoded by these genes is known in the art and is publicly available.

The present inventors have produced several different long-term, conditionally immortalized stem cells using the method of the present invention and using different combinations of protooncogenes and anti-apoptotic genes, including the following combinations: *MYC*-ER and Bcl-2; *MYC*-ER and hTERT (reverse transcriptase component of the human telomerase); ICN-1-ER and Bcl-2; ICN-1-ER and hTERT; and *MYC*-ER and ICN-1-ER.

It is noted that with regard to either of the protooncogene or the gene encoding an anti-apoptosis protein used in the present method, it is not required that the entire gene be used in the constructs described herein, since any portion of the gene or a nucleic acid sequence (*e.g.,* cDNA) that encodes the desired functional protein product, a functional portion thereof, or a functional homologue thereof is encompassed by the invention. Accordingly, reference generally herein to the genes or transgenes used to transfect stem cells is to be understood to be exemplary and to include the use of any nucleic acid molecules encoding the entire gene, the entire coding region of the gene, or portions of the genes or homologues thereof, as long as such nucleic acid sequences encode functional proteins suitable for use in the present invention.

In one embodiment of the present invention, the present method additional includes the use of shRNAs or siRNAs that are directed against RNAs encoding proapoptotic proteins, such as the pro-apoptotic members of the Bcl-2 family, namely those of the BH3-only type (Bim, Bax, Bak, Puma, Noxa, etc.). The disruption of a pro-apoptotic gene in the context of a regulated oncogene is expected to result in a more efficient immortalization of certain stem cell populations. RNA interference (RNAi) is a process whereby double stranded RNA, and in mammalian systems, short interfering RNA (siRNA) or short hairpin RNA (shRNA), is used to inhibit or silence expression of complementary genes. In the target cell, siRNA are unwound and associate with an RNA induced silencing complex (RISC), which is then guided to the mRNA sequences that are complementary to the siRNA,

whereby the RISC cleaves the mRNA. shRNA is transfected into a target cell in a vector where it is transcribed, and then processed by DICER enzymes to form siRNA-like molecules that activate RISC, which, as with siRNA, is then guided to the mRNA sequences that are complementary to the shRNA, whereby the RISC cleaves the mRNA.

The stem cells can be transfected with the vectors comprising the protooncogene and encoding the anti-apoptosis protein using any suitable method of transfecting cells, and particularly mammalian cells, including by using combinations of techniques. The present inventors have discovered that it is the particular coordination between the genes (or constructs) that are expressed that have resulted in the generation of conditionally immortalized, long term stem cells as described herein. The Examples have demonstrated the use of retroviral vectors, but other methods include, but are not limited to, the use of other viruses and viral vectors derived therefrom, including, but not limited to, lentivirus vectors, parvovirus, vaccinia virus, coronavirus, calicivirus, papilloma virus, flavivirus, orthomixovirus, togavirus, picornavirus, adenoviral vectors, modified and attenuated herpesviruses. Any such virus can further be modified with specific surface expressed molecules that target these to HSCs or other stem cells, such as membrane bound SCF, or other stem-cell specific growth factor ligands. Other methods of transfection of mammalian cells include, but are not limited to, direct electroporation of mammalian expression vectors, such as by using NUCLEOFECTOR™ technology (AMAXA Biosystems). This technology is a highly efficient non-viral gene transfer method for most primary cells and for hard-to-transfect cell lines, which is an improvement on the long-known method of electroporation, based on the use of cell-type specific combinations of electrical current and solutions to transfer polyanionic macromolecules directly into the nucleus. Additionally, suitable methods of transfection can include any bacterial, yeast or other artificial methods of gene delivery that are known in the art.

The step of expanding the transfected stem cells or culturing the stem cells and exogenous fusion proteins (*e.g.,* the Tat-fusion proteins described in the variations of this method described below) in the presence of suitable growth factors can include the use of any suitable culture conditions, including those specifically described herein. The combination of suitable stem cell growth factors can include any stem cell factors that allow transfected (*e.g.,*transduced) cells of the invention to grow, survive and proliferate in culture. While specific combinations are described herein, and while this is an important step of the present method, this step can be simply described as providing any combination of growth

factors that are suitable for the growth, proliferation and survival of stem cells, and include any combinations that are known in the art. Accordingly, the invention is not limited to a particular combination. One preferred combination of growth factors includes: interleukin-6 (IL-6), IL-3 and stem cell factor (SCF). Another preferred combination of growth factors includes stem cell factor (SCF), thrombopoietin (TPO), insulin-like Growth Factor 2 (IGF-2) and fibroblast Growth Factor 1 (FGF-1), in serum-free media. This latter combination was recently described in Zhang and Lodich (2005; Murine hematopoietic stem cells change their surface phenotype during ex vivo expansion, *Blood* 105, 4314-20). The stem cells transfected with nucleic acid molecules encoding the combinations proteins described herein (*e.g.*, MYC-ER and Bcl-2 as described in the examples) are expected to also become conditionally immortalized in this cocktail of growth factors, as with the cocktail described in the Examples above (using IL-3, IL-6 and SCF). Other growth factors for use in the invention include, but are not limited to, angiopoietin-like proteins (*e.g.*, Agptl2, Angptl3, Angptl5, Angptl7, etc.), proliferin-2 (PLF2), glycogen synthase kinase-3 inhibitors, inducers of the wnt and Notch signaling pathways, Flt3L and related cytokines, fibroblast growth factor 2 (FGF2) and related cytokines, wnt-1 and other activators of the Wnt pathway, Sonic hedghog (shh-1) and other activators of that pathway. Other suitable combinations of growth factors will be applicable to the method of the present invention and will be apparent to those of skill in the art. Indeed, the cell lines generated using the method of the present invention can readily be used to screen for additional cytokines and growth factors that could be used for expanding long-term stem cells, or any of their derived progenitors, *in vitro* under neutral or directed conditions.

According to the present invention, a medium suitable for culture of animal cells can include any available medium which has been developed for culture of animal cells and particularly, mammalian cells, or which can be prepared in the laboratory with the appropriate components necessary for animal cell growth, such as assimilable carbon, nitrogen and micronutrients. Such a medium comprises a base medium, which is any base medium suitable for animal cell growth, including, but not limited to, Iscove's Modified Dulbecco's Medium (IMDM), Dulbecco's modified Eagles medium (DMEM), alpha MEM (Gibco), RPMI 1640, or any other suitable commercially available media. To the base medium, assimilable sources of carbon, nitrogen and micro-nutrients are added including, but not limited to, a serum source, growth factors, amino acids, antibiotics, vitamins, reducing agents, and/or sugar sources. It is noted that completed mediums comprising a

base medium and many of the additional components necessary for animal cell growth are commercially available, and some media are available for particular types of cell culture. In addition, many serum-free media are available and may be particularly suited for the culture of stem cells according to the invention.

Cells and Compositions

Another embodiment of the present invention relates to a cell, cell line, or population of cells produced according to the method of the present invention as described herein. Also included in the invention are compositions comprising such cells, cell lines or populations of cells. For therapeutic methods, such compositions can include a pharmaceutically acceptable carrier, which includes pharmaceutically acceptable excipients and/or delivery vehicles, for delivering the cells, cell lines, or cell populations to a patient. As used herein, a pharmaceutically acceptable carrier refers to any substance suitable for delivering a therapeutic composition useful in the method of the present invention to a suitable *in vivo* site.

Adaptation of the Method of the Invention to Produce Cell Lineages at Intermediate Stages of Development

Another embodiment of the present invention relates to adaptations of the novel methods described herein to generate cell lines that capture intermediate stages of development for the hematopoietic lineages. According to the present invention, an "intermediate" stage of development or differentiation refers to a pluripotent stage of cell development or differentiation that is downstream of the stage of development or differentiation of the stem cell from which the "intermediate" cell was derived, but is upstream of the final, or terminal, point of differentiation of a cell. For example, a pre-B cell is an intermediate stage of a hematopoietic stem cell, which can still differentiate into a mature B cell. Intermediate stages of development or differentiation will be understood by those of skill in the art.

More particularly, for many therapeutic and discovery or research applications, as well as for storage of cells lines, it is desirable that the cell lines have a stable phenotype and retain their ability to further differentiate along their committed pathway once the active oncogene with which the cell has been transfected is turned off. Accordingly, the present invention encompasses additional steps of producing cells that have not fully differentiated (are not terminally differentiated), but rather, are at an intermediate stage of differentiation. In one non-limiting example of this embodiment, long-term stem cells produced using the

method described above are randomly differentiated *in vitro* following withdrawal of the conditions that maintain the activity of the protooncogene or other gene that promotes cell survival and proliferation (*e.g.,* 4-OHT in the case of the tamoxifen-dependent protooncogenes), or by applying the appropriate conditions that turn off (inactivate) the protooncogene/oncogene. This step can be performed while maintaining the culture in neutral cytokine growth conditions (*e.g.,* IL-3, IL-6 and SCF), or by replacing those cytokines which could specifically direct differentiation towards a certain lineage (*e.g.,* IL-7 and Notch ligands for lymphoid lineages, GM-CSF and IL-4 for dendritic cells, G-CSF for myelomonocytic cells, etc.) with cytokines that are neutral for differentiation (do not direct or drive differentiation of the cells). Once the cultures begin to display differentiation markers consistent with a specific lineage, the culture media is again supplemented with the conditions that activate the protooncogene (*e.g.,* 4-OHT) or exposed to the conditions that otherwise reactivating the protooncogene, in order to stabilize the phenotype and generate cell lines having a stable, intermediate differentiation phenotype.

By way of exemplification of this method, the inventors have generated CD4+, αβ+ T cells *in vitro* from ABM42 cells (lt-HSC produced by the method of the invention; see Examples) by withdrawal of 4-OHT from the media, and re-addition of 4OHT after differentiation. The inventors have also generated dendritic cell lines by incubating ABM46 cells (see Examples) in GM-CSF, IL-4 and FLT3L and then placing the cultures back in the presence of 4-OHT after differentiation.

