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HEMATOPOIETIC STEM CELL GENE THERAPY: ASSESSING THE RELEVANCE OF PRE-CLINICAL MODELS

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Abstract

The modern laboratory mouse has become a central tool for biomedical research with a notable influence in the field of hematopoiesis. Application of retroviral-based gene transfer approaches to mouse hematopoietic stem cells (HSCs) has led to a sophisticated understanding of the hematopoietic hierarchy in this model. However, the assumption that gene transfer methodologies developed in the mouse could be similarly applied to human HSCs for the treatment of human diseases left the field of gene therapy in a decade-long quandary. It is not until more relevant humanized xenograft mouse models and phylogenetically related large animal species were used to optimize gene transfer methodologies that unequivocal clinical successes were achieved. However, the subsequent reporting of severe adverse events in these clinical trials casted doubts on the predictive value of conventional pre-clinical testing, and encouraged the development of new assays for assessing the relative genotoxicity of various vector designs.

Introduction

Hematopoietic stem cells (HSCs) are indispensable for lifelong blood production. HSCs can sustain long-term and functional hematopoiesis due to their ability to both differentiate to produce mature progeny of all myeloid and lymphoid blood lineages or to self-renew to replace the cells that become progressively committed to differentiation. The majority of HSCs, however, are quiescent and do not contribute to daily production of mature blood cells. Our understanding of the nature and properties of HSCs has been greatly influenced by the seminal murine studies of Till and McCulloch^{1,2} over five decades ago. Since then, the highly standardized and easily accessible laboratory mouse has continued to dominate the field of hematopoiesis because durable, long-term *in vivo* reconstitution of the hematopoietic system of a recipient animal after transplantation is the only operational means of unequivocally identifying HSCs, raising an obvious impediment to studying human HSCs. The introduction of genetic markers into mouse HSCs and their progeny using retroviral vectors was instrumental in providing both conceptual and methodological insights for the identification and characterization of individual stem cells, leading to a refined understanding of murine stem cell behavior *in vivo* over time.

The potential of applying similar gene transfer approaches to human HSCs is considerable, as it offers a powerful methodology for the characterization of these cells and an approach to permanent correction of various inherited or acquired hematologic, metabolic and

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immunologic disorders. Gene transfer of a therapeutic gene into human HSCs is necessary to achieve long-lasting correction; mature cells and committed progenitors do not have the proliferative capacity for long-term reconstitution of the entire hematopoietic system and must be replenished from HSCs. However, direct application of gene transfer techniques developed in the mouse to human HSCs initially met with limited success. Recent efforts have centered on the optimization of existing gene transfer approaches using more predictive models to achieve efficient gene delivery into human HSCs.³ The clinical successes that ensued were tarnished by the development of malignancies linked to insertional genotoxicity, forcing the scientific community to further re-evaluate and refine pre-clinical models to be used for testing of potentially safer approaches for HSC gene therapy. This review summarizes the benefits and drawbacks of the laboratory mouse model in the development and safety evaluation of methodologies used for the genetic manipulation of human HSCs for gene therapy applications.

Development of methodologies for the genetic manipulation of human HSCs: the influence of mouse transplantation models

Gene transfer into mouse HSCs

Murine gene marking studies—Early murine transplantation experiments stressed the importance of genetic markers to follow the progeny of HSCs after reconstitution of an ablated syngeneic recipient.⁴ The use of donor versus host genetic differences, including enzyme isotypes or polymorphic hemoglobin and immunoglobulin markers, led to the demonstration that all mature blood cell types in the reconstituted recipient mouse were donor derived but the limited resolution (only two possible markers) of the donor versus host marker system did not permit a definition of the developmental potential, self-renewal capability and overall proliferative capacity of individual stem cells. An important refinement to the transplantation system was achieved with the use of X-ray induced random chromosomal abnormalities as markers for individual stem cells and the clones derived from them.^{5–8} Although clonally precise, this strategy suffered from low-efficiency as well as marker visibility limited to actively dividing cells, and could reflect abnormal hematopoiesis linked to major mutational events.

Several groups sought to extend the early *in vivo* clonal analyses by stably integrating new genetic information into the genomic DNA of murine HSCs via transmissible retroviral vectors.^{9–12} Gammaretroviral vectors (γ -RV) based on murine leukemia virus (MLV), a well-characterized member of the *Retroviridae* family of viruses, were used in these initial studies. For successful transduction with MLV-based vectors, the target cells must be replicating at the time of infection in order for the vector to enter the nucleus.¹³ This requirement for active cell division is a disadvantage of MLV-based gene transfer vectors for use in the quiescent HSC targets. Active growth stimulation *ex vivo* by 3 or more cytokines (e.g. interleukin-3 (IL3), interleukin-6 (IL6) and stem cell factor (SCF)) for 3–4 days was used to coax HSCs into cycle and allow efficient vector entry and integration.¹⁴

Marking with provirus provided a more efficient, quantifiable and less detrimental approach than other means of genetic marking. Because of the largely random nature of integration of retroviruses, each cell in an infected population carries the integrated retrovirus at a unique and permanent location. These identifiable integration sites provide a genetic tag to follow the progeny of HSCs after *in vivo* reconstitution of an ablated recipient. Initial applications of the retroviral marking strategy yielded results that extended earlier classical studies. The observation of lymphoid and myeloid cells harboring the same proviral integrant 10–20 weeks after transplantation confirmed the existence of pluripotent stem cells capable of contributing to all cell lineages.^{9,11,12} In addition, the ability to accurately quantitate the

extent to which a given tissue was repopulated by progeny of marked stem cells made possible a rigorous demonstration of the ability of a single stem cell to reconstitute the entire murine hematopoietic system.⁹ Molecular analysis of the spectra of proviral integration sites found in each fractionated cell population also provided evidence for the existence of lineage restricted stem cells, as previously proposed.^{5,8}

Murine gene therapy preclinical models for evaluation of MLV-based vectors

—The ability of MLV-based retroviral vectors to permanently introduce marker genes into murine cells with lifelong repopulating ability led investigators to test whether this approach was feasible when clinically relevant genes were used. Genetic disorders with high morbidity and mortality and with no effective conventional treatments were considered prime candidates for preclinical evaluation.

Severe combined immunodeficiency disease (SCID): SCID resulting from adenosine deaminase (ADA) deficiency was initially chosen and stable expression of functional human ADA was demonstrated in all hematopoietic lineages at levels near endogenous murine levels in reconstituted murine transplants.^{15–20} The efficiencies of gene transfer and ADA levels achieved in these preclinical models, together with the anticipated *in vivo* selective survival advantage of transduced T cells, were thought to be predictive of successful correction of lymphoid dysfunction in patients with ADA deficiency.²¹ Gamma-retroviral vector-mediated gene transfer has also been used successfully to evaluate gene therapy strategies in several murine models of human immunodeficiencies, including those caused by deficiency of the common γ -chain expressed in T-cell cytokine receptors (X-SCID),^{22–24} Jak3 kinase deficiency,²⁵ deficiency in the zap70 protein,²⁶ and recombination-activating gene-2 (RAG-2) deficiency.²⁷

Gaucher disease: Gaucher disease is an inherited deficiency of the lysosomal enzyme glucocerebrosidase (GC) and the associated accumulation of glucocerebroside in the lysosomes of macrophages results in multisystem damage, including hepatosplenomegaly, gradual replacement of bone marrow (BM), skeletal deterioration and neuropathology in some cases of Gaucher disease. Correction of enzyme deficiency in macrophages by HSC gene therapy has been considered an attractive therapeutic option for these patients. A transgenic GC-deficient mouse model has been created but, due to alternative physiological pathways of lysosomal metabolism in rodents, the resulting phenotype was significantly different from that observed in humans.²⁸ The profoundly severe phenotype observed in this model resulted in perinatal lethality that precluded its use in most gene transfer studies. However, normal mouse BM transplant models have been invaluable for initial evaluation of MLV-based gene transfer vectors developed for Gaucher disease.^{29–34} These studies established the feasibility of efficient transfer of the GC gene to normal mouse HSCs and long-term expression in their progeny after reconstitution, strengthening the rationale for gene therapy as a treatment option for Gaucher disease.

Hemoglobinopathies: Hemoglobinopathies, including β -thalassemia and sickle cell disease, were also among the first diseases selected as targets for genetically based therapeutic approaches. Transfer of the human β -globin gene into murine HSCs proved more challenging due to the requirement to include specific endogenous regulatory elements from the β -globin locus that were obligatory to achieve clinically relevant expression. Early preclinical studies demonstrated that MLV vectors containing the β -globin gene and its promoter could transduce murine HSCs. However, human β -globin gene expression was either absent or very low, usually varying between 0% and 2% of mouse β -globin RNA levels.^{35–41} As outlined below, it is not until new vector designs became available that

successful genetic correction of β -thalassemia was first demonstrated in murine preclinical models, laying the foundation for a recent clinical trial of gene therapy for β -thalassemia.⁴²

Chronic granulomatous disease (CGD): CGD results from mutations in any one of four genes encoding the essential subunits of the phagocytic antimicrobial system NADPH phagocyte oxidase (phox)⁴³, including gp91^{phox}, p22^{phox}, p47^{phox}, and p67^{phox}, rendering individuals born with CGD particularly susceptible to bacterial and fungal microorganisms. MLV-based gene transfer vectors have been tested in two CGD knockout mouse models. In studies utilizing the gp91^{phox}^{-/-} (X-CGD) mouse, BM cells were transduced with a γ -RV harboring the murine gp91^{phox} cDNA and transplanted into lethally irradiated syngeneic X-CGD recipients.^{44,45} Long-term (18 months) restoration of NADPH oxidase activity was demonstrated in 50–80% of peripheral blood neutrophils and gene corrected neutrophils were detected in secondary transplants, indicating successful transduction of long-term reconstituting murine HSCs. Improved resistance to respiratory challenge with *Aspergillus fumigatus* was achieved in all mice with >10% gene-corrected neutrophils, consistent with observations in human X-CGD carriers in which women with low levels of functional neutrophils (5–20%) were usually resistant to fungal infections.^{46,47} In another study, recipient p47^{phox}^{-/-} animals received a sublethal dose of radiation prior to transplantation of p47^{phox}^{-/-} BM transduced with a MLV-based retroviral vector carrying the p47^{phox} gene.⁴⁸ The percentage of superoxide-generating peripheral blood neutrophils increased up to 17% in individual mice but long-term expression was not detected.⁴⁸ Nevertheless, mice challenged with *B. cepacia* at a time when ~3% oxidase-positive neutrophils were present in the peripheral blood had significantly prolonged survival compared to untreated mice. Taken together, these studies suggested that gene transfer into murine HSCs is feasible and that partial reconstitution of NADPH oxidase activity achieved after retroviral gene transfer can improve host defense if an adequate number of phagocytes exhibit enzyme activity.