Another approach for creating such cell lines involves introducing the ctlt-HSC cells into mice to allow for differentiation, and arresting, or stabilizing the phenotypes *in vivo* after injections of 4-OHT. This method is described in detail in Example 8. Briefly, and by way of example, lt-HSC generated by the present method are injected into immuno-compromised animals (*e.g.,* immuno-compromised mice). The oncogene in the lt-HSCs is reactivated using injections of the activating agent (*e.g.,* 4-OHT), cells are later collected, and then the cells can be cultured *in vitro* to differentiate the cells, and then stored or used as desired. This approach, and the other described above, can be used for both murine and human ctlt-HSC cell lines, such as by using either NOD/SCID mice as the recipients, or neonatal Rag-$1^{-/-}$ mice, which will be given intrahepatic injections.

Application of the Method of the Invention to Embryonic Stem Cells

Another embodiment of the invention relates to the application of the method of conditionally immortalizing stem cells to embryonic stem (ES) cells. Such methods will be

useful for generating cell lines that are more readily derived from ES cells, such as cells of the neuronal linage, including neuronal stem cells.

In this embodiment, the method of the present invention, comprising the transduction of cells (in this case, ES cells) with a protooncogene and a gene that inhibits apoptosis (*e.g.*, MYC-ER and Bcl-2) can be applied to ES cells to further control the directed differentiation of these cells. In this embodiment, such cells can be used to generate transgenic mice, for example, and in addition, any ES cell and relevant progenitor cell population derived therefrom can be subjected to the activation of the protooncogene by exposure to the activating agent, hence allowing for the generation of novel conditionally transformed stem cell lines (different tissue types), or mature cell lines for the tissue type of interest. In addition, the directed differentiation of transduced ES cells *in vitro* can also be used to capture intermediate states of differentiation by as described above. The use of ES cells or ES-derived cells in this manner provides a novel platform for drug discovery and target identification in the setting of different diseases.

For example, neuronal stem cells can be employed in this embodiment of the invention, as well as the directed differentiation of ES cells into the neuronal pathway using the method of the invention. The isolation and transduction of neuronal stem cells from the hippocampus has been previously described for mice. The culture conditions for neurospheres would enable the proliferation of those cells, rendering them susceptible to viral-mediated transduction of the genes of the invention (*e.g.*, MYC-ER and Bcl-2), in order to generate conditionally transformed neuronal stem cell lines. Their differentiation *in vitro* as well as *in vivo* following implantation can be monitored by virtue of the virally encoded reporter genes as well as previously defined markers of neuronal differentiation. In addition, the administration of the activating agent (*e.g.*, 4-OHT) to the mice following transplantation of the conditionally transformed neuronal stem cell lines may lead to the development of a neurological malignancy (neuroblastoma, glioblastoma, etc.). Those tumors would provide a novel model for preclinical studies and target identification.

The directed differentiation of ES cells that had been transduced with, for example, MYC-ER and Bcl-2, can be carried out in the presence of a previously defined growth medium, as well as cytokines. The addition of the activating agent (*e.g.*, 4-OHT) at any time during the culture will enable the stabilization of the cells at an intermediate phenotype, and leads to the generation of cell lines that still retain the capacity to undergo further differentiation. For instance, the generation of dopaminergic neurons from ES cells is

normally done by the addition of Retinoic acid and FGF8. This type of neuron would be ideal for repairing brain lesions observed in Alzheimer's patients. However, the transplantation of fully differentiated neuronal cells may preclude their successful implantation and engraftment. A conditionally transformed cell line that was committed to the dopaminergic neuronal pathway, but still retained its ability to further differentiate after transplant, as envisioned herein, is expected to greatly increase the chances of implantation and successful engraftment. A similar scenario can be proposed for the generation of motor neurons from ES cells, by adding Retinoic acid and a sonic hedgehog agonist to the cultures. Those neuronal cells could help repair spinal cord injuries. Once again, fully differentiated cells would not be used in this embodiment, but rather, the committed progenitor cells that retain the capacity to differentiate (produced by the method of the invention) would be employed.

Variations or Modifications of the Method of Conditional Immortalization for the Removal of the Transgene

In one embodiment of the invention, in order to avoid taking the risk of introducing stem cells that harbor transgenes such as those described herein (*e.g.,* MYC-ER) into humans and/or mice, the recombinant constructs are designed so that these DNA fragments will be excised. This embodiment can be achieved using any suitable method of first establishing the long-term stem cells according to the method of the invention, and then exposing the cells (or a patient) to conditions under which the recombinant DNA will be removed, excised or completely silenced.

For example, in one aspect of the invention, a bacterial recombinase approach is used. In this aspect of the invention, preferably, two different recombinases are used in order to allow control over which one of the two genes is excised at any one point in time. Two examples of such recombinases are the Cre and Flp recombinases, which are well-known in the art. Briefly, the recognition substrate sequences (RSS's) for one of the recombinases is introduced into the retroviral constructs such that they flank the open reading frame of the oncogene, as well as the reporter gene (*e.g.,* GFP or Thy1.1). In this case, the cells are incubated in media containing a Tat-Cre fusion protein (*i.e.,* HIV or other retroviral Tat protein fused to Cre). This recombinant protein has been previously described and shown to be able to passively enter cells, and mediate loxP site-dependent recombination of genomic DNA. Other methods of gene (nucleic acid molecule) excision

are known to those of skill in the art and could readily be applied to the present invention. Examples 5 and 13 exemplify this embodiment of the invention.

In another embodiment of the invention, to provide another method of avoiding the risk of introducing stem cells that harbor transgenes such as those described herein into humans and/or other animals (*e.g.,* mice), instead of transfecting the stem cells with the combination of the recombinant constructs for the protooncogene or the anti-apoptosis protein, the invention is performed by making use of Tat-fusion proteins as a method to allow the proteins access to the inside of the cell without having to introduce transgenes into the cell. For example, recombinant constructs that encode tat-protooncogene or tat-anti-apoptosis genes (*e.g.,* Tat-*MYC*-ER or Tat-Bcl-2) may be used to conditionally immortalize stem cells. In this embodiment of the invention, the target stem cells will be cultured under suitable culture conditions, in media that contains purified recombinant Tat-fusion proteins encoded by the specific gene combination selected (*e.g.,* MYC-ER and Bcl-2). In this embodiment of the invention, the protooncogene product or similar gene product can be inducible, as in the embodiments above. Alternatively, or in addition, the action of this protein can be regulated simply by providing or removing the protein from the culture. While the cell lines that are generated with this approach will be continuously dependent upon the addition of the exogenous Tat-fusion proteins, they will not have a specific exogenous nucleotide sequence introduced into them. The absence of foreign oncogene sequences is expected to improve the clinical deployment of the method of the present invention. Human immunodeficiency virus-1 (HIV-1) Tat, is one exemplary Tat protein, although other retroviral Tat proteins are known in the art. As a non-limiting example, the nucleic acid sequence encoding HIV-1 Tat is represented herein as SEQ ID NO:9, which encodes an amino acid sequence represented herein by SEQ ID NO:10.

In another embodiment, to provide another method of avoiding the risk of introducing stem cells that harbor transgenes such as those described herein into humans and/or other animals (*e.g.,* mice), instead of transfecting the stem cells with the combination of the recombinant constructs for the protooncogene or the anti-apoptosis protein, the invention is performed by introducing proteins (*e.g.,* MYC and Bcl-2) into a cell using aptamer technology. Aptamers are short strands of synthetic nucleic acids (usually RNA but also DNA) selected from randomized combinatorial nucleic acid libraries by virtue of their ability to bind to a predetermined specific target molecule with high affinity and specificity. Aptamers assume a defined three-dimensional structure and are capable of discriminating

between compounds with very small differences in structure. Accordingly aptamers can be conjugated with the proteins used in the invention or with non-integrating cDNA encoding the proteins, for example, and used to deliver the proteins or DNA to the cells. In addition, aptamers can readily be used to deliver siRNA to cells, for example, when one disrupts proapoptotic proteins according to the present invention. Aptamer technology is discussed, for example, in Davidson, 2006, *Nature Biotechnol.* 24(8):951-952; and McNamara et al., 2006, *Nature Biotechnol.* 24(8):1005-1015). Again, the absence of foreign oncogene sequences is expected to improve the clinical deployment of the method of the present invention.

In another embodiment, to provide another method of avoiding the risk of introducing stem cells that harbor transgenes such as those described herein into humans and/or other animals (*e.g.*, mice), instead of transfecting the stem cells with the combination of the recombinant constructs for the protooncogene or the anti-apoptosis protein, the invention is performed by introducing the protooncogene and/or anti-apoptosis protein into a cell using CHARIOT™ technology (Krackeler Scientific, Inc., Albany, NY). With this technology, a non-covalent bond is formed between a CHARIOT™ peptide and the protein of interest. This protects the protein from degradation and preserves its natural characteristics during the transfection process. Upon delivery to a cell, the complex dissociates and CHARIOT™ is transported to the nucleus, while the delivered protein is biologically active and free to proceed to its cellular target. Efficient delivery can occur in the presence or absence of serum, and is independent of the endosomal pathway, which can modify macromolecules during internalization. This delivery system also bypasses the transcription-translation process. Accordingly, the proteins useful in the present invention can be delivered to a cell and released to conditionally immortalize the cell, without the need for the introduction of a protoooncogene or oncogenes to the cell. As above, the absence of foreign oncogene sequences is expected to improve the clinical deployment of the method of the present invention.

As yet another alternative (or additional) means to control for the possibility of an insertion of a protooncogene into the host cell genome by the various viral approaches described herein, and thereby avoid a transforming event, a drug sensitivity (drug susceptibility) cassette can be introduced into the viral constructs to be used such that it will be expressed in every transduced cell and its differentiated progeny. A drug sensitivity cassette or a drug susceptibility cassette is a nucleic acid sequence encoding a protein that

renders a cell susceptible or sensitive to the presence of a particular drug, so that upon exposure to the drug, the cell activity is inhibited and preferably, undergoes apoptosis. Those patients in which the levels of a particular blood cell population increases without apparent cause (*e.g.,* infection, trauma, stress, etc.), can be given a course of the drug to which sensitivity has been introduced in order to ablate those cells and mitigate any possible additional complications involving cells in which the genetic insertions may have inadvertently caused an oncogenic mutation. Accordingly, as a non-limiting example, one could introduce into a construct used in the method of the invention a cassette that encodes the cDNA for HPRT in order to render the transduced cells susceptible to 6-thioguanine. Another non-limiting example is the introduction of the thymidine kinase cDNA from a Herpes-simplex virus family member (HSV-TK), in order to render the transduced cells susceptible to relevant inhibitors such as Ganciclovir, Acyclovir, and any relevant derivatives. In addition, any other such drug sensitivity cassettes and their relevant agonists would work in this context.