Wiskott-aldrich syndrome (WAS): WAS is an X-linked complex primary immunodeficiency disorder caused by mutations in the gene that encodes the WAS protein (WASP)⁴⁹. It is characterized by an increased susceptibility to recurrent infections associated with adaptive and innate immune deficiency, thrombocytopenia, eczema and autoimmunity.^{50,51} The generation of two WASP-deficient mice have facilitated preclinical safety and efficacy studies of MLV-based vectors for the treatment of WAS. In one study,⁵² the WAS gene was inserted into hemizygous WASP-deficient animals BM cells using a γ -RV vector, followed by transplantation into lethally irradiated WASP⁻ recipients. Vector-mediated WASP expression was shown to correct the T-cell proliferative and cytokine secretory defects, as well as the defective secondary T-cell response to influenza virus infection in WASP⁻ mice. In a similar study, investigators also demonstrated rescue of T-cell signaling and amelioration of colitis upon transplantation of transduced WAS HSCs in mice, supporting the development of gene therapy approaches for WAS.⁵³

Gene transfer into human HSCs: lessons from the first generation gene transfer trials

Because of the absence of in vivo assays that measure the repopulating capacity of human HSCs, gene transfer protocols employed in early clinical trials were adapted from the murine studies described above, and initially tested using human in vitro colony forming cell (CFC) assays that detect committed progenitor cells, and long-term bone marrow culture (LTBMC) assays that detect a cell capable of maintaining production of CFC for at least 5 weeks on a layer of stromal cells. Notwithstanding the fact that progenitors do not have the same biological properties as stem cells, investigators were initially encouraged when high gene transfer efficiency (up to 100%) was observed in these in vitro progenitor assays using gene transfer vectors and transduction conditions comparable to those employed in the mouse.^{54–56} Demonstration of correction of GC and ADA deficiency after retroviral vector-

mediated gene transfer into progenitors from patients with Gaucher disease⁵⁷ and ADA-SCID,⁵⁸ respectively, provided even further impetus to regulators and investigators to initiate a first generation of human HSC gene transfer clinical trials, including gene marking studies and gene therapy trials with therapeutic intent (Table 1-First generation HSC gene therapy clinical trials). However, it was not long before the drawbacks of relying on murine studies and in vitro assays as surrogates for optimization of gene transfer in human HSCs became overtly apparent to investigators anxious to see patients in need benefit from this procedure.

Human gene marking studies—As previously done in the mouse BM transplantation model, Brenner and colleagues utilized MLV-based retroviral vectors as a tool for marking human HSCs in patients with acute myeloid leukemia (AML) or neuroblastoma undergoing autologous BM transplant after consolidation therapy to determine whether contaminating tumor cells in the transplant contributed to tumor relapse and to establish if transduced HSCs could contribute to long-term hematopoietic reconstitution.^{59–63} Several patients were shown to relapse with genetically marked cells, implying that the “remission” BM contained tumor cells that contributed to relapse. The presence of the marker gene was also followed in non-malignant hematopoietic cells. Gene-marked cells contributed for only 0.1–1% of the total BM but detection of the marker gene in T cells and B cells for as long as 18 months after transplantation was consistent with low level transduction of primitive hematopoietic cells with multilineage capacity. In a similar marking study, Deisseroth et al. determined that autologous BM used for transplantation in patients with chronic myelogenous leukemia (CML) following intensive therapy also contained cells that contributed to relapse.⁶⁴ Other gene marking trials involving patients with multiple myeloma^{65–67}, breast cancer,^{66,67} follicular lymphoma,⁶⁸ and AML⁶⁹ failed to show stable levels of marked cells of more than 0.1% after transplantation with autologous gene marked grafts, contrasting with the high levels marking observed in preclinical mouse models.

Gene therapy trials with therapeutic intent—In spite of the low transduction efficiency observed in human gene marking studies, a wealth of clinical protocols with therapeutic intent were subsequently approved throughout the world (Table 1-First generation HSC gene therapy clinical trials). As in the murine preclinical models, SCID resulting from ADA deficiency has been the focus of the initial gene therapy attempts. T cells,^{70,71} BM,^{72,73} or cord blood (CB) CD34+ cells⁷⁴ were used as targets of transduction. In one study,⁷⁴ the continued presence and expression of the ADA gene for 18 months demonstrated that CB cells had been genetically modified with retroviral vectors and could engraft in neonates. However, only 0.01% of the patient total BM cells were shown to contain the transferred gene, indicating that the anticipated survival advantage of transduced T cells was not substantial and far below clinical benefit.

Modeling preclinical murine transplantation models, gene therapy was also attempted for Gaucher disease.⁷⁵ Akin the previous gene therapy trials, no conditioning was used in these patients prior to infusion of G-CSF mobilized or BM CD34+ cells transduced with MLV-based retroviral vectors carrying a normal GC cDNA. Unlike results obtained in the mouse, low numbers of gene corrected cells were again detected, with little or no expression and no disease correction following transplantation.

Similar results were obtained in a clinical trial for an autosomal recessive form of CGD.⁷⁶ Five patients received transduced G-CSF mobilized CD34+ cells without preconditioning. Corrected granulocytes were detected in the peripheral blood of all individuals for up to 6 months after infusion but the levels (0.004–0.05%) were below the desired 5–10% required for therapeutic effects.

Murine transplantation models: poor predictors of gene transfer efficiency in human HSCs

—While these initial studies established the proof of principle of transduction of primitive human repopulating hematopoietic cells, they uniformly failed to reach and maintain therapeutically relevant levels of genetically modified cells. This striking difference in outcome observed between mouse and human studies is thought to result from intrinsic differences between mice and humans, resulting in a different susceptibility to retroviral transduction and a different ability of transduced HSCs to engraft. Mice and humans differ in size, environmental exposure and lifespan, imposing different selective proliferative pressures on HSCs from each species. As a result, the balance between self-renewal and proliferation, as well as quiescence and proliferation, is altered in human compared to mouse HSCs. For instance, the number of red blood cells (RBCs) produced by mice in a 2-year lifespan is comparable to the number of RBCs produced daily by a healthy adult individual.⁷⁷ Moreover, competitive transplantation studies in mice have estimated that murine HSCs divide every 2.5 weeks *in vivo*,^{78,79} significantly faster than human HSCs estimated to divide every 40–45 weeks.^{80,81} This difference is further amplified by a decreased sensitivity of mouse HSCs to cytotoxic agents compared to human HSCs,⁸² allowing the administration of 5-fluorouracil to donor mice prior to collection of HSCs to increase cell cycling of HSCs without decreasing HSC numbers significantly. These considerations are important for gene transfer with MLV-based retroviral vectors given the inability of these vectors to transduce quiescent cells.⁸³ The minimal expression of amphotropic surface receptors used by MLV-based gene transfer vectors on human HSCs has also been proposed for the poor susceptibility of these cells to retroviral vectors.⁸⁴

While culture of early mouse hematopoietic cells under stimulatory conditions improved gene transfer efficiency, these *ex vivo* culture conditions were subsequently shown to result in loss of at least 75% *in vivo* repopulating stem cell activity, compared to non-cultured BM.^{85–87} A similar loss in repopulating activity has also been reported after culture of human^{88,89} and rhesus macaque⁹⁰ HSCs. This observation has recently been proposed to result from the disruption of an organized membrane domain on repopulating cells as a result of increased cell cycling during *ex vivo* culture⁹¹, consistent with the finding that progenitor and stem cells in G₂/S/M phase of the cell cycle engraft poorly compared to cells in G₀ and G₁.⁹² However, because mouse strains used in biomedical research are inbred and maintained in a protected pathogen-free environment, unlike genetically diverse human populations exposed to more complex environmental stimuli, murine engraftment and survival could occur even when a small number of transduced HSCs were transplanted. Therefore, detection of transduced HSCs and their progeny after transplantation was robust, circumventing the need to improve upon gene transfer protocols or ensure retention of HSC functional activity during culture and transduction.

The recognition of differences in HSC behavior between mice and humans and the disappointing results in the early human HSC gene therapy clinical trials underscored the need for alternative assays similar to those available in mice that permit direct identification and characterization of human long-term reconstituting cells and their susceptibility to gene transfer. These assays allowed investigators to refocus efforts on better understanding of target cells and vector biology, optimization of *in vitro* transduction conditions, and use of conditioning regimens to favor engraftment of transduced cells.

Optimization of human HSC gene transfer protocols: the role of mouse xenotransplant and large animal models

Development of preclinical animal models for investigating gene transfer into human HSCs

Large animal models: Since prolonged follow-up of *in vivo* hematopoiesis is the most reliable parameter to identify human HSCs, large animals are more adapted than mice for evaluation of gene transfer to long-term repopulating cells, given their lifespan and their size, allowing repetitive blood and marrow sampling. The group of Zanjani, capitalizing on the immunologically tolerant environment of the fetal sheep between 50 and 60 days of gestation, successfully showed engraftment and persistence of human cells several years after intraperitoneal administration *in utero* of primitive human hematopoietic cells from CB or BM.⁹³⁻⁹⁵ Among fetuses reaching maturity, at least 50% showed long-term persistence of human cells and demonstration that retrovirally transduced human cells could be detected,⁹⁶ suggesting transduction of primitive human HSCs. However, the procedure was hampered by low-level engraftment, a high rate of fetal loss, and impracticality for most research groups.

An alternative approach based on autologous HSC transplant in dogs and non-human primates, including baboons and Old World rhesus macaques, has proven to be invaluable in gene transfer preclinical research. Cells from these species cross-react with key anti-human antibodies found on progenitor and stem cells (e.g. CD34), respond to human cytokines and have stem cell dynamics approximating those found in humans. In contrast to murine studies, results from early clinical trials were very similar to data obtained in non-human primates and dogs using similar vector systems and transduction conditions,⁹⁷ validating the importance of large animal models for the optimization of gene therapy strategies. The value of these models for preclinical testing was also illustrated when aggressive T cell lymphomas developed in three of ten rhesus macaques transplanted with BM cells transduced with retroviral vector stocks contaminated with replication-competent retrovirus (RCR).⁹⁸ This finding resulted in the introduction of more stringent requirements for preventing and detecting RCR in vector formulations developed for clinical applications. However, given the high purchase costs of these animals, the space requirements for husbandry, and the sophisticated training required to collect stem cells and support them through myeloablative transplantation, mouse xenotransplant models have been exploited as a more practical alternative approach for preclinical gene transfer testing in human HSCs.

Mouse xenotransplant models: The most widely used murine xenotransplant model was developed using a strategy closely modeled on human BM transplantation and conventional murine HSC assays. Initially, large numbers of human BM cells were intravenously injected into sub-lethally irradiated mice lacking a functional immune system to prevent rejection of the injected human cells, including SCID and beige/nude/xid (bnx) mice.^{99,100} With regular treatment of engrafted SCID mice with a combination of human hematopoietic cytokines, human BM cells that migrated to the mouse marrow and spleen gave rise to a small but sustained pool of myeloid progenitors and B cells for several months, indicating that the engraftment was long-term and multipotent, fulfilling two key criteria used to define HSCs.¹⁰⁰

The SCID mouse used in these initial studies can spontaneously generate murine T and B cells with age and has high levels of natural killer (NK) cell activity, impeding efficient and prolonged xenograft. To improve upon the available immunodeficient mouse strains, the SCID mutation was backcrossed onto the non-obese diabetic (NOD) background.¹⁰¹ The resultant NOD-SCID mouse has reduced innate immunity and superior engraftment of human hematopoietic cells.¹⁰² However, this strain has a high incidence of spontaneous

thymic lymphomas resulting in a short lifespan, a striking preferential development of human B cells after transplantation, and a persistence of murine NK cells resulting in a lack of human T- and NK-cell differentiation in this strain. Reducing or abolishing NK activity in NOD-SCID mice by infusion of antibodies against NK1.1 or the IL2 receptor β chain (IL2R β , CD122),^{103,104} or genetic manipulation by introduction of the IL2 receptor γ chain c (IL2R γ c) deletion (NSG mice) or truncation (NOG mice) strikingly improved permissiveness towards human T and NK lymphoid differentiation, decreased incidence of thymic lymphoma, and murine T and B cell leakiness. This strain is currently the most widely used humanized mouse model for gene therapy pre-clinical testing.^{105–107}

The immunodeficient mouse model assays a human cell population operationally defined as SCID-repopulating cells (SRCs). In contrast to preclinical standard murine transplantation studies and human in vitro progenitor assays, the xenotransplantation model was shown to provide a more accurate prediction of the low levels of HSC gene marking reported in human clinical trials and large animal models; whereas CFC and long-term culture initiating cells (LTCIC) were efficiently transduced using gene marking approaches similar to those used in mouse transplant studies and early clinical trials, SRC were rarely transduced and therefore distinct from progenitor cells.⁵⁶ Using improved transduction conditions (see below), Guenechea G. et al.¹⁰⁸ subsequently showed that individual engrafted and marked human SRCs could produce a large clone of differentiated progeny with engraftment potential in secondary NOD-SCID recipients, demonstrating the proliferative and self-renewal capacity of SRCs. Although this study did not contain a direct analysis of individual lineages, a recent investigation by the same group¹⁰⁹ successfully tracked self-renewal and multilineage output of single human cells purified using a complex set of markers (CD34+CD38-CD45RA-CD90+CD49f+Rho^{lo}) for at least 8 months after transplantation in NSG mice. Together, these studies fulfilled the proliferative, self-renewal and multipotential criteria previously used to define murine HSCs, providing a compelling characterization of human HSCs and relevance for preclinical testing of human HSC gene therapy.