Other methods of introducing nucleic acids or proteins according to the present invention into a cell will be apparent to those of skill in the art. Those that minimize or eliminate the risk of introducing recombinant DNA into a host cell genome are preferred by the invention, many such examples being described above.

Methods of Use for Conditionally Immortalized Cells of the Invention

Another embodiment of the present invention includes any of the stem cell populations, including mixed and clonal populations, that are produced by the method of the invention, as well as the use of the stem cells of the invention in any of the methods described herein, including differentiation into a desired cell type, and any method of transplantation, cell replacement, disease therapy, genetic engineering, drug discovery, and investigation of cell development and differentiation as described herein.

Since one can now produce virtually unlimited supplies of homogeneous stem cells that can readily be stored, recovered, expanded and manipulated, such stem cells can be used as stem cells or differentiated into various cell lineages and used in assays to test various compounds for effects on cell differentiation, gene expression, and cell processes. Therefore, one embodiment of the invention relates to a method to identify compounds that effect cell differentiation, gene expression, and/or cell processes. The method generally includes the steps of contacting stem cells produced by the method of the present invention with a compound to be tested, and measuring a particular result, and particularly a desired

result, such as gene expression, a biological activity, cell differentiation, cell growth, cell proliferation, etc. (see below), as compared to in the absence of the compound, to determine whether or not the test compound had the desired effect on the stem cell. This method can be used to test for virtually any aspect of cell differentiation, cell activity or gene expression. In one aspect, the stem cells are manipulated prior to contact with the compounds, such as by genetic manipulation. Stem cells from individuals with genetic defects can be evaluated in such assays in order to identify therapeutic compounds (*e.g.,* cancer therapeutics) and to evaluate gene replacement therapies, for example. Indeed, the technology of the present invention provides an opportunity to target the cells of a specific individual to identify drug candidates and therapeutic candidates and strategies that are "tailored" to the cells of an individual. Furthermore, as discussed above, such assays can also be used to identify other growth factors or culture conditions that are suitable for maintaining the stem cells of the invention in culture. An example of such an assay is described in detail below in Example 7, although the invention is not limited to this assay.

Another embodiment of the invention relates to a method to study cell lineage commitment and/or differentiation and development of cells from a stem cell, which generally comprises culturing the conditionally immortalized stem cells of the present invention and evaluating such cells for genetic and biological markers related to cell development and differentiation under various conditions and in the presence and absence of compounds or agents that may affect cell lineage commitment or differentiation. As discussed above, prior to the present invention, such studies were severely hampered by the lack of access to and the inability to generate sufficient numbers of the desired cell population to perform desired experiments. For example, in order to identify or screen for intermediates in the differentiation of a particular progenitor cell line, a sufficient number of cells must be obtained to provide meaningful and reproducible results. Using technologies available at the time of the invention, this was not possible. However, the present invention solves the problem by providing expandable and essentially unlimited supplies of homogeneous stem cells that can be used in a variety of experiments. This technology will greatly enhance research capabilities in the area of cell differentiation and discovery. In one aspect, conditionally immortalized stem cells of the invention are expanded, and then a subset are cultured in the absence of the conditions that maintain the cells in the conditionally immortalized state (*e.g.,* in the absence of tamoxifen, according to the exemplary method illustrated herein). The cells can be evaluated for changes in gene

expression, cell surface markers, secretion of biomolecules, or any other genotypic or phenotypic marker, to study the process of cell differentiation and lineage commitment. Growth factors or other factors can be added to the cultures, for example to drive differentiation down a particular cell lineage pathway, and the changes in the cells can be evaluated in the presence or absence of such factors. Furthermore, the cells can be used to evaluate culture conditions, *in vivo* conditions, factors, and agents that influence (regulate) cell differentiation and development.

Various methods of detection of changes in genotypic or phenotypic characteristics of cells in any of the assays of the invention are known in the art. Examples of methods that can be used to measure or detect gene sequence or expression include, but are not limited to, polymerase chain reaction (PCR), reverse transcriptase-PCR (RT-PCR), *in situ* PCR, quantitative PCR (q-PCR), *in situ* hybridization, Southern blot, Northern blot, sequence analysis, microarray analysis, detection of a reporter gene, or other DNA/RNA hybridization platforms. Methods to measure protein levels, include, but are not limited to: Western blot, immunoblot, enzyme-linked immunosorbant assay (ELISA), radioimmunoassay (RIA), immunoprecipitation, surface plasmon resonance, chemiluminescence, fluorescent polarization, phosphorescence, immunohistochemical analysis, matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry, microcytometry, microarray, microscopy, fluorescence activated cell sorting (FACS), flow cytometry, and assays based on a property of the protein including but not limited to DNA binding, ligand binding, interaction with other protein partners, cell signal transduction, enzyme activity, and secretion of soluble factors or proteins.

In drug screening assays, the term "test compound", "putative inhibitory compound" or "putative regulatory compound" refers to compounds having an unknown or previously unappreciated regulatory activity in a particular process. As such, the term "identify" with regard to methods to identify compounds is intended to include all compounds, the usefulness of which as a compound for a particular purpose (*e.g.,* regulation of cell differentiation) is determined by a method of the present invention, preferably in the presence and absence of such a compound. Compounds to be screened in the methods of the invention include known organic compounds such as antibodies, products of peptide libraries, and products of chemical combinatorial libraries. Compounds may also be identified using rational drug design. Such methods are known to those of skill in the art and can involve the use of three-dimensional imaging software programs. For example, various

methods of drug design, useful to design or select mimetics or other therapeutic compounds useful in the present invention are disclosed in Maulik et al., 1997, *Molecular Biotechnology: Therapeutic Applications and Strategies*, Wiley-Liss, Inc., which is incorporated herein by reference in its entirety.

In any of the above-described assays, the conditions under which a cell, cell lysate, nucleic acid molecule or protein of the present invention is exposed to or contacted with a putative regulatory compound, such as by mixing, are any suitable culture or assay conditions, which can include the use of an effective medium in which the cell can be cultured (*e.g.*, as described above) or in which the cell lysate can be evaluated in the presence and absence of a putative regulatory compound. Cells of the present invention can be cultured in a variety of containers including, but not limited to, tissue culture flasks, test tubes, microtiter dishes, and petri plates. Culturing is carried out at a temperature, pH and carbon dioxide content appropriate for the cell. Such culturing conditions are also within the skill in the art, and particularly suitable conditions for culturing conditionally immortalized stem cells of the present invention are described in detail elsewhere herein. Cells are contacted with a putative regulatory compound under conditions which take into account the number of cells per container contacted, the concentration of putative regulatory compound(s) administered to a cell, the incubation time of the putative regulatory compound with the cell, and the concentration of compound administered to a cell. Determination of effective protocols can be accomplished by those skilled in the art based on variables such as the size of the container, the volume of liquid in the container, conditions known to be suitable for the culture of the particular cell type used in the assay, and the chemical composition of the putative regulatory compound (*i.e.*, size, charge etc.) being tested.

In one embodiment of the invention, the cells and methods of the invention are useful for methods directed at evaluating pluripotency of ctlt-HSCs derived from human cord blood, CD34+ cells, or adult CD34+ cells isolated from peripheral blood. Such a method is described in Example 11.

Yet another embodiment of the invention relates to the use of ctlt-HSC cell lines as a platform to generate novel models of Acute Myeloid Leukemia (AML). More particularly, the present inventors have generated a mouse model of acute myeloid leukemia using the ctlt-HSCs of the invention. These are leukemias composed of cells that resemble HSCs, based on their surface marker expression. In order to generate ctlt-HSCs to promote leukemia in mice, 10^3-10^5 ctlt-HSCs are transferred along with 10^5 Rag-$1^{-/-}$ whole bone

marrow cells into lethally irradiated recipient mice. The mice are given weekly doses of 4-OHT in order to maintain oncogene activity, and monitored for clinical signs associated with leukemia, as known in the art. Tumors have been recovered from these animals and they can be propagated in culture in the absence of 4-OHT. Those cells retain their HSC-like phenotype, indicating that they are no longer exquisitely dependent upon MYC hyperactivity in order for proliferation, survival and arrested differentiation. The leukemic cell lines can also confer the disease upon secondary transplantation to irradiated recipient mice. These tools provide a novel platform for studying the biology and exporting new therapeutic avenues for AML and related diseases. Furthermore, the introduction of ctlt-HSC cell lines into mice that are treated with 4-OHT will provide a good built-in positive control for therapy: the withdrawal of 4-OHT. The secondary cell lines that arose after the establishment of tumors *in vivo* can also be used to understand the relevant therapeutic targets for drug resistant forms of AML.

Other embodiments of the present invention relate to the use of the stem cells generated by the method of the present invention, as well as cells differentiated from those stem cells, in a variety of therapeutic and health-related methods. These methods generally include the steps of obtaining a population, culture or line of conditionally immortalized stem cells produced by the method of the present invention, removing the conditions under which such cells are conditionally immortalized, and then using the cells in a therapeutic protocol. For example, the cells can be administered directly to an individual in need of the cells or the cells can be differentiated into a desired cell type *in vitro* and then administered to an individual. In addition, prior to or just after the removal of the conditions under which the cells are immortalized, the cells can be genetically modified *in vitro* to express or silence a gene or genes, as a novel method of gene therapy under a controlled environment. The cells can then be administered to an individual as stem cells or first differentiated *in vitro* to a desired cell lineage.

To obtain the stem cells, in one embodiment, stem cells are obtained from the individual to be treated, and are then conditionally immortalized according to the method of the invention. These cells can be expanded extensively, stored (*e.g.*, frozen or cryopreserved), and then retrieved and expanded again, manipulated, and/or used repeatedly as required. In another embodiment, one obtains the stem cells by accessing a previously stored source of conditionally immortalized stem cells from the individual to be treated. In yet another embodiment, the stem cells are obtained from a panel of human stem cell lines

that were previously generated and which cover a significant percentage of the population according to the current criteria used to identify "matching" donors. In one embodiment, the cells are obtained from fresh, or cryopreserved cord blood, hematopoietic progenitor populations that can be derived from the directed differentiation of ES cells *in vitro*, HSCs obtained from the peripheral blood of normal, or G-CSF treated patients who have been induced to mobilize their lt-HSCs to the peripheral circulation. Other sources of stem cells will be apparent to those of skill in the art. The cells are cultured according to the methods described previously herein and the conditions controlling immortalization can be removed at the appropriate time. In addition, prior to administration of the cells to an individual, the cells can be manipulated to excise the genes or constructs that are responsible for the conditional immortalization (*i.e.*, the protooncogene and/or the anti-apoptosis encoding gene), or if the cells are maintained through the use of soluble fusion proteins in the culture medium, as described above for the Tat-fusions, these soluble proteins can be removed from the culture gradually or immediately.

Therefore, the present invention includes the delivery of stem cells produced by the method of the invention (including compositions comprising such stem cells), or cells differentiated from these cells, to an individual (which can include any animal). Since the stem cells used in these methods are produced *in vitro*, even if stem cells were initially isolated from the patient, the entire administration process of the cells is essentially an *ex vivo* administration protocol. *Ex vivo* administration refers to performing part of the regulatory step outside of the patient, such producing the conditionally immortalized stem cells that were removed from an individual (which can include producing genetically modified stem cells in addition to essentially normal stem cells), and returning the cells, or cells differentiated from these cells, to the patient. The stem cells produced according to the present invention or cells differentiated therefrom can be returned to an individual, or administered to an individual, by any suitable mode of administration. Such administration can be systemic, mucosal and/or proximal to the location of a target site. The preferred routes of administration will be apparent to those of skill in the art, depending on the type of condition to be prevented or treated or the reason for administration. Preferred methods of administration include, but are not limited to, intravenous administration, intraperitoneal administration, intramuscular administration, intranodal administration, intracoronary administration, intraarterial administration (e.g., into a carotid artery), subcutaneous administration, transdermal delivery, intratracheal administration, subcutaneous

administration, intraarticular administration, intraventricular administration, intraspinal, pulmonary administration, impregnation of a catheter, and direct injection into a tissue (*e.g.*, such as cannulation of the liver, for example).

The cells can be administered with carriers or pharmaceutically acceptable excipients. Carriers are typically compounds that increase the half-life of a therapeutic composition in the treated individual. Suitable carriers include, but are not limited to, polymeric controlled release formulations, biodegradable implants, liposomes, oils, esters, and glycols. As used herein, a pharmaceutically acceptable excipient refers to any substance suitable for delivering cells produced by the method of the present invention to a suitable *in vivo* site. Preferred pharmaceutically acceptable excipients are capable of maintaining a cells in a form that, upon arrival of the cells at a target tissue or site in the body, the cells are capable of functioning in a manner that is beneficial to the individual.

According to the present invention, an effective administration protocol comprises suitable dose parameters and modes of administration that result in delivery of a useful number of functional cells to a patient in order to provide a transient or long-term benefit to the patient. Effective dose parameters can be determined using methods standard in the art for a particular condition or disease. Such methods include, for example, determination of survival rates, side effects (i.e., toxicity) and progression or regression of disease.

A suitable single dose of stem cells or cells differentiated therefrom according to the present invention is a dose that is capable of providing a beneficial number of cells to a patient, when administered one or more times over a suitable time period. For example, a preferred single dose of stem cells according to the present invention is from about 0.5×10^4 to about 5.5×10^8, or from about 0.5×10^5 to about 5.5×10^7, or from about 0.5×10^6 to about 5.5×10^{10} stem cells per individual per administration, with doses from about 1×10^8 to about 5.5×10^{10} being even more preferred. Any dose in between 0.5×10^4 and about 5.5×10^{10} is encompassed by the invention, in increments of 10^2 cells. Higher or lower doses will be known to those of skill in the art depending on the type of stem cell or differentiated cell to be administered, and also depending on the route of administration. It will be obvious to one of skill in the art that the number of doses administered to an animal is dependent upon the extent of the condition or disease and the response of an individual patient to the treatment. Thus, it is within the scope of the present invention that a suitable number of doses includes any number required to treat a given disease.

As used herein, the phrase "protected from a disease" refers to reducing the symptoms of the disease; reducing the occurrence of the disease, and/or reducing the severity of the disease. Protecting an animal (an individual, a subject) can refer to the ability of cells produced according to the present invention, when administered to an animal, to prevent a disease from occurring and/or to cure or to alleviate disease symptoms, signs or causes. As such, to protect an animal from a disease includes both preventing disease occurrence (prophylactic treatment) and treating an animal that has a disease or that is experiencing initial symptoms of a disease (therapeutic treatment). The term, "disease" refers to any deviation from the normal health of a mammal and includes a state when disease symptoms are present, as well as conditions in which a deviation (e.g., infection, gene mutation, genetic defect, etc.) has occurred, but symptoms are not yet manifested.

As discussed above, the stem cells of the present invention can be administered to an individual to treat or prevent a variety of conditions. For example, the stem cell lines of the present invention provide a unique source of expandable stem cells for use in a variety of transplantation and therapeutic strategies, including the treatment of cancer, and particularly, cancer that is treated by radiation. In addition, a variety of immune deficiency disorders and anemia disorders (*e.g.*, aplastic anemia or hemolytic anemia) will also benefit greatly from this technology, since the present invention provides the ability to repopulate hematopoietic cells of an individual as needed by the individual. Another application of the present invention relates to the generation of continuously expandable and renewable hair follicle stem cells, for use, for example in the context of reconstructive surgery for burn victims, for any individual that undergoes chemotherapy and/or radiation therapy resulting in the irreversible loss of hair growth, as well as patients following any surgical procedure affecting the skull or in elective procedures that involve the induction of hair growth in individuals affected by hereditary pattern baldness. Similarly, application of the present invention to stem cells of the skin will be invaluable for use in wound healing and treatment of burn victims, as well as plastic reconstructive surgery for trauma and other patients, as well as elective surgeries, including, but not limited to, cosmetic surgery. Such cells can be additionally genetically manipulated to correct inborn or acquired genetic defects in young and aged individuals. One of skill in the art will understand based on this disclosure that benefits can be derived from the use of the present invention on various other stem cell populations, including, but not limited to, stem cells derived from lung, breast, and intestinal epithelium and stem cells derived from neural and cardiac tissue, to name just a few.

In addition, as discussed above, the present invention provides the unique opportunity for an individual to have access to expandable supplies of autologous stem cells and cells differentiated therefrom as needed throughout the life of the individual. Such stem cells generated by the present method can be stored and used as part of therapeutic protocols during the lifetime of the individual, should they be needed (*e.g.,* in the event the individual develops a cancer or immune deficiency disease).

Genetic defects can now be corrected or beneficial gene modifications can be introduced into somatic cells by manipulating autologous stem cells obtained from an individual that have been conditionally immortalized and expanded using the method of the present invention. The stem cells can then be reintroduced into the individual from whom they were obtained.

Additional applications of the present invention include the use of stem cell lines to repair lung injury that occurs as a result of COPD, IPF, emphysema, asthma and smoking. In addition, such cells could be used to treat blood vessel damage in the heart, and help in autoimmune diseases after lethal irradiation (*e.g.,* SLE, diabetes, RA).

In the method of the present invention, cells produced according to the method of the invention and compositions comprising the cells can be administered to any animal, including any member of the Vertebrate class, Mammalia, including, without limitation, primates, rodents, livestock and domestic pets. A preferred mammal to treat is a human.

Various aspects of the present invention are described in more detail in the following Examples and the attached figures. However, the present invention is not limited to these examples and illustrations of the invention.

Examples

Example 1

The following example describes the development of a method to reversibly immortalize long-term hematopoietic stem cells (lt-HSCs).

Elucidation of the molecular basis of the impairment in hematopoietic lineage development has been complicated historically by the low frequency of relevant cell populations, which prevents biochemical analysis of signaling and downstream responses. In fact, this has been a major limiting factor in all studies of hematopoiesis. In addition, the

limited availability of LT-HSCs has also been a major obstacle in the treatment of many types of cancer as well as several kinds of immune deficiencies in humans.

In an effort to overcome this limitation, the present inventors developed a method to produce conditionally transformed cell lines representing early hematopoietic stem cell progenitors. The initial strategy involved retroviral transduction of bone marrow stem cells from 5FU treated young and immunologically aged 3-83 mice. The inventors utilized the pMSCV bisistronic retroviral vector with inserts encoding Bcl-2 and GFP, and *MYC*-ER and GFP [Van Parijs, L., Y. Refaeli, A.K. Abbas, and D. Baltimore. (1999) Autoimmunity as a consequence of retrovirus-mediated expression of C-FLIP in lymphocytes. Immunity, 11, 763-70]. These genes were selected because the present inventors knew that *MYC* has the ability to replace cytokine derived survival and proliferative signals in lymphocytes. By restricting the target cell, the inventors hypothesized that stem cell tumors might form. Importantly, *MYC*-ER function is tamoxifen dependent in this setting, allowing the termination of *MYC* function and transformation by withdrawing tamoxifen from the animal or cultures. In cells transduced with MYC-ER, the fusion protein is produced, but is retained in the cytoplasm until exposed to tamoxifen.

More specifically, stem cell populations from 5FU treated mice were transduced with both retroviruses (encoding *MYC*-ER and Bcl-2) and transferred into lethally irradiated recipient mice (1200 rads). Ten days later, weekly intraperitoneal injections of 1 mg/mouse of 4-hydroxytamoxifen (40HT) emulsified in oil were initiated to activate *MYC* function (Fig. 1). Within four weeks, recipients of young (but not old) transduced stem cells developed tumors. The tumors were harvested from bone marrow, spleen and lymph nodes and cultured *in vitro* with tamoxifen, but without added cytokines. These cells grew for about 10 days, but then growth stopped and the cells eventually died. the inventors suspected that the cells were differentiating and considered that this might have been due to requirements for cytokines for growth of the cells. Referring to Fig. 1, the curves represent the kinetics of mortality after transplantation and activation of *MYC* function *in vivo*. The mice uniformly succumbed to leukemias. While the overexpression of MYC can replace the cytokine-dependent proliferation and survival function, it does not seem to be involved in the cytokine-derived differentiation signals.