Although, in practical terms, the above studies served to validate the murine xenotransplant model as a sound surrogate assay system for human stem cells, a number of limitations have cast doubt on its usefulness to the study of human HSCs. For instance, the various human cell lineages that differentiate and proliferate from transplanted SRCs may not be detected simultaneously, with an early (2–4 weeks) but usually non-persistent RBC contribution and a late (>12 weeks) T cell detection. Thus, a careful kinetic analysis is required when evaluating human cell engraftment in these mice. This caveat is compounded by the practical 8–12 week-post-transplant endpoint adopted by most investigators for assessment of engraftment, perhaps limiting the ability to distinguish between long-term and short-term repopulating cells.^{109,110} A study in non-human primates (baboon) which compared autologous reconstitution of retrovirally marked cells infused in parallel in the donor non-human primate and NOD-SCID mice have suggested that clones detected in NOD-SCID mice were only found early after transplantation in the baboon but did not contribute to long-term (>6 months) hematopoiesis.¹¹¹ The authors deduced that most cells assayed in murine xenografts must represent short-term repopulating cells, but their conclusion was derived from the analysis of only two clones from one baboon.

The development of better assays to evaluate gene transfer efficiency in human repopulating cells has culminated over the past two decades in various strategies to improve gene transfer protocols, including: 1- New retroviral vector designs; 2- Optimized transduction conditions; and 3- Use of conditioning regimens to favor engraftment of transduced cells.

Use of alternative gene transfer vectors based on lentiviruses—Early preclinical murine studies established MLV-based vectors as a tool of choice for efficient transduction

of mouse HSCs but the contrasting poor in vivo marking levels observed in more relevant preclinical models and in actual gene therapy trials led investigators to explore alternative gene transfer vehicles for human HSCs. In the late 1990's, retroviral vectors based on lentiviruses (e.g. human immunodeficiency virus-1, HIV-1) were designed to overcome the shortcomings of MLV-based vectors. Unlike γ -retroviral vectors, lentiviral vectors harbor several viral elements that enhance nuclear translocation and localization, thus allowing enhanced transduction of non-dividing cells such as HSCs.^{112–122} However, it is also generally agreed that cells must exit G0 and enter G1 for efficient transduction by HIV-1-based vectors.^{123–125} Because of safety concerns regarding recombination with endogenous HIV, a “self-inactivating (SIN)” feature was incorporated in these vectors by eliminating a portion of the 3'-LTR, which on proviral integration replaces and thus inactivates the 5'-LTR.¹²⁶ For these SIN vectors, the efficiency of transgene expression is highly dependent on the addition of a ubiquitous internal promoter, such as murine stem cell virus (MSCV), human elongation factor-1 α (EF-1 α), human phosphoglycerate kinase (PGK), spleen focus-forming virus (SFFV), gibbon-ape leukemia virus (GALV), or the hybrid chicken actin promoter containing the CMV enhancer region (CAG). Wild-type HIV-1 virions infect cells that express the CD4 receptor and an appropriate co-receptor. Because murine and large animal HSCs do not express CD4, wild-type HIV or any lentiviral vectors using the HIV envelope cannot be used in HSC gene therapy applications. Expansion of the cellular tropism of HIV-1-based vectors can be accomplished by substituting the wild-type envelope protein with an envelope protein from a different virus, a process referred to as pseudotyping.¹²⁷ Superior transduction of HSCs was achieved using the alternative GALV envelope protein, the cat endogenous retroviral glycoprotein (RD114), and the vesicular stomatitis virus-G protein (VSV-G).^{128–131}

Preclinical evaluation of lentiviral vectors using murine xenotransplantation models:

Given the established lack of predictability of standard murine transplantation models for evaluation of HSC transduction efficiency in humans, investigators initially chose the murine xenotransplant assay to validate the ability of HIV-1-based vectors to efficiently transduce human hematopoietic cells, including CD34+ cells and the more primitive CD34+/CD38- subset. Several groups reported efficient gene transfer in SRCs derived from human CB^{132–136} and mobilized peripheral blood^{137,138} under conditions where MLV vectors were ineffective. High level GFP transgene expression in SRCs capable of secondary¹³⁶ and tertiary¹³⁹ multilineage repopulation in NOD-SCID mice suggested transduction of primitive human HSCs with pluripotential, proliferative, and self-renewing capabilities.

Murine xenograft models also provided unique experimental systems to assess disease-specific lentiviral gene transfer vectors for their ability to improve disease phenotype after gene therapy. In one study, immune-deficient mice were transplanted with BM cells from patients with thalassemia major transduced with a SIN-lentiviral vector carrying the human β -globin gene and LCR regulatory sequences.¹⁴⁰ Effective human erythropoiesis was achieved with circulating β -globin producing human erythroid cells in the genetically corrected xenografts, at levels comparable to normal BM xenograft controls. Preclinical evaluation has also been documented for X-linked adrenoleukodystrophy (ALD), an inherited demyelinating disorder of the central nervous system caused by mutations in *ABCD1*, a gene encoding the ALD protein (ALDP) whose function involves peroxisomal import of fatty acids in the organelle.^{137,141} Xenotransplantation of lentivirally transduced human ALD CD34+ cells into NOD-SCID mice demonstrated in vivo expression of ALDP in human monocytes and macrophages derived from engrafted human HSCs. Human BM-derived cells migrated into the brain of transplanted mice where they differentiated into microglia expressing the human ALDP. As described below, the validity of these preclinical

data has recently been confirmed in the context of clinical trials for ALD¹⁴² and β -thalassemia.⁴²

Murine xenotransplantation has also been utilized to establish preclinical safety and efficacy of HIV-1-based gene transfer vectors for the treatment of WAS, CGD, SCID, and lysosomal storage diseases. As reported below, patients with WAS have been treated using an MLV-based vector methodology,¹⁴³ and phase I/II gene therapy clinical protocols based on infusion of lentivirally transduced autologous CD34+ cells have also recently started.¹⁴⁴ In a preclinical study, Aiuti and colleagues¹⁴⁵ transduced human CD34+ cells derived from the BM or mobilized blood of WAS patients using a good manufacturing practice (GMP)-grade lentiviral vector encoding WASP. Transduced human cells infused in immunodeficient mice could repopulate and differentiate into multiple lineages with a polyclonal pattern of integration in the absence of vector shedding or germline transmission, providing a rationale for the use of this vector in patients.¹⁴⁵ Similar conclusions were derived from xenotransplant preclinical studies for X-CGD; sustained gp91phox expression and correction of the defective oxidase function was achieved in the lentivirally transduced human X-CGD myeloid cells arising from the human xenograft in the BM of NOD-SCID mice, suggesting efficacy of lentiviral vectors for clinical applications in CGD.^{146,147} HIV-1-based vectors for SCID gene therapy have also been investigated in immunodeficient mice.¹⁴⁸ Human CD34+ cells from SCID patients have been transduced with a SIN lentiviral vector containing the Artemis or RAG-1 gene, followed by transplantation into NOD-SCID mice. Transduced cells differentiated into functionally mature B cells, with human IgM present in the serum of the recipient mice, providing a useful model for evaluation of gene transfer efficiency in human SCID forms affecting B cell development. The feasibility of lentiviralbased HSC gene therapy was also investigated in NOD-SCID mice for mucopolysaccharidosis type VII (MPSVII), a lysosomal storage disease (LSD) caused by β -glucuronidase (GUSB) deficiency.¹⁴⁹ Human GUSB-deficient mobilized peripheral blood CD34+ cells from a patient with MPSVII were transduced with HIV-1-based vectors encoding human GUSB and xenotransplanted in murine recipients that were also GUSB-deficient. Approximately 10% of cells expressed the defective protein and the corrected cells distributed throughout recipient tissues, resulting in therapeutic improvement of the disease phenotype and indication of potential clinical value.

Preclinical evaluation of lentiviral vectors using large animals models: Demonstration of the utility of HIV-1-based lentiviral vectors to transduce hematopoietic cells with long-term repopulating potential was initially met with limited success in rhesus macaques^{150,151} and baboons.¹⁵² These Old World monkeys were found to possess cellular antiviral factors, including tripartite motif-containing 5 isoform- α (TRIM5 α) and apolipoprotein B mRNA-editing catalytic polypeptide 3G (APOBEC3G), responsible for the observed resistance to HIV-1 infection. In contrast, HIV-1-based lentiviral vectors could mediate efficient gene transfer to long-term repopulating cells in the canine¹⁵³ and pigtailed macaque models.¹⁵⁴ The TRIM5 α -mediated restriction to HIV-1 infection in rhesus macaques was alleviated by the use of an alternative lentiviral vector based on the simian immunodeficiency virus (SIV).^{155–159} Modification of HIV-1-based vectors by introduction of mutations in the cyclophilin A (CypA) binding site^{160,161} or by substituting SIV capsid and SIV viral infectivity factor (Vif) in HIV-1 vectors were shown to escape TRIM5 α resistance, resulting in superior in vivo marking levels (up to 30%) in all blood lineages in rhesus macaques 3 to 7 months post-infusion.¹⁶² Thus, rhesus macaques provide a unique model for preclinical testing of lentiviral vectors intended for clinical applications, as recently shown with a lentiviral vector (TNS9) based on HIV-1 encoding the human β -globin gene flanked by regulatory sequences.¹⁶³

Only rare human disease phenotypes that can be targeted by gene therapy of HSCs have been recapitulated in large animal models (reviewed in Bauer et al.¹⁶⁴). Gene therapy has been investigated in a canine model of Glanzmann thrombasthenia (GT), a platelet adhesion and aggregation disorder resulting from a defect in one of two glycoproteins (GPs), GPIIb or GPIIIa, and leading to bleeding episodes involving mucosal membranes.¹⁶⁵ Autologous canine GT CD34+ cells were collected, transduced using a SIN lentiviral vector carrying a human GPIIb promoter driving the canine GPIIb cDNA, and reinfused into the affected animals after non-myeloablative conditioning. Long-term follow-up revealed expression of the GPIIb/GPIIIa heterodimers in 10% of circulating platelets, buccal bleeding was reduced, and animals were less susceptible to bruising.¹⁶⁶ Gamma-retroviral vectors were investigated for in vivo and ex vivo gene therapy of canine X-SCID¹⁶⁷ and leukocyte adhesion deficiency (CLAD),¹⁶⁸ respectively, and a foamy virus-based vector has been used to phenotypically correct CD18 integrin deficiency in a canine model of LAD¹⁶⁹, but no other reports of preclinical testing of lentiviral vectors in large animal disease models are available.

Preclinical evaluation of lentiviral vectors using standard murine transplantation

models: Despite the lack of predictability of standard murine transplantation studies for evaluation of gene transfer into human HSCs, mouse disease models developed by gene targeting or arising from spontaneous gene mutations may represent the only available option for preclinical testing of the impact of gene transfer vectors on disease phenotype; large animal disease models do not exist for most disorders treated by gene therapy, and for a number of orphan diseases that are common targets of gene transfer protocols, it is impractical to obtain biospecimens from a large cohort of patients to perform preclinical murine xenotransplant efficacy studies.

A large number of investigations using murine disease models as surrogates in gene therapy preclinical studies have shown partial or complete correction of the underlying abnormal phenotype and thus have encouraged in some cases instigation of new clinical trials. All disorders with active HSC gene therapy clinical trials have employed murine models of human diseases to evaluate efficacy of lentiviral vectors for correction of disease phenotype, including ALD,¹⁴² WAS,^{170–175} β -thalassemia,^{176–179} SCID,^{180–184} and CGD.¹⁸⁵ Human gene therapy trials employing lentiviral vectors are currently underway for ALD, β -thalassemia and WAS. However, in several cases, these murine homologues were limited as translational models by the fact that mutations in the affected gene do not faithfully reflect the clinical manifestations of such mutations in humans. For instance, because the ALD mice do not develop cerebral demyelination,¹⁸⁶ the neuropathological and clinical effects of lentiviral gene transfer could not be assessed in this model. Also, expression of human proteins in a murine disease model may not provide optimal correction of the human disease characteristics. This is illustrated in β -thalassemia mouse models using vectors encoding the human β -globin gene; tetramers of human β -globin must form with mouse α -globin, likely underestimating the degree of correction that would be achieved with similar vectors in human cells, where natural tetramers of human α and β globin would be formed.

Optimization of transduction conditions

Cytokine combinations: Various procedures have been refined by different laboratories to optimize retrovirus-mediated transduction in HSCs. A balance must be reached to reconcile the need for cell cycling for productive transduction without impairing the repopulating ability of HSCs. In the mid-1990's, the addition of *fms*-related tyrosine kinase 3 ligand (Flt3L) to the cytokine combination IL3, IL6 and SCF used in original murine studies helped preserve human CD34+ cells to sustain long-term hematopoiesis in the murine xenotransplant model after retroviral-mediated transduction.¹⁸⁷ Subsequently, consistent

with evidence that the early acting hematopoietic growth factor thrombopoietin (TPO) or its truncated homologue, megakaryocyte growth and development factor (MGDF), could better support primitive human hematopoietic cells in vitro,^{188,189} studies in non-human primates showed that IL3 and IL6 could be replaced by MGDF during ex vivo transduction.^{190–192} While the addition of IL3 during transduction was shown to impair the engraftment of murine HSCs cultured ex vivo,^{193,194} this finding was not confirmed in large animal models¹⁹¹ and most groups have thus continued to use IL3 during transduction of human HSCs in clinical applications. The mechanism of action of these early acting cytokines is generally related to their effect on cell cycle status, but they have also been proposed to enhance transduction by down-regulating proteasome activity in HSCs.^{195,196} Overall, the current consensus based on large animal and murine xenograft models favors a transduction step in the presence of an early-acting cytokine cocktail composed of SCF, Flt3L, TPO/MGDF, with the optional addition of IL3.

Use of Fibronectin during transduction: The function of HSCs depends upon the signals from surrounding stromal cells (e.g. fibroblasts, osteoblasts) and extracellular matrix molecules (e.g. fibronectin, FN) found within the highly specialized BM microenvironment. In murine studies, co-culture of the hematopoietic target cells with the fibroblast-derived retroviral producer cells has been shown to be the most efficient gene transfer method. However, this approach is inappropriate for use in human clinical trials because of the risk of co-infusing the producer cells into patients along with the transduced hematopoietic cells.

To expand clinical applicability of murine gene transfer protocols, several investigators showed increased gene transfer in human hematopoietic cells adherent to autologous or allogeneic BM stromal cells using in vitro assays.^{197–199} Similarly, addition of autologous stromal cells during the transduction period promoted gene transfer into HSCs in the rhesus macaque model.²⁰⁰ However, the technical difficulties associated with extensive scale-up and the lack of clear benefit in a gene marking clinical trial have limited widespread clinical application of this approach.⁶⁷ Moritz et al. took a different tactic by transducing human hematopoietic cells cultured in vessels coated with the chemotryptic 35-kd carboxy-terminal fragment of human fibronectin (FN35) and noted enhanced transduction by retroviral vectors.²⁰¹ A recombinant version of this fragment (CH-296), commercially available as Retronectin (Takara Biomedical, Otsu, Japan), was shown to enhance gene transfer in human CD34+ cells by co-localization of the cells with the vector,^{202–204} unless an excess of retroviral particles was used during transduction.²⁰⁵ The colocalization of vectors and target cells can be enhanced using spinoculation, a neologism coined to describe low speed centrifugation used at the start of transduction to augment gene transfer.²⁰⁶ The enhancement effect achieved with FN was also attributed to biological effects on HSCs, such as preservation of repopulating potential,^{203,207–209} and decreased apoptosis.²¹⁰ Extensive pre-clinical studies showed successful gene transfer into murine long-term repopulating HSCs as well as into human and non-human primate CD34+ cells derived from BM, CB or mobilized peripheral blood when transduction was performed in vitro^{210–213} or in vivo²¹³ with retroviral vectors and Retronectin. Correspondingly, in most recent clinical gene therapy trials showing therapeutic benefits, retroviral transduction of human CD34+ cells has been conducted in the presence of human recombinant FN.

Conditioning regimens to enhance in vivo gene marking—Engraftment of HSCs is a competitive process between endogenous and infused stem cells. Conditioning of the patient, traditionally achieved by delivering chemotherapy agents with or without radiation before cell infusion, damages or destroys endogenous stem cells and thus provides a competitive advantage to the infused HSCs. This is of particular interest to enhance engraftment of low numbers of genetically marked HSCs in gene therapy applications. In preclinical models^{190,200} and in patients with malignancies,^{60,66,67} myeloablative regimens

have been used routinely to enable engraftment of gene-modified primitive hematopoietic cells. However, many of the diseases that could be targeted by gene therapy are chronic, indolent disorders in which the risks of myeloablative regimens may outweigh the potential benefits.

Reduced intensity (non-myeloablative) conditioning regimens were tested in preclinical models to assess engraftment of marked HSCs while reducing transplant-related toxicities. Retrovirally modified hematopoietic cells have been detected at low levels (<1%) in hematologically normal mice even with no myeloablation but infusion of extraordinarily high cell doses obtained from multiple syngeneic donors, impossible to achieve in large animals or humans, was required.²¹⁴ Moderate-dose irradiation or antimetabolite-based non-myeloablative conditioning allowed correction of the CGD phenotype in knockout mice receiving cells transduced with a retroviral vector containing a normal copy of the defective gene.^{48,215–218} Similarly, improved immune reconstitution was detected in a mouse model of X-SCID by applying mild conditioning prior to infusion of genetically corrected BM cells.²¹⁹ Alternative conditioning strategies to promote engraftment of infused HSCs with increased safety have been investigated in mice and are of potential relevance for gene therapy applications. For instance, administration of an antibody that blocks c-kit, the receptor for SCF, transiently reduced endogenous murine HSCs, facilitating engraftment with donor HSCs in immunodeficient Rag2^{-/-}/γc^{-/-} mice but not in immunocompetent mice.²²⁰ Combination of this antibody with low-dose irradiation profoundly decreased endogenous repopulating activity, enabling efficient and durable engraftment of fresh or lentivirus-transduced BM cells in wild-type and CGD mice.²²¹ In another study, HSC mobilization with AMD3100, a CXCR4 antagonist with a favorable safety profile in clinical studies, was shown to vacate niches in the mouse BM microenvironment and thus could be used in this model as a preparative regimen for HSC transplantation.²²²

In large animal models, no engraftment with corrected cells has been observed without conditioning, except for rare detectable neomycin-resistant (Neo^R) marrow CFU-GM in dogs receiving cells transduced over a 3-week period in a long-term culture system.²²³ In one study, 12% gene marked leukocytes persisted in the peripheral blood of a rhesus macaque up to 33 weeks after low dose non-myeloablative total body irradiation.²²⁴ In other studies, autologous transplantation of either γ-retrovirus- or lentivirus-transduced HSCs in non-human primates conditioned with low-dose irradiation or busulfan have generally resulted in low but measurable (~1%) long-term marking,^{158,225–227} providing proof-of-principle that partial marrow cytoablation allowed engraftment of gene-modified cells without significant toxicity. A possible concern is the unexpected finding that in partially ablated recipient mice, in which the BM is a more competitive environment for repopulation compared to the fully ablated marrow, HSCs carrying survival- or proliferation-activating lentiviral insertions had an advantage for engraftment, perhaps increasing the risk of leukemic progression.²²⁸

Initial gene therapy efforts using HSCs for non-malignant disorders did not administer preparative regimens to avoid potential toxicities from chemotherapy agents when benefits of the procedure were unproven (Table 1-First generation HSC gene therapy clinical trials).^{72,74,76} It was hypothesized that the low marking levels achieved in HSCs in these trials could only lead to clinical benefits if the cells derived from the transduced HSCs had a biological selective advantage in vivo. Modeling conditioning protocols developed in preclinical assays, subsequent gene therapy trials for ADA-SCID,^{229–233} X-CGD,^{234–236} WAS,¹⁴³ and β-thalassemia⁴² introduced partial myeloablation with busulfan or melphalan prior to infusion of the genetically corrected cells (Table 1). As outlined below, in most cases, successes were detected after non-myeloablative conditioning when augmented by a recognized biological selection for successfully treated cells in vivo or by retroviral-

mediated clonal expansion. As predicted by preclinical studies, it appears that reduced intensity regimens employed to date for disorders that lack a biological selective advantage in gene-corrected cells, such as CGD, may be insufficient to mediate substantial HSC engraftment and that more ablative approaches may be necessary. The recent clinical success achieved in X-linked ALD using a conventional myeloablative conditioning (cyclophosphamide 200mg/Kg and busulfan 16mg/Kg) is a useful example of a relatively non-toxic regimen that resulted in clinically relevant levels of HSC marking (10–15%) and long-term myeloid engraftment in the absence of a selective advantage (Table 1).¹⁴²

Optimized gene therapy protocols—The preclinical studies above (Figure 1, upper left panel), augmented by the clinical experience of the early gene therapy efforts, have led to an optimized protocol for ex vivo manipulation of HSCs that has been employed with success in recent clinical trials (Figure 1, lower panel).^{237,238} Hematopoietic stem and progenitor cells expressing the CD34 cell surface marker are purified from BM harvests or granulocyte-colony stimulating factor (G-CSF)-mobilized peripheral blood cell (MPBC) collections. Following a brief (~24 hours) ex vivo culture in conditions that favor cell cycle transition from G₀ to G₁ (e.g. X-vivo medium supplemented with SCF, Flt3L, TPO/MGDF +/- IL3), the CD34+ cells are incubated on a surface coated with the C-terminal fragment of FN in the presence of the same cytokines for an additional 72 hours with MLV-based vectors or for an additional 24 hours with VSV-G-pseudotyped SIN HIV-1-based vectors expressing the desired therapeutic gene from an internal promoter. As discussed below, the increased incidence of genotoxicity in patients transplanted with cells transduced with standard MLV-based vectors has led investigators and regulators to abandon their use in further HSC gene therapy applications.²³⁹ For disorders in which corrected cells do not have a competitive repopulating advantage over uncorrected endogenous HSCs and their progeny, the patient is conditioned with a reduced intensity (e.g. Busulfan 2–10mg/Kg) or a fully ablative regimen (e.g. busulfan 16 mg/kg and cyclophosphamide 200 mg/kg), prior to intravenous reinfusion of the treated cells. After autologous transplantation, transduced cells home to the BM where they initiate hematopoiesis. Transduction efficiency and safety of the procedure are evaluated by periodic collection of peripheral blood samples over extended periods of time.