When ill, the mice were euthanized. Bone marrow, spleen and lymph node cells were harvested and placed in culture with tamoxifen and a stem cell growth factor cocktail (IL-6, IL-3 and stem cell factor (SCF)). In parallel, cells were analyzed by flow cytometry

(Fig. 2). Referring to Fig. 2, the dot plots represent the flow cytometric data for the forward (FSC) and side (SSC) scatter characteristics of the HSCs after three days in culture with IL-3, IL-6 and SCF. These two criteria correlate with cell size (FSC) and granularity (SSC). The two populations have similar profiles. The histograms represent the levels of GFP expressed in each cell population. This reflects the efficiency of retroviral transduction in vitro with retroviruses that encode cDNAs for *MYC*-ER and Bcl-2.

In all cases, *ex vivo* GFP^+ cells were >90% $Sca\text{-}1^+$ and Lineage marker negative. After a few days in culture, cells began to grow and approximately 400 lines were frozen for later study. After propagation, these cells retained expression of EGFP and were homogeneously positive for SCA1 and negative for CD34, Flk2 and lineage markers (Fig. 3). The only difference in marker expression between young mouse-derived and aged mouse-derived markers was increased expression of c-kit in young. Without being bound by theory, the present inventors believe that this may have resulted from longer culture (3 months vs. 3 weeks) of aged lines in c-kit ligand before markers were analyzed. Finally, the inventors discovered that these lines can be recovered easily after freezing and retained their original phenotype. Importantly, these cell lines are homogenous in phenotype and exhibit the phenotype of lt-HSC that provide all long term reconstitution in mice (Reya, T., Duncan, A.W., Ailles, L., Domen, J., Scherer, D.C., Willert, K., Hintz, L., Nusse, R., and Weissman, I.L. (2003). A role for Wnt signaling in self-renewal of hematopoietic stem cells. Nature 423, 409-14).

Recently, the inventors thawed 10 bone marrow derived lines produced as described above, and were able to recover 9 our of 10 of these lines easily by culture in the cytokine cocktail and 4OHT. The inventors phenotyped these tumors, and the results were extremely promising. Specifically, each line contained two distinct cell populations based on forward and 90° light scatter. The nine lines differed only in the proportionality of these populations. The larger of these populations in cell size were uniformly GFP bright and positive for Sca1, Endoglin and ckit but negative for Flt3, B220, CD19 and mIgM. $CD34^-$ also appeared to be negative, although this required confirmation (Fig. 3). This phenotype corresponds perfectly with the published characteristics of long term repopulating pluripotent stem cells (Reya et al., *supra*). The inventors observed the same initial phenotype on the cell lines that they recently obtained from leukemias that developed from transduced HSCs obtained from young donor mice (Fig. 3).

To test the ability of these cells to differentiate, representative lines were cultured with and without tamoxifen and in the presence of IL-3, IL-6 and SCF to terminate MYC-ER function for 7 days before analyzing phenotypic markers. As shown in Fig. 4, a significant proportion of cells acquired B lineage markers including B220 (~12%), CD19 (~10%) and mIgM (~10%). In addition, the inventors have been able to generate the following lineages *in vitro* by withdrawal of 4OHT from the cultures: CD4+ ab T-cells, myeloid cells (Mac-1+), ter-119+ erythroid progenitor cells, NK1.1 expressing cells, neutrophils (Gr-1+ cells). Further experiments will assess the ability of these cells to give rise to other lineages, as well as the effect of altering the cytokine regimen on differentiation. Although the comparison has not been performed, the present inventors expect differentiation from young animals, as compared to aged animals to be much more efficient in B cell production. To the best of the present inventors' knowledge, this is the first example of a conditionally immortal hematopoietic stem cell line that can be induced to differentiate *in vitro*.

Example 2

The following example describes the results of adoptive transfer of LT-HSC lines into lethally irradiated recipients.

If the HSC lines described in Example 1 are to be appropriate subjects for analysis of the basis of defective B cell lymphopoiesis in aged animals, they should recapitulate the defect *in vivo*. The inventors have begun to address this question by adoptive transfer of LT-HSC lines into lethally irradiated recipients. In initial experiments, lines from aged animals (>60% ID$^-$) were transferred along with RAG2$^{-/-}$ bone marrow, and recipients were not treated with tamoxifen in order to silence MYC-ER. Six weeks later recipient bone marrow and spleen cells were harvested and the recovery and phenotype of GFP$^+$ cells (GFP marks cells derived from HSC lines) was analyzed (Fig. 5).

In the data from three mice presented in Fig. 5, one mouse received the aged HSC line ABM42, and two mice received aged HSC line ABM46. Depending upon the line transferred, 30 to 70% of cells in the lymphoid scatter gate were GFP$^+$. As shown in Fig. 5, both lines tested (ABM46 and ABM42) gave rise to B (CD19$^+$) and T (TCR$^+$, CD4$^+$, CD8$^+$) cells, macrophages (CD11b$^+$) and granulocytes (GR1$^+$). There was some recipient to recipient variation in the proportionality of these lineages. However, importantly, while both lines tested gave rise to mature CD4 and CD8 single positive T cells (Fig. 7), B cell development did not proceed beyond the progenitor stage (Fig. 6). While B220$^+$, CD19$^+$ cells

developed, they did not progress to the mIg^+ stage. This is precisely the outcome predicted by results of experiments involving autoreconstitution and adoptive reconstitution using BM HSC from immunologically aged mice (Johnson, S.A., S.J. Rozzo, and J.C. Cambier, Aging-dependent exclusion of antigen-inexperienced cells from the peripheral B cell repertoire. J Immunol, 2002. 168(10): p. 5014-23). In other words, the same developmental arrest is observed when whole bone marrow from immunologically aged mice is used for transplantation.

The inventors have found that this system can be taken a step further, successfully re-establishing LT-HSC lines from bone marrow of adoptive recipients of the original HSC lines (data not shown). This was accomplished simply by culturing bone marrow cells in stem cell cytokines plus tamoxifen to reactivate MYC. These cells are now growing and exhibit the original phenotype.

Example 3

The following example describes a method for reversibly immortalizing HSCs using a method conducted entirely *in vitro*.

In addition to the method for generating conditionally immortalized long term HSC cell lines described previously herein, the inventors have been able to carry out this procedure completely *in vitro*. The method described above relies upon introducing the transduced HSC's into mice, and inducing their transformation *in vivo*. The advantage of carrying this procedure out *in vitro* is that every aspect of the process is carried out in a controlled environment.

The method first includes the treatment of donor mice with 5-fluorouracil (5-FU) in order to enrich for HSCs and induce these cells to proliferate. 5FU enriched hematopoietic stem cells from the tibia and femurs of mice were collected and then plated in 24 well tissue culture plates in DMEM media containing 15% heat inactivated fetal calf serum and IL-3, IL-6 and SCF, at a density of 1.8-2.0 x 10^6 cells per well. The cells were subjected to three rounds of spin infection in order to retrovirally transduce the cells with retroviral vectors encoding *MYC*-ER and Bcl-2. Briefly, the cells were transfected with pMIG-MYC.ER or pMIT-Bcl2. The virus containing supernatants were collected and supplemented with 4 µg/ml of polybrene and 10mM HEPES, and passed through a 0.45µm filter. The two different viral supernatants were mixed at a 1:1 ratio and added to the wells. The cells were then centrifuged at 2000 rpm for one hour. The viral supernatants were replaced at the end of each spin infection. 24 hours after the last round infection, the levels of transduction were

determined by flow cytometric analysis in order to determine the transduction efficiency. The transduced cells were then incubated in DMEM medium containing IL-3, IL-6, SCF and 10nM 4OHT. The medium was replaced every 3 days and special emphasis was placed on ensuring a fresh supply of cytokines and 4OHT. Cells are passed slowly, and as needed.

Using this *in vitro* approach, the inventors have been able to generate conditionally immortalized cell lines with the following combinations of genes: *MYC*-ER and Bcl-2; *MYC*-ER and hTERT (reverse transcriptase component of the human telomerase); ICN-1-ER (ER-regulated active element of the intracellular portion of Notch-1) and Bcl-2; ICN-1-ER and hTERT; and *MYC*-ER and ICN-1-ER. The data presented in Figs. 8-11 show the initial characterization of most of these cell lines. They yielded lines composed of c-kit+, Sca-1+, CD34-, flk2- cells, which is a phenotype that is consistent with the one presented by normal long-term hematopoietic stem cells. The data presented in Figs. 8-11 is derived from the flow cytometric analysis of retrovirally encoded reporter genes (GFP and thy1.1), as well as four markers for stem cells: c-kit, sca-1, CD34 and flk-2. The cell lines shown in Figs. 8-11 had been in culture for 5 weeks prior to phenotyping. These cells have been expanded and divided in continuous culture for over 35 days to date.

Referring to Fig. 8, this figure shows the phenotypic comparison of cell lines derived from HSCs obtained from young C57/BL6 mice that were retrovirally transduced with BCL-2 and *MYC*-ER and maintained in continuous *in vitro* culture for >90 days. Shown is the phenotype of representative clones 3 (young) months after 90 days of continuous of culture.

Referring to Fig. 9, this figure shows the phenotypic comparison of cell lines derived from HSCs obtained from young C57/BL6 mice that were retrovirally transduced with *different combinations* of oncogenes and maintained in continuous *in vitro* culture for >90 days. 5FU enriched HSCs were retroviral transduced with pMIG-*MYC* and pMIT-Bcl-2 (top panels), pMIG-MYC.ER and pMIG-hTERT (middle panels), or pMIG-ICN.1.ER and pMIT-Bcl-2. The cells were maintained in DMEM supplemented with 15% fetal calf serum, and a cocktail of IL-6, IL-3 and SCF. Shown is the phenotype of representative clones 3 (young) months after 90 days of continuous of culture. The panels represent the results of the flow cytometric analysis for expression of the viral expression markers (GFP and Thy1.1), as well as four markers required to define long-term HSCs in mice, Sca-1, c-kit, CD34 and Flk-2. The four cell lines contained subpopulations that retained the phenotypes of lt-HSCs (Sca-1+, c-kit+, CD34-, flk-2-).