Clinical benefits in gene therapy trials using protocols optimized in preclinical studies

The advances derived from preclinical models were rapidly applied in a second generation of clinical trials, with actual therapeutic intent, for immunodeficiency disorders, including X-SCID,^{240–245} ADA-SCID,^{229–231,233} CGD,^{236,246} and WAS^{143,247} (Figure 2, Table 1). Third generation HSC gene therapy trials have recently emerged, pioneering the use of SIN-lentiviral vectors for correction of ALD¹⁴² and β -thalassemia⁴² (Figure 2, Table 1).

Second generation HSC gene therapy clinical trials

Severe combined immunodeficiency disease: The first HSC gene therapy trial demonstrating unequivocal clinical benefit was led by Fischer and Cavazzana-Calvo at the Necker Hospital in France^{240,243,244}. Ten boys with X-SCID were treated, and each patient received autologous CD34+ BM cells, transduced with a γ -retroviral vector expressing the corrective IL2R γ gene and reinfused without conditioning. Rapid functional B and T cell immune reconstitution was observed in all but one child. The same vector insertion site could be detected in both myeloid and lymphoid cells, suggesting that at least some true HSCs had been corrected. Unfortunately, the elation after this success was short-lived; four subjects in the trial developed acute T cell leukemia^{248–250}. The gene therapy vector had inserted near the locus for *LMO2*, *CCND* or *BMI1* resulting in increased expression of these proto-oncogenes through the vector's enhancer activity. Chemotherapy led to sustained remission in 3 of the 4 cases of T-lineage acute lymphoblastic leukemia (T-ALL), but failed in the fourth. Patients that were successfully treated with chemotherapy continued to benefit

from therapeutic gene transfer as a result of restoration of polyclonal transduced T cell populations after chemotherapy.

A similar gene therapy trial was also conducted in London on ten children with X-SCID. All patients experienced substantial immunological recovery and in most patients this was accompanied by recovery of humoral immunity and withdrawal of immunoglobulin therapy^{232,242,251}. Similar to the first clinical study of gene therapy for X-SCID, a single insertion 35 kb upstream of the transcription start site caused substantial overexpression of *LMO2* and neighboring genes in one of ten patients²⁵². Leukemogenesis was thought to have been precipitated by the acquisition of other genetic abnormalities, including a gain-of-function mutation in *NOTCH1*, deletion of the tumor suppressor gene locus *CDKN2A*, and translocation of the TCR- β region to the *STIL-TAL1* locus. These data indicated that conventional murine γ -retroviral vectors (based on MLV) present a high risk of leukemogenesis as a result of their powerful enhancer sequences in the intact LTR regions. While gene therapy has been effective in infants with X-SCID, minimal clinical improvement was detected in 2 of 3 pre-adolescents despite effective transduction and engraftment of G-CSF mobilized CD34+ cells²⁴¹, and complete failure of gene therapy in two adult patients was reported after transplantation of transduced BM CD34+ cells²⁴⁵.

Bordignon's and Thrasher's group also reported sustained engraftment of engineered HSCs and good immune reconstitution in patients with SCID resulting from ADA enzyme deficiency following transplantation of BM-derived transduced CD34+ cells^{230,233,253}. No cases of leukemia have been reported to date in these trials consistent with the long-term analysis of integration sites revealing a polyclonal pattern along with a lack of *in vivo* skewing for risky insertions.

Chronic granulomatous disease: In an attempt to genetically correct the defect in CGD patients, Manuel Grez and collaborators in Switzerland obtained G-CSF-mobilized CD34+ cells from two CGD patients and, using a vector similar to that used in the X-SCID trials, inserted a corrective copy of one gp91^{phox} gene needed to make a functional NADPH oxidase²³⁶. Unlike other CGD trials,^{76,234,235} three weeks after the cells were reinfused into the patients, a surprisingly large fraction of circulating myeloid cells, more than 20%, carried the corrective gene. This sustained engraftment of functionally corrected cells with therapeutically relevant levels of NADPH oxidase was unexpectedly followed by further *in vivo* expansion of cell clones containing insertionally activated growth-promoting genes, including *MDS1-EVII*, *PRDM16* or *SETBP1*. These activating insertions facilitated expansion of the gene-corrected clones in both individuals, with up to 60% of their white blood cells containing the corrective gene by a year after transplantation. However, a progressive decline in blood counts was observed in both CGD patients at 15 and 28 months, respectively, after gene therapy.^{239,246} BM examination was consistent with a myelodysplastic syndrome (MDS). Recent evidence suggests that overexpression of *EVII* could have been an initiating event that then resulted in chromosomal instability, stimulating further chromosomal abnormalities, such as loss of chromosome 7, and progression to MDS^{239,246}. Despite the persistent high frequency of vector-corrected neutrophils, expression of NADPH oxidase dropped precipitously in both subjects over time. The silencing of NADPH oxidase occurred through progressive CpG methylation of the promoter contained in the long terminal repeat (LTR) of the vector, a region important for transgene expression. These events led to a series of infections and eventual death of one patient. The second subject was referred for unrelated donor stem cell transplantation while still infection free.

Wiskott-Aldrich syndrome: A German group has recently reported long-term (up to 5 years) correction of WAS in 9 of 10 patients through γ -retroviral infection of G-CSF

mobilized CD34+ cells transfused after busulfan-induced transient myelosuppression, as evidenced by a decreased frequency and severity of infections, and resolution of signs and symptoms of autoimmunity, including autoimmune hemolytic anemia, thrombocytopenia, neutropenia and eczema.^{143,247} However, in an initial report, 2 of 9 patients that achieved an efficient correction of the disease developed T-ALL 5 years and 16 months after gene therapy, respectively. Two additional patients also developed T-ALL more recently (unpublished data). In 3 of 4 patients with T-ALL analyzed to date, an increase of a cell clone harboring an integration site upstream of LMO2 could be observed at the onset of leukemia, the same gene locus activated by vector insertion in most of the X-SCID patients that developed T-ALL. One patient underwent an allogeneic stem cell transplant and the other individuals have responded to chemotherapy with recovery of a polyclonal integration site pattern.

Third generation gene therapy clinical trials

Adrenoleukodystrophy: A third generation of clinical trials have been designed, supported by preclinical data suggesting that HIV-derived lentiviral vectors may be safer and more efficient for transduction of HSCs than vectors based on γ -retroviral vectors^{113,125,154,156,254–257}. The first use of a lentiviral vector for HSC gene therapy was reported for the treatment of two children with X-linked ALD¹⁴². This is also the first study using a conventional myeloablative conditioning regimen before reinfusion of the genetically manipulated G-CSF mobilized CD34+ cells. Functional myelomonocytic cells derived from corrected CD34+ cells migrated into the patient's central nervous system to replace diseased microglia cells. At 24 and 30 months post-transplantation, both patients had highly polyclonal reconstitution of hematopoiesis and normal levels of ALD protein, which appeared to retard the progressive cerebral demyelination process. No evidence of genotoxicity has yet been reported in this trial.

β -thalassemia: Cavazzana-Calvo and colleagues⁴² have recently provided another example of the clinical potential of gene therapy using lentiviral vectors by treating an 18-year-old male patient suffering from transfusion-dependent β^E/β^0 -thalassemia. CD34+ cells were isolated from the individual's BM and transduced with an HIV-derived lentiviral vector containing a functional β -globin gene. Compared to previous trials, a conditioning regimen with higher doses of busulfan (12.8 mg/kg) was used in this study. The levels of genetically modified cells gradually rose up to 11% at 33 months post-transplant with concomitant increases in levels of the normal β -globin protein and improved production and quality of normal RBCs. Remarkably, a year after treatment, the patient no longer needed RBC transfusions. This therapeutic benefit, however, was observed in the setting of clonal expansion resulting from integration of lentiviral vectors in the high mobility group AT-hook 2 (HMGA2) gene²⁵⁸. Marked expansion of a single corrected clone, persisting without malignant transformation for many years, has been documented in an early ADA-SCID gene therapy trial,²⁵⁹ suggesting that clonal expansion does not irrevocably progress to malignancy, but the known association between HMGA2 overexpression and benign/malignant neoplasias imposes further caution.^{258,260,261}

EVALUATION OF INSERTIONAL GENOTOXICITY USING MOUSE MODELS

MLV-based retroviral vectors pose a high risk of insertional mutagenesis

Studies performed prior to the availability of the human and murine genome sequences and without high-throughput sequencing methodologies suggested the paradigm that retroviral integration was random, and that insertional mutagenesis was thus likely to be an exceedingly rare event in the absence of replication competent vectors.²⁶² Given the powerful tumor induction models reported by mouse geneticists and cancer biologists, who

injected replication-competent MLV viruses into neonatal mice to produce hematopoietic tumors at a high rate, allowing identification of novel proto-oncogenes,^{263,264} it seems surprising that the issue of insertional mutagenesis was not further seriously considered until the first child enrolled in the X-SCID gene therapy trial developed leukemia in 2003. This paradigm was so pervasive that a paper reporting what in retrospect was clearly a murine myeloid leukemia resulting from a single insertion activating the EVI1 locus with a replication-incompetent MLV vector instead attempted to link the leukemia to aberrant signaling from the truncated nerve growth factor receptor (NGFR) marker gene.²⁶⁵ Another paper suggesting that the multidrug resistance gene 1 (MDR1) could be oncogenic, due to a high rate of leukemia in mice transplanted with cells transduced with MDR1 versus control Neo^R vectors, can also be reinterpreted in retrospect as almost certainly representing insertional genotoxicity, given the very high titer and vector copy number associated with a novel Harvey sarcoma virus vector carrying the MDR1 transgene, compared to a standard MLV control Neo^R vector.²⁶⁶

Standard murine transplantation models: poor predictors of insertional genotoxicity

Standard murine gene transfer experiments, as performed for twenty years, do not provide robust information on genotoxicity, for a number of reasons. The accepted time point of analysis to document successful HSC gene transfer is only 4–6 months, far shorter than time to induction of murine tumors via insertional mutagenesis and the clinical experience with such tumors, given the multistep nature of their pathogenesis. Mice receive ablative irradiation in most studies, and have such a high rate of radiation-induced tumors that longer term follow-up is challenging, even when a study is designed to monitor insertional mutagenesis.²⁶⁷ A survey of the literature and unpublished studies completed following the 2003 reports of human leukemias in the X-SCID trial confirmed lack of follow-up of longer than a few months in the vast majority of murine studies.²⁶⁸

Most studies utilize the equivalent of one million starting nucleated marrow cells (i.e. ~50 HSCs) to transduce and then transplant per recipient mouse. Ex vivo transduction conditions result in gene transfer efficiencies of less than 50% even in progenitors and in loss of at least 75% repopulating activity, compared to fresh marrow.⁸⁵ In addition, relatively low-titer vector was used to transduce murine HSCs, resulting in vector copy number per transduced cell of only 1–2. The net result of these factors is transplantation of each mouse with very few transduced HSCs, and thus very limited numbers of insertions to follow for genotoxicity long-term. Early clonal tracking studies utilizing Southern blot documented oligoclonal patterns of contribution from vector-containing cells.¹⁰ Even more modern studies, utilizing ligation-mediated PCR (LM-PCR) to retrieve vector insertions and improved transduction conditions, generally only catalog 2–5 insertions per mouse.^{269,270} Therefore, even cohorts of 10 or more mice per experimental group interrogate less than 100 viral insertions, far fewer than the thousands of insertions documented in the X-SCID and other trials.^{251,271}

Preclinical models to assess the risks of insertional mutagenesis

The high rate of leukemia induction first in the X-SCID clinical trial, followed by similar issues in trials for CGD and WAS, accelerated the paradigm shift towards the realization that all integrating vectors have a risk for insertional oncogenesis, and a focus on the development of predictive models to prevent further unexpected complications in human clinical trials of HSC gene therapy.^{246,249,252,257} The availability of complete sequences for human, murine and other model organism genomes, and the development of PCR and high-throughput sequencing methodologies for insertion site retrieval from highly complex and polyclonal samples have concurrently permitted a much deeper understanding of the integration patterns and biases inherent to different vector classes and target cells. Over the

past decade, many investigators and regulators have thus focused on the development of predictive models of insertional mutagenesis.