Referring to Fig. 10, this figure shows the phenotypic comparison of cell lines derived from HSCs obtained from young C57/BL6 mice that were retrovirally transduced with *different combinations* of oncogenes and maintained in continuous in vitro culture for >90 days. 5FU enriched HSCs were retroviral transduced with pMIG- ICN.1.ER and pMIT-Bcl-2 (top panels), pMIG-ICN.1 and pMIT-Bcl-2 (second row panels), or pMIG-ICN.1 and pMIG-Bcl-2 (third row panels), or pMIG-hTERT and pMIT-Bcl-2 (bottom panels). The cells were maintained in DMEM supplemented with 15% fetal calf serum, and a cocktail of IL-6, IL-3 and SCF. Shown is the phenotype of representative clones 3 (young) months after 90 days of continuous of culture. The panels represent the results of the flow cytometric analysis for expression of the viral expression markers (GFP and Thy1.1), as well as four markers required to define long-term HSCs in mice, Sca-1, c-kit, CD34 and Flk-2. The four cell lines contained subpopulations that retained the phenotypes of lt-HSCs (Sca-1+, c-kit+, CD34-, flk-2-).

Referring to Fig. 11, this figure shows the phenotypic comparison of cell lines derived from HSCs obtained from young C57/BL6 mice that were retrovirally transduced with *different combinations* of oncogenes and maintained in continuous in vitro culture for >90 days. 5FU enriched HSCs were retroviral transduced with pMIG-*MYC* and pMIG-ICN.1 (top panels), pMIG-MYC.ER and pMIG-ICN.1 (middle panels), or pMIG-ICN.1.ER and pMIG-MYC. The cells were maintained in DMEM supplemented with 15% fetal calf serum, and a cocktail of IL-6, IL-3 and SCF. Shown is the phenotype of representative clones 3 (young) months after 90 days of continuous of culture. The panels represent the results of the flow cytometric analysis for expression of the viral expression markers (GFP and Thy1.1), as well as four markers required to define long-term HSCs in mice, Sca-1, c-kit, CD34 and Flk-2. The four cell lines contained subpopulations that retained the phenotypes of lt-HSCs (Sca-1+, c-kit+, CD34-, flk-2-).

These cell lines have also been used to reconstitute cellular compartments *in vivo*. Referring to Fig. 12, this figures shows the results of *in vivo* reconstitution of T cell and B cell compartments from cell lines derived from HSCs obtained from young C57/BL6 mice that were retrovirally transduced with different combinations of oncogenes and maintained in continuous in vitro culture for >90 days. Briefly, 5FU enriched HSCs were retroviral transduced with pMIG-ICN.1-ER and pMIG-hTERT (top panels), pMIG-MYC.ER and pMIG-hTERT (middle panels), or pMIG-MYC-ER and pMIT-Bcl-2 (lower panels). The cell lines were maintained in DMEM supplemented with 15% fetal calf serum, and a cocktail of

IL-6, IL-3 and SCF. Lethally irradiated young C57/BL6 mice were reconstituted using bone marrow stem cells from Rag2-/- mice and LT-HSC lines generated *in vitro*. Six weeks later, bone marrow was harvested and stained with a panel of specific lineage markers. The development of mature CD4 and B220 positive/GFP positive cells can readily be observed. Data from four representative mice are presented in this figure. In each group, approximately 30% of the mice retain GFP marker.

Example 4

The following example describes an extension of the method for reversibly immortalizing human cord blood and bone marrow derived HSCs *in vitro*.

One additional application of this technology is the ability to expand human long-term hematopoietic stem cells *in vitro* through their conditional immortalization. The inventors have therefore adapted the *in vitro* method described in the previous examples for human cells with a few changes. First, the retroviruses are packaged preferably with amphotrophic envelopes in order to enable efficient transduction of human cells. In addition, the source of the cells is human cord blood obtained anonymously from the a cord blood bank, following all rules and regulations set forth by the Institutional Review Boards of the inventors' institutions. The resulting cells will express reporter genes that may ultimately be useful for isolating a pure population by high speed cell sorting. The inventors have noticed that many mature cells resulting from the murine lt-HSC cell lines lose expression of the surface markers, potentially due to the methylation of the retroviral genome upon lineage determination and differentiation. The inventors expect to see similar behavior in the human cells, in which case the lt-HSCs and their prevalence in transplant recipients can be monitored by the presence of reporter genes in such cells, in combination with cell surface markers for that population of cells.

Example 5

The following example describes an approach to the sequential excision of the DNA fragments encoding *MYC*-ER and Bcl-2 from conditionally immortalized HSC cells.

In order to avoid taking the risk of introducing HSCs that harbor transgenes encoding *MYC*.ER and Bcl-2 into humans and/or mice, these two DNA fragments will be excised using a bacterial recombinase approach. Two different recombinases will be used in order to allow control over which one of the two genes is excised at any one point in time. Two examples of such recombinases are the Cre and Flp recombinases. Briefly, the recognition substrate sequences (RSS's) for one of the recombinases is introduced into the retroviral

constructs such that they flank the open reading frame of the oncogene, as well as the reporter gene (GFP or Thy1.1). In this case, the cells are incubated in media containing a Tat-Cre fusion protein. This recombinant protein has been previously described and shown to be able to passively enter cells, and mediate loxP site-dependent recombination of genomic DNA.

This approach will allow the achievement of a number of things in order to enable the generation of many HSCs for differentiation *in vitro* and *in vivo*. First, the cells can gradually be weaned from the high levels of proliferative and survival signals they had become accustomed to during the conditional transformation process. Second, the cells can be re-adapted to depend on normal cytokines for their homeostatic functions and differentiation. Third, the sequential loss of reporter expression will allow the definition of the status and degree of deletion of each one of the genes in question. Accordingly, cells that express both reporter genes (GFP and Thy1.1) harbor both sequences (MYC and Bcl-2, respectively), cells that express Thy1.1 but no GFP have successfully deleted the MYC encoding sequences, but still contain Bcl-2 genes, and lastly, cells that do not express either GFP or Thy1.1 have deleted both of those alleles. Fig. 13 represents this approach in a diagram.

In addition, this approach is tested in mice by obtaining 5FU enriched BM-HSCs from a strain of mice in which the expression of a human *MYC* transgene can be induced by the withdrawal of tetracycline and the presence of a bacterial protein called tTA (tetracycline transactivator protein). The human *MYC* cDNA was cloned downstream of a tetracycline regulatory transcription element (TRE). The TRE-MYC mice are treated with 5FU and used to harvest BM-HSCs. Those cells are transduced *in vitro* with retroviruses expressing Bcl-2 and tTA (pMIT-Bcl2 and pMIG-tTA). The cells are cultured in the continuous presence of Doxycycline in order to maintain the *MYC* transgene silent. Once the cells are analyzed by flow cytometry, they can be used for transplantation back into mice that will not be maintained on a doxycycline containing diet (this is a more stable form of tetracycline is normally used *in vivo*).

Once the lt-HSC cell lines are generated, the effect of culturing them in the presence of doxycycline *in vitro* will be examined in parallel with *MYC*.ER harboring cell lines that will be cultured in the absence of 4OHT. The protein levels of *MYC* are monitored by western blots and intracellular staining approaches throughout.

Example 6

The following example describes the generation of many hematopoietic lineages *in vitro*, following the withdrawal of 4OHT from the liquid tissue culture media.

The traditional methods used to determine the potency of an HSC involve the use of semi-solid media (methycellulose) with defined cytokines in order to potentiate the differentiation of HSCs into specific lineages. The inventors were interested in determining the pluripotency of this cell population created using the method of the present invention *in vitro*. In order to examine this issue, the ABM42 and ABM46 cell lines described herein were maintained in media containing IL-3, IL-6 and SCF, but without 4OHT. In addition to the lineages that the inventors were able to detect in the reconstituted mice (*i.e.*, lymphoid, myeloid and granulocytic), GFP+ cells could also be detected that expressed NK1.1 or ter-119 (Fig. 14). The NK1.1 cells could either be NK-cell, or NK-T cells. The ter-119 expressing cells are of the erythroid lineage. These findings indicate that these cell lines are capable of giving rise to all of the elements of a normal hematopoietic system and that the cells will be useful for generation of large quantities of specific elements to be used for passive therapies. In addition, they will be of great use and importance to study the early events in hematopoiesis and to identify novel therapy for therapeutic intervention in genetic disorders, or complications that arise the normal course of chemotherapy, or even infectious disease.

Example 7

The following example describes a method for high throughput screens of small molecules or biological agents that induce or inhibit differentiation in conditionally transformed long term HSCs.

The following is a general method for screening small molecules or biological agents that induce or inhibit HSC differentiation. Previously, these types of large screens were prohibited by the fact that large numbers of stem cells were unobtainable. With the present inventors current ability to conditionally immortalize long term HSCs, it is now feasible to propose such technologies.

By way of example, one such method is a myeloid differentiation read-out that has been adapted from Schneider, et al. (Schneider, T., and Issekutz, A.C. (1996). Quantitation of eosinophil and neutrophil infiltration into rat lung by basic assays for eosinophil peroxidase and myeloperoxidase. Application in a Brown Norway rat model of allergic pulmonary inflammation. J Immunol Methods 198, 1-14). Briefly, conditionally transformed long term HSCs are plated in 96 well, flat bottom plates at various

concentrations of cell numbers (usually $2x10^4$-$5x10^4$ cells/well). The screens are carried out either in complete media (DMEM +15% heat inactivated fetal calf serum, 1X penicillin/streptomycin, 1X l-glutamine and 1X non-essential amino acids, supplemented with IL-3, IL-6 and SCF) with added 4OHT in order to maintain the cells in an undifferentiated state, or in the absence of added 4OHT in order to induce differentiation. These conditions have been shown to give rise to Mac-1+ cells, consistent with a myeloid differentiation pattern. Additional cytokines can be added to direct differentiation in specific paths, although this system can also be used to screen for specific functions of a panel of cytokines. In this instance, the complete media will be added without supplementation with IL-3, IL-6 and SCF, but instead with the given cytokines to be tested or used to direct differentiation (*e.g.*, CSF-1, G-CSF, GM-CSF, EPO, TEPO, etc.).

Small molecules, biological agents or positive control substances (*e.g.*, Arsenic 0_3) are titrated across the 96 well plate and incubated with the ltHSCs for time frames ranging from 24 to 72 hours, or longer, if needed and as determined based on the agents or molecules to be tested. After incubation, the cells are washed with PBS and resuspended in PBS for overnight storage at -80°C to lyse the cells. The cells are then thawed at room temperature and the plates are centrifuged for 10 min at 3,000 rpm. The supernatant is then transferred to a new 96 well plate and mixed with tetramethybenzidine (TMB) for 40 min. The reaction is stopped with 4N H_2SO_4 and the O.D. is read at 450 nm. This type of high-throughput assay can be used to test small molecules or biological agents for the ability to induce or block the differentiation of conditionally transformed long term HSCs into a wide variety of cell types. Results of these screens can then further be tested for the ability to induce or inhibit HSC differentiation *in vivo*. Variations on this assay format will be apparent to those of skill in the art and are encompassed by the present invention.

Example 8

The following example describes the use of the method of the invention to generate cell lines of an intermediate hematopoietic lineage.

The following protocol can be used to induce the development of cell lines representing intermediate stages of hematopoietic lineage development following transplantation of conditionally immortalized lt-HSC cell lines into lethally irradiated mice. First, 10^3–10^5 conditionally transformed lt-HSC cell lines generated according to the method of the invention are transferred into cohorts of lethally irradiated recipient mice. The transplants will also include 10^5 Rag-$1^{-/-}$ cells as carriers in order to ensure the initial survival

of the irradiated mice. The mice are treated with weekly injections of 1mg tamoxifen, intraperitoneally, in order to immortalize partially differentiated cells derived from the conditionally transformed lt-HSC cell lines. Injections begin either 3 days-1 week after the initial transplant, or 8 weeks after the transplant, once the mice have been fully reconstituted by the conditionally transformed lt-HSC cell lines. Cells are collected from the spleen and bone marrow cells from mice three days after treatment with tamoxifen, or when they show clinical signs associated with leukemias. The cells are cultured in either the standard bone marrow culture conditions with 4-OHT (DMEM, 15% fetal calf serum, pen/strep, L-glut, non essential amino acids, IL-3, IL-6 and SCF), or in the presence of other cytokines and medium used for different hematopoietic cell types. Cell lines are frozen and/or expanded, and cell lines are also single-cell cloned by limiting dilution and defined by PCR amplification of proviral integrations, frozen, and then characterized for surface marker expression by flow cytometry. These types of approaches are used for both murine and human ctlt-HSC cell lines, using either NOD/SCID mice as the recipients, or neonatal Rag-1-/- mice, which will be given intrahepatic injections.

Example 9

The following example describes the use of the method of the invention and the adoption of protocols used to generate mature CD4+ αβ T-cells *in vitro* to develop cell lines representing intermediate stages of T-cell development.

In this experiment, conditionally immortalized lt-HSC cell lines generated according to the method of the invention are plated in the presence of the normal cytokine cocktail, supplemented with IL-7 and without tamoxifen. Parallel cultures are established on a layer of OP-9 stromal cells that express Jagged, a Notch-1 ligand. Cells are stained for T-cell lineage markers every 48 hours after the cultures are initiated to monitor for signs of T-cell development. The wells that show signs of T-lineage commitment and development are switched to media containing tamoxifen in order to stabilize the phenotype and establish cell lines. The resulting cell lines are expanded, cloned and characterized as described in Example 8. The T-cell lines are specifically stained for individual TCR-Vβ alleles in order to determine their T-cell receptor repertoire usage. Some mature T-cell lines, or cell lines representing progenitor populations, are transplanted into Rag-$1^{-/-}$ mice in order to evaluate their ability to conform to normal tolerance and homeostatic mechanisms *in vivo*, as well as their ability to further differentiate *in vivo*, when appropriate. Finally, their ability to respond to antigenic stimulation is evaluated *in vitro* and *in vivo*.

Example 10

The following example describes the use of the method of the invention and the adoption of protocols used for the directed differentiation of HSCs into myeloid cell lineages to develop intermediate developmental cell lines and myeloid leukemia models.

In this experiment, conditionally immortalized lt-HSC cell lines generated according to the methods of the present invention are plated in the presence of the normal cytokine cocktail, supplemented with G-CSF and without tamoxifen. Cells are stained for myeloid lineage markers every 48 hours after the cultures are initiated to monitor for signs of myeloid development. The wells that show signs of myeloid lineage commitment and development are switched to media containing tamoxifen in order to stabilize the phenotype and establish cell lines. The resulting cell lines are expanded, cloned and characterized as described in Example 8. Some of the resulting cell lines are transplanted back into mice in order to monitor their ability to repopulate Op/Op mice (mutant mice that naturally lack macrophages). Those cell lines are also transplanted into wild type mice that will be maintained on tamoxifen throughout, in order to determine if these cell lines will also give rise to myeloid leukemias similar to human AML, CML and APL. These novel tumors provide novel models for preclinical therapeutics.

Example 11

The following example describes the generation of Human adult ctlt-HSC cell lines and examination of their pluripotential *in vivo* using NOD/SCID or $RAG^{-/-}$ xenotransplant models.

In this experiment, CD34+ cells (from mobilized blood or cord blood) are transduced *in vitro* with retroviral vectors encoding MYC-ER, Bcl-2 and GFP (for later detection of transplanted cells), packaged using amphotrophic envelopes (according to the methods of the present invention). lt-HSC are selected by propagation *in vitro* in the presence of 4OHT and growth factors, as described above using murine HSCs. Pluripotency of the selected cells is evaluated by transplantation of lt-HSC lines into sublethally irradiated NOD/SCID or NOD/SCID/ß-$2M^{-/-}$ or Rag-$1^{-/-}$ or Rag-$2^{-/-}$ mice, followed 6-12 weeks later by analysis of all blood cell lineages by immunofluorescence flow cytometry. More particularly, following the generation of ctlt-HSC cell lines using the method of the present invention, one can use two different and complimentary approaches to examine their pluripotency. In a first approach, varying amounts of clonal ctlt-HSC cell lines are introduced into sublethally irradiated NOD/SCID mice or NOD/SCID/ß-$2M^{-/-}$ mice. In this instance, 10^3-10^5 cells

derived from a human ctlt-HSC cell lines are transferred intravenously after the mice are subjected to a sublethal irradiation regimen (0.3 Gy). The mice are analyzed for reconstitution at 6-12 weeks after transplantation. Second, 10^3-10^5 cells derived from a human ctlt-HSC cell lines are introduced into the liver of neonatal Rag-$1^{-/-}$ or Rag-$2^{-/-}$ mice by direct injection. Those xenotransplants will also be analyzed for appropriate reconstitution 6-12 weeks after transplantation.

Example 12

The following example describes the use of conditional approaches to abrogate expression of MYC and Bcl-2 from the ctlt-HSCs after transplantation.

In this experiment, viruses (viral vectors) used to transform stem cells are re-engineered to contain two loxP sites flanking the MYC-ER, Bcl-2 and GFP open reading frames (ORFS). When the cells are transplanted, a regulated form of Cre or CRE-TAT fusion protein will be used to delete the oncogene-encoding sequences, thus eliminating risk of insert-driven malignancy in recipients. This approach is first developed in mice, then applied to human lt-HSCs.

In a second approach, lt-HSCs from TRE-MYC mice are used to generate the cell lines with retroviruses that encode Bcl-2 or rtTA. These are transplanted into mice. Mice are fed Doxycycline to abrogate the expression of MYC. One can use lt-HSCs obtained from TRE-MYCxTRE-Bcl-2 bigenic mice that can be transduced with a pMIG-rtTA retrovirus to eliminate MYC and Bcl2 expression.

Example 13

The following example describes the use of HIV-1 Tat protein fusions with MYC and/or Bcl-2 to attain conditional transformation without genetic modification of the lt-HSCs.

MYC-Tat and Bcl-2-Tat fusion proteins are generated and purified using established protocols. The fusion proteins are tested by treatment of cells in which one can easily assay the effects of overexpressed Bcl-2 (*e.g.*, activated T cells, B-cell lymphoma cell lines that are rendered resistant to BCMA-Fc, etc.) or MYC (*e.g.*, anergic B-cells, naïve T-cells, activated T-cells). Combinations of MYC-Tat and Bcl-2-Tat proteins are used to allow propagation of lt-HSCs prior to transplantation. This approach is readily developed and tested in the mouse system, then applied to human.

The entire disclosure of each of U.S. Provisional Patent Application No. 60/728,131 and U.S. Provisional Patent Application No. 60/765,993 is incorporated herein by reference.

While various embodiments of the present invention have been described in detail, it is apparent that modifications and adaptations of those embodiments will occur to those skilled in the art. It is to be expressly understood, however, that such modifications and adaptations are within the scope of the present invention, as set forth in the following claims.

What is claimed is:

1. A method to produce conditionally immortalized adult stem cells, comprising:

a) obtaining an expanded population of adult stem cells;

b) transfecting the stem cells with a nucleic acid molecule comprising a protooncogene or biologically active fragment or homologue thereof that promotes cell survival and proliferation, wherein the protooncogene is inducible;

c) transfecting the stem cells with a nucleic acid molecule encoding a protein that inhibits apoptosis of the cell; and

d) expanding the transfected cells in the presence of a combination of stem cell growth factors under conditions whereby the protooncogene is active, to produce conditionally immortalized adult stem cells.

2. The method of Claim 1, wherein the nucleic acid molecule of (b) and/or (c) is contained in an integrating vector.

3. The method of Claim 1, wherein the nucleic acid molecule of (b) and/or (c) is transfected into the cells using a virus or viral vector selected from the group consisting of: retroviral vectors, lentivirus vectors, parvovirus, vaccinia virus, coronavirus, calicivirus, papilloma virus, flavivirus, orthomixovirus, togavirus, picornavirus, adenoviral vectors, modified and attenuated herpesviruses.