In vitro immortalization assays—The quickest, simplest and most quantitative models have utilized murine cells in vitro to document behavior consistent with malignant transformation. Factor-dependent immortalized myeloid cell lines such as 32D convert to cytokine-independence as a result of insertional events.²⁷² Primary murine BM cells transduced with vectors at a high MOI become immortalized at a low rate, and this process can be semi-quantitated, allowing comparisons between different vector backbones.^{273,274} Both assays monitor only myeloid transformation events, and are skewed very markedly towards a few genes in each assay, those involved in cytokine signaling pathways in the first instance, and EVI1 or genes that upregulate EVI1 in the second. The relevance to human cell immortalization and transformation is not clear, given the inability to create factor-dependent similar human myeloid cell lines, or immortalize human cells via similar approaches or assays.

Murine transplantation assays

Optimization of insertional load using improved transduction and transplantation conditions: Based on the drawbacks of the standard murine transplantation assays detailed above, a number of investigators have attempted to improve their relevance, reproducibility, and speed. Transduction of murine HSCs in the presence of improved cytokine combinations and Retronectin support and using concentrated vector supernatants has increased gene transfer efficiency and vector copy number per cell, and likely maintained a higher number of HSCs during culture and transduction, resulting in a much higher “insertional load” per recipient mouse. Animals are followed longer and secondary transplants further extend follow-up and provide additional selective pressure to help identify dominant or eventually leukemic clones.

A series of landmark papers from Baum’s group reported important insights into vector safety and hematopoiesis, using serial transplantation to enhance detection.^{269,275,276} Only a relatively small number of clonal insertions leading to dominance or leukemia could be studied, 29 in the initial paper, expanded to 276 via combining information from a number of laboratories. Twenty two percent overlapped with cancer genes identified using retroviral insertional mutagenesis by Copeland and coworkers (the RTCGD database²⁷⁷), and both EVI1 as well as LMO2, the two loci linked to leukemias most frequently in the human gene therapy clinical trials, were detected in these murine transplantation assays. The RTCGD database had already been shown to predict genes dysregulated in spontaneous human AML.²⁷⁸

Tumor-prone mouse models: In order to speed the detection process and have a readout directly linked to cancer, instead of simply clonal dominance, several groups have utilized murine “tumor-prone” models. The Cdkn2a gene product is a tumor suppressor and has a central role in controlling hematopoietic cell senescence and preventing transformation. It is inactivated in a large fraction of human cancers, including leukemias, and was a secondary event, preceding full leukemic transformation, in at least two of the X-SCID leukemias. All mice transplanted with Cdkn2a^{-/-} marrow develop both lymphoid and myeloid leukemias relatively rapidly. Elegant studies from Naldini’s group have utilized this model to study the impact of transducing Cdkn2a^{-/-} marrow with various vectors on latency of leukemia development and tumor type.^{279,280} The model reads out both myeloid and lymphoid tumors, and the total number of integrations administered and the vector copy number per cell are relevant. The relative risk for leukemia induction could be compared, and MLV vectors with an intact LTR were found to be most potent in shortening latency, followed by

lentiviral vectors with an MLV enhancer inserted into their LTR regions. Lentiviral vectors with an internal enhancer/promoter, even a very strong one such as an MLV LTR, were not active in enhancing leukemia induction in this model, and MLV vectors with deletion of the LTR enhancer (SIN design) or lentiviral vectors with an internal non-viral promoter were also no different than mock-transduced cells in leukemia induction. These studies could be carried out in less than a year and with practical mouse cohort sizes of 15–30. That the results from these studies are predictive of genotoxicity in more relevant clinical situations is supported by the lack of clonal dominance and known “dangerous clones” such as EVI1 and LMO2 when comparing standard MLV insertions to LV insertions, even with the presence of a strong viral internal promoter, in both rhesus macaque long-term follow-up studies and human clinical trials.^{142,156,281–283}

Large animal models—Large animal models have provided important information validating the murine models, uniquely provided very long-term follow-up of a much larger number of insertions than have been followed in mice, and uncovered risks associated with specific transgenes or integration sites that were not apparent from the murine models. Soon after the report of T-ALL linked to vector integration in the X-SCID trial, there was intense consternation and attempts by investigators to blame the adverse events on the IL2R γ transgene or the underlying patient population, instead of integration events alone.^{284,285} The initial combined data regarding primate and dog HSC gene marking studies was reassuring, with all animals remaining polyclonal and healthy in our initial report, however, few animals in this cohort had high level marking, and actual insertion sites were not identified.²⁸⁶ Therefore it was a shock to us and an alarm for regulators and clinicians when we observed the development of an acute myeloid clonal vector-linked leukemia in a rhesus macaque 5 years following transplantation, with a vector containing only marker genes.²⁸⁷ The insertion site was in the Bcl2A1 gene, encoding an anti-apoptotic protein. We and others then rapidly completed surveys of large numbers of insertions in monkeys and dogs, providing the first evidence in primary cells for a number of very important principles, including a pattern of integrations favoring expressed genes with both MLV- and lentivirus-based vectors, and transcription start sites for MLV-based vectors,²⁸³ and marked over-representation of integrations in specific proto-oncogenes such as EVI1, MDS1, HDAC7 and others, in a manner suggesting *in vivo* selection.^{282,288} The identification of EVI1/MDS1 as a particularly worrisome locus was prescient, as the CGD trial adverse events demonstrated a few years later.²⁴⁶ Novel vectors were reported as having much less concerning integration patterns in large animal models, including human foamy virus²⁸⁹ and avian leucosis sarcoma virus.²⁹⁰

Kiem and coworkers have demonstrated the unique importance of large animals in their report of the consequences of inclusion of homeobox B4 (HOXB4) in gene transfer vectors. Years of research in the murine model suggested that HOXB4 overexpression from a retrovirus vector could facilitate a benign and still homeostatically-controlled expansion of HSCs, with many potential clinical applications in gene therapy and stem cell transplantation.²⁹¹ However, Kiem first showed that the impact on large animal HSCs was much less pronounced than in rodents in terms of long-term repopulating stem cell expansion,²⁹² and then reported that two of two dogs and one of two rhesus macaques transplanted with CD34+ cells transduced with a HOXB4 retrovirus vector developed acute leukemias within two years of transplantation, and more recently have shown that other rhesus macaques developed a myelodysplasia-like syndrome.^{293,294} These findings have convinced the community that any approach utilizing HOXB4 in a gene transfer vector is not safe for clinical applications.

Approach to evaluate the risks of insertional genotoxicity

We believe the most practical, prudent and informative approach to the investigation of relative genotoxicity of gene transfer vectors would involve initial screening utilizing the in vitro immortalization assays, testing of a subset of candidate vectors in optimized murine transplant models or, preferably, in the murine tumor-prone models, followed by testing of promising novel vectors in long-term primate or canine transplantation studies, allowing retrieval of a large panel of insertions and very long-term follow-up. Large animals are not practical for screening of new vectors, and in contrast to gene transfer efficiency predictions, more modern rodent models have proven useful and overall predictive for genotoxicity (Figure 1, top right panel).

CONCLUSIONS AND FUTURE DIRECTIONS

In the hierarchy of laboratory animal species, the mouse rules and has become a central tool of biomedical research. However, the efficiency of gene transfer into human HSCs is poorly predicted by gene transfer studies in mouse HSCs and conventional murine transplant models have fallen short of predicting the risks of insertional mutagenesis. Instead, more modern mouse transplantation assays, namely the xenotransplant and tumor-prone mouse models, together with large animal systems have provided the essential preclinical platform for advancing approaches to improve the efficacy and safety of gene transfer into human HSCs that have underpinned the recent successful clinical applications.

The influence of modern mouse transplant assays and large animal models on approaches to gene therapy is likely to continue growing as new prospects in HSC engineering are being developed. Current preclinical studies are evaluating gene transfer vectors containing a suicide gene, such as the human-derived dimerizable caspase-9 gene,^{295,296} which would allow ablation of the vector-containing cells in the event of an adverse outcome. Approaches are also being developed to restrict expression of a transgene to a given target cell population, either by modification of the vector envelope to restrict tropism (transductional targeting) or by insertion of a tissue-specific promoter upstream of the therapeutic transgene (transcriptional targeting; reviewed in Frecha C. et al.²⁹⁷). Another promising methodology in gene therapy is the targeting of transgene delivery to a predetermined chromosomal location or the repair of a mutated locus using homologous recombination (HR). Maximization of HR efficiency is a sine qua non goal to achieve clinical relevance, and various techniques have been explored, including the transient expression of an endonuclease, which can be directed to a specific sequence using modular zinc finger proteins,²⁹⁸ homing endonucleases,²⁹⁹ or transcription activator-like effectors (TALEs).³⁰⁰ Xenograft mouse models and large animal studies will be required to assess off-target genotoxicity and efficiency of long-term HSC correction using these methodologies. Finally, the advent of patient-specific induced pluripotent stem cells (iPSCs) may offer a new avenue to generate and select genetically corrected hematopoietic cells, as well as to perform extensive efficacy and biosafety testing in the selected clonal derivatives using murine xenograft and large animal models. The inability to efficiently generate hematopoietic progenitors from iPSCs has limited this approach but recent progress in directly reprogramming somatic cells to a multipotent progenitor via introduction of a single transcription factor (Oct-4), may provide an alternative cell type with therapeutic potential in gene therapy applications.³⁰¹

We anticipate that the trend established over the past decade will continue as investigators hoping to use these novel technologies to treat humans will need to provide substantial safety and efficacy data in a variety of comparative murine and large animal assays before returning to the clinic.

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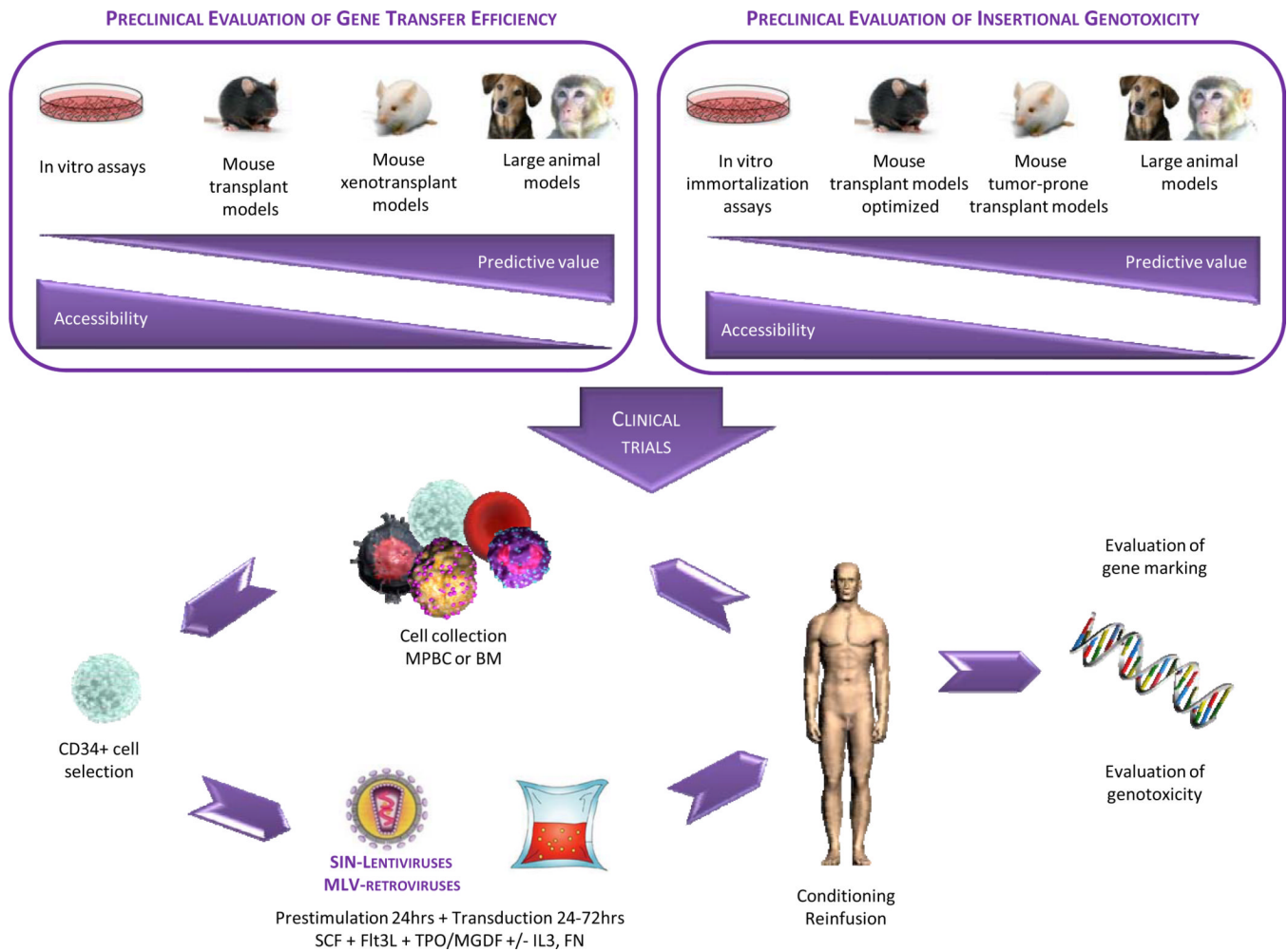


Figure 1. Approach for the genetic manipulation of hematopoietic stem cells (HSCs)

The upper panel compares the predictive value and accessibility of various preclinical models in the evaluation of gene transfer efficiency and insertional genotoxicity of vectors used in HSC gene therapy trials. The lower panel depicts the optimized protocol for transduction of hematopoietic stem and progenitor cells, as used in recent clinical trials. BM (bone marrow); Flt3L (*flms*-related tyrosine kinase 3 ligand); FN (fibronectin); IL3 (interleukin 3); MGDF (megakaryocyte growth and development factor); MLV (murine leukemia virus); MPBC (mobilized peripheral blood cells); SCF (stem cell factor); SIN (self-inactivating); TPO (thrombopoietin)

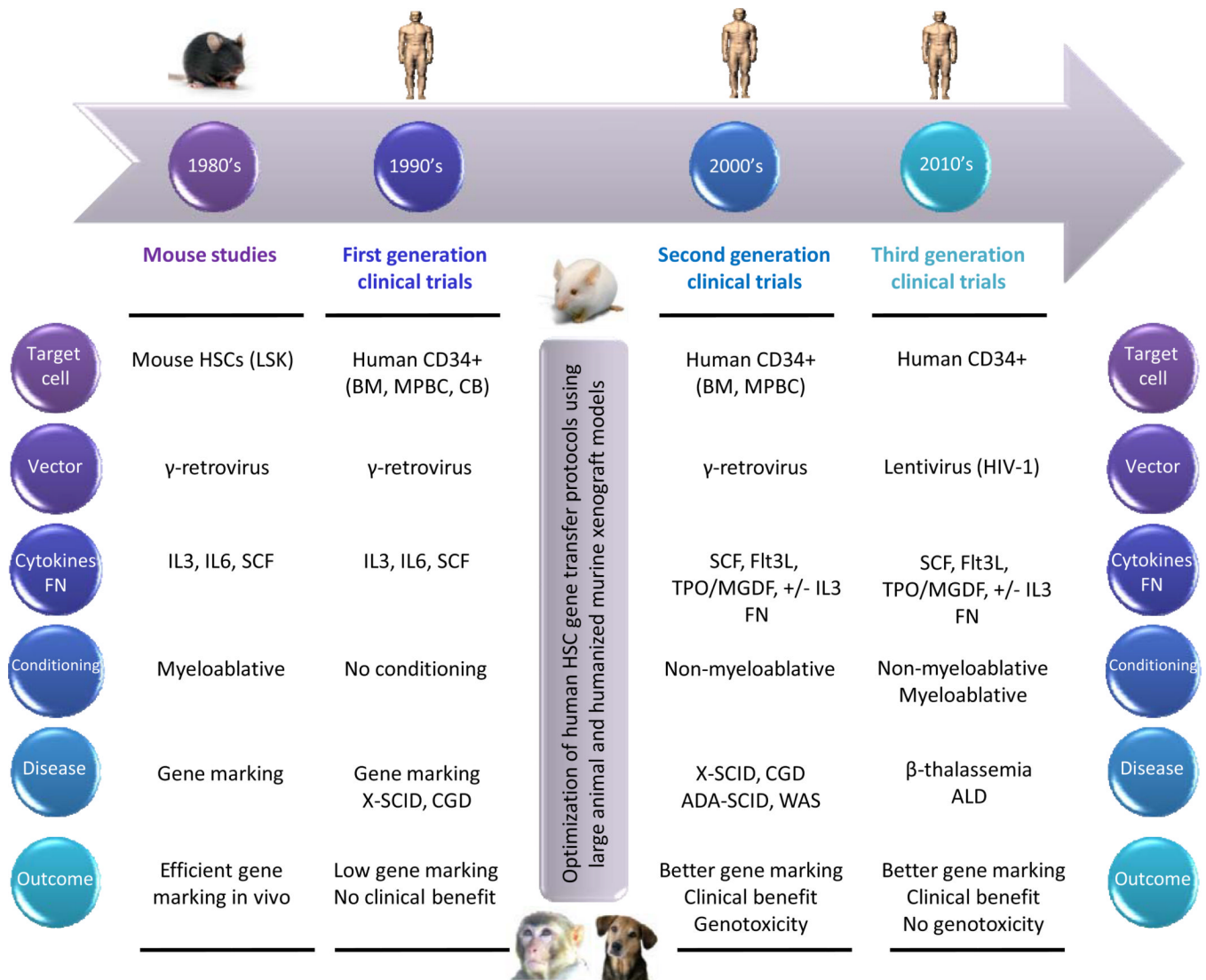


Figure 2. Timeline for the development of human gene therapy protocols targeting hematopoietic stem cells (HSCs)

The main phases in the evolution of HSC gene therapy clinical trials are ordered chronologically. The six principal features defining each phase are outlined.

ADA (adenosine deaminase); ALD (adrenoleukodystrophy); BM (bone marrow); CB (cord blood); CGD (chronic granulomatous disease); Flt3L (*fms*-related tyrosine kinase 3 ligand); FN (fibronectin); HIV (human immunodeficiency virus); IL3 (interleukin 3); IL6 (interleukin 6); LSK (Lin^- , $Sca1^+$, Kit^+); MGDF (megakaryocyte growth and development factor); MPBC (mobilized peripheral blood cells); SCF (stem cell factor); SCID (severe combined immunodeficiency disease); TPO (thrombopoietin); WAS (Wiskott-Aldrich syndrome)

Table 1

First, Second and Third Generation HSC Gene Therapy Clinical Trials

FIRST GENERATION HSC GENE THERAPY CLINICAL TRIALS									
Reference	Indication	Gene	CD34+ cells	Transduction		Vector	Conditioning	Outcome	
				Cytokines and FN	Duration (MOI)			Gene marking (# patients)	Genotoxicity (# patients)
Brenner MK et al. (1993) ⁵⁹	Gene marking (AML)	Neo ^R	BM	No cytokines No FN	P: 0hr T: 6hrs (MOI=10)	γ-RV Ampho env MLV-LTR promoter	Busulfan Cyclophosphamide	Low long-term gene marking	No
Brenner MK et al. (1995) ⁶⁰	Gene marking (AML, neuroblastoma)	Neo ^R	BM	No cytokines No FN	P: 0hr T: 6hrs (MOI=10)	γ-RV Ampho env MLV-LTR promoter	Bu/Cy (AML) Carboplatin/Etoposide (neuroblastoma)	Low long-term gene marking	No
Rill DR et al. (1994) ⁶²	Gene marking (Neuroblastoma)	Neo ^R	BM/MNC	No cytokines No FN	P: 0hr T: 6hrs (MOI=10)	γ-RV Ampho env MLV-LTR promoter	Carboplatin Etoposide	Low long-term gene marking	No
Deisseroth AB et al. (1994) ⁶⁴	Gene marking (CML)	Neo ^R	BM	No cytokines No FN	P: 0hr T: 6hrs (MOI=10)	γ-RV Ampho env MLV-LTR promoter	TBI Cyclophosphamide Etoposide	Low long-term gene marking	No
Dunbar CE et al. (1995) ⁶⁶	Gene marking (MM and BC)	Neo ^R	BM MPBC	IL3, SCF +/- IL6 No FN	P: 0hr T: 72hrs	γ-RV Ampho env MLV-LTR promoter	Melphalan/TBI (MM) or ICE chemotherapy (BC)	Low long-term gene marking	No
Cornetta K et al. (1996) ⁶⁹	Gene marking (AML and ALL)	Neo ^R	BM	No cytokines No FN	P: 0hr T: 4hrs	γ-RV Ampho env MLV-LTR promoter	Busulfan Cyclophosphamide	Low long-term gene marking	No
Emmons RV et al. (1997) ⁸⁷	Gene marking (MM and BC)	Neo ^R	BM MPBC	No cytokines +/- Stroma No FN	P: 0hr T: 6-72hrs	γ-RV Ampho env MLV-LTR promoter	Melphalan/TBI (MM) or ICE chemotherapy (BC)	Low long-term gene marking	No
Bachier CR et al. (1999) ⁶⁸	Gene marking (NHL)	Neo ^R	BM MPBC	No cytokines No FN	P: 0hr T: 6hrs (MOI=10)	γ-RV Ampho env MLV-LTR promoter	TBI Cyclophosphamide Etoposide	Low long-term gene marking	No
Alici E et al. (2007) ⁶⁵	Gene marking (MM)	Neo ^R	BM MPBC	IL3, IL6, SCF, bFGF No FN	P: 0hr T: 12hrs (MOI=5)	γ-RV Ampho env MLV-LTR promoter	Melphalan	Low long-term gene marking	No
Bordignon C et al. (1995) ⁷²	ADA-SCID	ADA	BM	Co-culture No cytokines No FN	P: 0hr T: 72hrs	γ-RV Ampho env MLV-LTR promoter	No conditioning	Low long-term gene marking	No
Kohn DB et al. (1995, 1998) ^{74,302}	ADA-SCID	ADA	CB	IL3, IL6, SCF FN	P: 0hr T: 72hrs	γ-RV Ampho env MLV-LTR promoter	No conditioning	Low long-term gene marking	No