4. The method of Claim 1, wherein the nucleic acid molecule of (b) and/or (c) is transfected into the cells using direct electroporation.

5. The method of Claim 1, wherein the nucleic acid molecule or (b) and/or (c) is contained in a vector comprising a nucleic acid sequence encoding a drug-sensitivity protein.

6. The method of Claim 1, wherein the nucleic acid molecule or (b) and/or (c) is contained in a vector comprising nucleic acid sequences encoding recognition substrate sequences for a recombinase flanking the nucleic acid molecule of (b) or (c).

7. The method of Claim 1, further comprising the steps of:

e) removing the conditions of (d) whereby the protooncogene is active; and

f) culturing the cells of (e) in media comprising growth factors that induce differentiation of the cells.

8. The method of Claim 7, further comprising:

g) adding to the cells of (f), the conditions of (d) whereby the protooncogene is active, to produce conditionally immortalized cells in an intermediate stage of cell differentiation.

9. A method to produce conditionally immortalized adult stem cells, comprising:

a) obtaining an expanded population of adult stem cells;

b) culturing the stem cells in the presence of:

(1) a combination of stem cell growth factors;

(2) a first Tat-fusion protein, wherein Tat is fused to a protein encoded by a protooncogene or biologically active fragment or homologue thereof that promotes cell survival and proliferation; and

(3) a second Tat-fusion protein, wherein Tat is fused to a protein that inhibits apoptosis in the stem cells.

10. A method to produce conditionally immortalized embryonic stem cells, comprising:

a) obtaining an expanded population of embryonic stem cells;

b) transfecting the stem cells with a nucleic acid molecule comprising a protooncogene or biologically active fragment or homologue thereof that promotes cell survival and proliferation, wherein the protooncogene is inducible;

c) transfecting the stem cells with a nucleic acid molecule encoding a protein that inhibits apoptosis of the cell; and

d) expanding the transfected cells in the presence of a combination of stem cell growth factors under conditions whereby the protooncogene is active, to produce conditionally immortalized embryonic stem cells.

11. The method of Claim 1, Claim 9 or Claim 10, wherein the protooncogene is selected from the group consisting of: MYC-ER and ICN-1-ER.

12. The method of Claim 1, Claim 9 or Claim 10, wherein the protein that inhibits apoptosis is a member of the Bcl-2 family that inhibits apoptosis.

13. The method of Claim 1, Claim 9 or Claim 10, wherein the protein that inhibits apoptosis is selected from the group consisting of: Bcl-2, Bcl-X, Bcl-w, BclXL, Mcl-1, Dad-1, or hTERT.

14. The method of Claim 1, Claim 9 or Claim 10, wherein the protooncogene is MYC-ER.

15. The method of Claim 14, wherein the conditions under which the protooncogene is active comprises the presence of tamoxifen or an agonist thereof.

16. The method of Claim 1, Claim 9 or Claim 10, wherein the protein that inhibits apoptosis is Bcl-2.

17. The method of Claim 1, Claim 9 or Claim 10, wherein the cells are transfected with *MYC*-ER and Bcl-2; *MYC*-ER and hTERT; ICN-1-ER and Bcl-2; ICN-1-ER and hTERT; or *MYC*-ER and ICN-1-ER.

18. The method of Claim 1, Claim 9 or Claim 10, wherein the cells are transfected with *MYC*-ER and Bcl-2.

19. The method of Claim 1, Claim 9 or Claim 10, wherein the step of expanding is conducted in a medium comprising interleukin-6 (IL-6), IL-3 and stem cell factor (SCF).

20. The method of Claim 1, Claim 9 or Claim 10, wherein the step of expanding is conducted in a serum-free medium comprising stem cell factor (SCF), thrombopoietin (TPO), insulin-like Growth Factor 2 (IGF-2) and fibroblast Growth Factor 1 (FGF-1).

21. The method of Claim 1, Claim 9 or Claim 10, wherein the adult stem cells are selected from the group consisting of: hematopoietic stem cells, intestinal stem cells, osteoblastic stem cells, mesenchymal stem cells, neural stem cells, epithelial stem cells, cardiac myocyte progenitor stem cells, skin stem cells, skeletal muscle stem cells, and liver stem cells.

22. The method of Claim 21, wherein the mesenchymal stem cells are selected from the group consisting of lung mesenchymal stem cells and bone marrow stromal cells.

23. The method of Claim 21, wherein the epithelial stem cells are selected from the group consisting of lung epithelial stem cells, breast epithelial stem cells, vascular epithelial stem cells and intestinal epithelial stem cells.

24. The method of Claim 21, wherein the skin stem cells are selected from the group consisting of epidermal stem cells and follicular stem cells (hair follicle stem cells).

25. The method of Claim 21, wherein the neural stem cells are selected from the group consisting of neuronal dopaminergic stem cells and motor-neuronal stem cells.

26. The method of Claim 21, wherein the stem cells are from fresh or cryopreserved cord blood.

27. The method of Claim 21, wherein the stem cells are hematopoietic progenitor cells obtained from the peripheral blood of normal or granulocyte colony-stimulating factor (G-CSF) treated patients.

28. The method of any one of Claims 1 to 27, further comprising genetically modifying the stem cells to correct a genetic defect in the cells.

29. The method of any one of Claims 1 to 27, further comprising genetically modifying the stem cells to silence the expression of a gene.

30. The method of any one of Claims 1 to 27, further comprising genetically modifying the stem cells to overexpress a gene.

31. The method of any one of Claims 1 to 30, further comprising storing the cells.

32. The method of Claim 31, further comprising retrieving the cells from storage and culturing the cells.

33. Cells produced by the method of any one of the preceding claims.

34. A method to provide adult stem cells, or cells differentiated therefrom, to an individual comprising:

a) providing a source of conditionally immortalized adult stem cells produced by the method of any one of Claims 1 to 32; and

b) removing the conditions under which the stem cells of (a) are conditionally immortalized; and

c) administering the stem cells or cells differentiated therefrom to the individual.

35. The method of Claim 34, wherein the cells were previously obtained from the individual in (c).

36. The method of Claim 34, wherein the cells were obtained from a previously frozen stock of said cells.

37. The method of Claim 34, wherein the cells are freshly obtained from the individual and conditionally immortalized by the method of any one of Claims 1 to 32.

38. The method of any one of Claims 34 to 37, wherein the individual has cancer.

39. The method of any one of Claims 34 to 37, wherein the individual has leukemia.

40. The method of any one of Claims 34 to 37, wherein the individual has an immune deficiency disorder.

41. The method of any one of Claims 34 to 37, wherein the individual has an anemia disorder.

42. The method of any one of Claims 34 to 37, wherein the individual is undergoing reconstructive surgery.

43. The method of any one of Claims 34 to 37, wherein the individual is undergoing elective cosmetic surgery.

44. The method of any one of Claims 34 to 37, wherein the individual is undergoing transplantation surgery.

45. The method of any one of Claims 34 to 37, wherein the individual is in need of stem cells, or cells differentiated therefrom, selected from the group consisting of: hematopoietic stem cells, intestinal stem cells, osteoblastic stem cells, mesenchymal stem cells, neural stem cells, epithelial stem cells, cardiac myocyte progenitor stem cells, skin stem cells, skeletal muscle stem cells, and liver stem cells.

46. The method of any one of Claims 34 to 37, wherein the individual is in need of improved immune cell function.

47. The method of any one of Claims 34 to 37, wherein the individual has a genetic defect that is corrected by the stem cell.

48. A method to identify compounds that regulate lineage commitment and/or cell differentiation and development, comprising:

a) contacting adult stem cells produced by the method of any one of Claims 1 to 32 with a compound to be tested; and

b) detecting at least one genotypic or phenotypic characteristic in the stem cells of (a), as compared to the stem cells in the absence of the compound, wherein detection of a difference in the characteristic in the presence of the compound indicates that the compound affects the characteristic in the stem cell.

49. A method to study lineage commitment and/or cell differentiation and development, comprising evaluating adult stem cells produced by the method of any one of Claims 1 to 32, or cells differentiated therefrom, to detect at least one genotypic or phenotypic characteristic of the cells.

50. Use of the cells produced by the method of any one of Claims 1 to 32 in a medicament for treating a condition or disease in which transplantation of stem cells is beneficial.

51. A mouse model of acute myeloid leukemia (AML), comprising a mouse produced by a method comprising:

a) lethally irradiating a mouse;

b) transferring conditionally immortalized long-term stem cells produced by the method of Claim 18 and whole bone marrow cells from a $Rag^{-/-}$ mouse into the mouse; and

c) injecting periodic doses of tamoxifen or an agonist thereof into the mouse until the mouse develops clinical signs of AML.

52. Tumor cells obtained from the mouse model of AML of Claim 50.

53. Use of the mouse model of AML for preclinical testing of drug candidates specific for human proteins; to identify, develop, and/or test a compound for use in the diagnosis of, study of, or treatment of AML; or to identify, develop, and/or test a target for use in the diagnosis of, study of, or treatment of AML.

54. A method to produce conditionally immortalized stem cells, comprising:

a) obtaining an expanded population of stem cells;

b) culturing the stem cells in the presence of:

(1) a combination of stem cell growth factors;

(2) a protein encoded by a protooncogene or biologically active fragment or homologue thereof that promotes cell survival and proliferation; and;

(3) a protein that inhibits apoptosis in the stem cells;

wherein the protein of (2) and (3) are delivered into the stem cells.

55. A method to produce conditionally immortalized adult stem cells, comprising:

a) obtaining an expanded population of adult stem cells;

b) delivering into the cells a protein encoded by a protooncogene or biologically active fragment or homologue thereof that promotes cell survival and proliferation, or a nucleic acid molecule encoding the same, wherein the protooncogene is inducible;

c) inhibiting apoptosis in the stem cells by delivering into the cells a protein that inhibits apoptosis of the cell, a nucleic acid molecule encoding the protein that inhibits apoptosis of the cell, or a nucleic acid molecule or protein that inhibits a proapoptotic protein in the cells; and

d) expanding the cells in the presence of a combination of stem cell growth factors under conditions whereby the protooncogene is active, to produce conditionally immortalized adult stem cells.