FIRST GENERATION HSC GENE THERAPY CLINICAL TRIALS									
Reference	Indication	Gene	CD34+ cells	Transduction			Conditioning	Outcome	
				Cytokines and FN	Duration (MOI)	Vector		Gene marking (# patients)	Genotoxicity (# patients)
Malech HL et al. (1997) ⁷⁶	CGD		MPBC	PIXY321, G-CSF No FN	P: 18hrs T: 72hrs	γ -RV Ampho env MLV-LTR promoter	No conditioning	Low long-term gene marking	No
Hesdorffer C et al. (1998) ³⁰³	Breast CA Ovarian CA Glioblastoma	MDR1	BM MPBC	IL3, IL6, SCF FN	P: 48hrs T: 24hrs	γ -RV Ampho env MLV-LTR promoter	High dose chemotherapy	Low long-term gene marking	No
Dunbar CE et al. (1998) ⁷⁵	Gaucher	GC	BM MPBC	IL3, IL6, SCF No FN	P: 0hr T: 72hrs	γ -RV Ampho env MLV-LTR promoter	No conditioning	Low long-term gene marking	No
Kohn DB et al. (1999) ³⁰⁴	HIV	RRED	BM	IL3, IL6, SCF +/- FN	P: 0hr T: 72hrs	γ -RV Ampho env MLV-LTR promoter	No conditioning	Low long-term gene marking	No
Cowan KH et al. (1999) ³⁰⁵	Breast CA	MDR1	BM MPBC	IL3, IL6, SCF No FN	P: 0hr T: 72hrs	γ -RV Ampho env MLV-LTR promoter	ICE chemotherapy	Low long-term gene marking	No
Liu JM et al. (1999) ³⁰⁶	FA	FANCC	BM MPBC	IL3, IL6, SCF No FN	P: 0hr T: 72hrs	γ -RV Ampho env MLV-LTR promoter	No conditioning	Low long-term gene marking	No
SECOND GENERATION HSC GENE THERAPY CLINICAL TRIALS									
Reference	Indication	Gene	CD34+ cells	Transduction			Conditioning	Outcome	
				Cytokines and FN	Duration (MOI)	Vector		Gene marking (# patients)	Genotoxicity (# patients)
Cavazzana-Calvo M et al. (2000) ^{240,243,244}	X-SCID	IL2R γ	BM	SCF, Flt3L, MGDF, IL3 FN	P: 24hrs T: 72hrs	γ -RV Ampho env MLV-LTR promoter	No conditioning	Correction of X-SCID (9/10)	T-ALL (4/9) LMO2, CCND2, BMI1 gene insertions ²⁴⁸⁻²⁵⁰
Abonour R et al. (2000) ²¹¹	Germ cell tumors	MDR1	MPBC	SCF, IL6 or SCF, MGDF, G-CSF FN	P: 48hrs T: 48hrs	γ -RV Ampho env HaMSV-LTR promoter	Etoposide 2250mg/m ² Carboplatin 2100 mg/ m ²	Low long-term gene marking (6/11)	No
Aitui A et al. (2002) ²⁵³	ADA-SCID	ADA	BM	SCF, Flt3L, TPO, IL3 FN	P: 24hrs T: 72hrs	γ -RV Ampho env MLV-LTR promoter	Busulfan 4mg/kg	Correction of ADA-SCID (2/2)	No
Amado RG et al. (2004) ^{307,308}	HIV (Phase I)	Anti-HIV1 ribozyme	MPBC	MGDF, SCF +/- FN	P: 18hrs T: 72hrs (MOI=5)	γ -RV Ampho env MLV-LTR promoter	No conditioning	Low long-term gene marking (10/10)	No

FIRST GENERATION HSC GENE THERAPY CLINICAL TRIALS									
Reference	Indication	Gene	CD34+ cells	Transduction			Conditioning	Outcome	
				Cytokines and FN	Duration (MOI)	Vector		Gene marking (# patients)	Genotoxicity (# patients)
Gaspar HB et al. (2004) ^{232,242,251}	X-SCID	IL2R γ	BM	SCF, Flt3L, TPO, IL3, FN	P: 40hrs T: 56hrs	γ -RV GALV env MLV-LTR promoter	No conditioning	Correction of X-SCID (10/10)	T-ALL (1/10) LMO2 gene insertion ²⁵²
Thrasher AJ et al. (2005) ²⁴⁵	X-SCID	IL2R γ	BM	SCF, Flt3L, MGDF, IL3, FN	P: 24hrs T: 72hrs	γ -RV Ampho env MLV-LTR promoter	No conditioning	Failure to correct X-SCID in older patients (2/2)	No
Ott MG et al. (2006) ²³⁶	X-CGD	gp91 ^{phox}	MPBC	SCF, Flt3L, TPO, IL3, FN	P: 36hrs T: 72hrs	γ -RV Ampho env SFV-LTR promoter	Busulfan 8mg/Kg	Correction of X-CGD (2/2)	MDS (2/2) MDS1-EV11, PRDM16, SETBP1 gene insertions ^{235,246}
Gaspar HB et al. (2006) ²³⁵	ADA-SCID	ADA	BM	SCF, Flt3L, TPO, IL3, FN	P: 40hrs T: 56hrs	γ -RV GALV env SFV-LTR promoter	Melphalan 140mg/m ²	Correction of ADA-SCID (1/1)	No
Chinen J et al. (2007) ²⁴¹	X-SCID	IL2R γ	MPBC	SCF, Flt3L, TPO, IL3, FN	P: 16hrs T: 96hrs (MOI=1-2)	γ -RV GALV env MLV-LTR promoter	No conditioning	Clinical improvement (3/3)	No
Mitsuyasu RT et al. (2009) ^{308,309}	HIV (Phase II)	Anti-HIV1 ribozyme	MPBC	MGDF, SCF, FN	P: 36hrs T: 48hrs (MOI=5)	γ -RV Ampho env MLV-LTR promoter	No conditioning	Lower HIV-1 viral load (10/10)	No
Aiuti A et al. (2009) ²³⁰	ADA-SCID	ADA	BM	SCF, Flt3L, TPO, IL3, FN	P: 24hrs T: 72hrs	γ -RV Ampho env MLV-LTR promoter	Busulfan 4mg/Kg	Correction of ADA-SCID (9/10)	No
Boztug K et al. (2010) ^{143,247}	WAS	WAS	MPBC	SCF, Flt3L, TPO, IL3, No FN	P: 48hrs T: 48hrs (MOI=5)	γ -RV GALV env MPSV promoter	Busulfan 8mg/Kg	Correction of WAS (9/10)	T-ALL (4/9) LMO2 +/- other gene insertions ²⁴⁷
Kang EM et al. (2010) ²³⁴	X-CGD	gp91 ^{phox}	MPBC	SCF, Flt3L, TPO, IL3, FN	P: 18hrs T: 96hrs (MOI=2)	γ -RV Ampho env MLV-LTR promoter	Busulfan 10mg/Kg	Long-term clinical benefits (2/3)	No
Kang HJ et al. (2011) ²³⁵	X-CGD	gp91 ^{phox}	MPBC	SCF, Flt3L, TPO, IL3, FN	P: 40hrs T: 40hrs (MOI=1-2)	γ -RV Ampho env MLV-LTR promoter	Fludarabine 120mg/m ² + Busulfan 1.6mg/Kg	Short-term clinical benefit (2/2)	No
Gaspar et al. (2011) ²³¹	ADA-SCID	ADA	BM	SCF, Flt3L, TPO, IL3, FN	P: 40hrs T: 56hrs	γ -RV GALV env SFV-LTR promoter	Melphalan 140mg/Kg or Busulfan 4mg/Kg	Correction ADA-SCID (4/6)	No

THIRD GENERATION HSC GENE THERAPY CLINICAL TRIALS						
Reference	Indication	Gene	CD34+ cells	Transduction	Conditioning	Outcome

FIRST GENERATION HSC GENE THERAPY CLINICAL TRIALS									
Reference	Indication	Gene	CD34+ cells	Transduction		Conditioning	Outcome		
				Cytokines and FN	Duration (MOI)		Vector	Gene marking (# patients)	Genotoxicity (# patients)
Cartier N et al. (2009) ¹⁴²	X-ALD	ABCD1	MPBC	SCF, Flt3L, MGDF, IL3, FN	P: 19hrs T: 17hrs (MOI=25)	Vector	Busulfan 16mg/Kg + Cyclophos 200mg/Kg	Gene marking Genotoxicity	
Cavazzana-Calvo et al. (2010) ⁴²	β -thalassemia	β -globin	BM	SCF, Flt3L, TPO, IL3, FN	P: 34hrs T: 18hrs	SIN-HIV-1 VSV-G env β -globin promoter β -LCR	Busulfex 12.8mg/Kg	Correction of X-ALD (2/2) Correction of β -thalassemia (1/1)	No Clonal dominance (1/1) HMGA2 insertion ⁴²

ADA (adenosine deaminase); ALD (adrenoleukodystrophy); ALL (acute lymphoblastic leukemia); AML (acute myelogenous leukemia); Ampho (amphotropic) BC (breast cancer); bFGF (basic fibroblast growth factor); BM (bone marrow); BMI1 (B lymphoma MLV insertion region 1 homolog); Bu (busulfan); CB (cord blood); CCND2 (cyclin D2); CGD (chronic granulomatous disease); CA (cancer); CML (chronic myelogenous leukemia); Cy (cyclophosphamide); Env (envelope); EVII (ecotropic virus integration site 1 protein homolog); FA (Fanconi anemia); FANCC (Fanconi anemia complementation group C); Flt3L (*fltns*-related tyrosine kinase 3 ligand); FN (fibronectin); GALV (gibbon-ape-leukemia-virus); GC (glucocerebrosidase); G-CSF (granulocyte-colony stimulating factor); HaMSV (Harvey murine sarcoma virus); HIV (human immunodeficiency virus); HMGA2 (high mobility group AT-hook 2); ICE (ifosfamide, carboxiplatin, etoposide); IL2R γ (interleukin 2 receptor γ chain); ABCD1 (ATP binding cassette subfamily D, member 1); IL-3 (interleukin 3); IL-6 (interleukin 6); LCR (locus control region); LMO2 (LIM domain only 2); LTR (long-terminal repeat); MDR1 (multidrug resistance gene 1); MDS (myelodysplastic syndrome); MGDF (megakaryocyte growth and development factor); MLV (murine leukemia virus); MM (multiple myeloma); MNC (mononuclear cells); MND (myeloproliferative sarcoma virus enhancer, negative control region deleted, dl587rev primer-binding site substituted); MOI (multiplicity of infection); MPBC (mobilized peripheral blood cells); MPSV (myeloproliferative sarcoma virus); Neo^R (neomycin resistance); NHL (non-Hodgkin's lymphoma); P (prestimulation); Phox (phagocyte oxidase); PRDM16 (PR domain containing 16); RRED (rev-responsive element decoy); RV (retroviruses); SCF (stem cell factor); SCID (severe combined immunodeficiency disease); SETBP1 (SET binding protein 1); SFFV (spleen focus forming virus); SIN (self-inactivating); T (transduction); T-ALL (T-lineage acute lymphoblastic leukemia); TBI (total body irradiation); TPO (thrombopoietin); VSV-G (vesicular stomatitis virus-G protein); WAS (Wiskott Aldrich syndrome).