

SOMATIC STEM CELL POPULATIONS AND STUDIES ON THE  
FUNCTIONAL ROLE AND REGULATION OF ABCG2

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FUNCTIONAL ROLE AND REGULATION OF ABCG2

by

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## SOMATIC STEM CELL POPULATIONS AND STUDIES ON THE FUNCTIONAL ROLE AND REGULATION OF ABCG2

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ATP binding cassette transporters use ATP to transport substances such as sterols, peptides, drugs and other toxins across membranes. Abcg2 is a member of the G family of transporters that was identified in breast cancer cells due to its ability to efflux chemotherapeutic drugs. Abcg2 can also efflux Hoechst 33342, resulting in a side population phenotype when stained cells are sorted by FACS. Recent studies have suggested that Abcg2 may be a marker for stem and progenitor cells. This paper presents experiments that were undertaken to further evaluate the functional role and regulation of Abcg2. Preliminary data obtained from a microarray performed on main and side population cells indicated that side population cells were enriched for genes that are important in cytoprotection and cell cycle control. To confirm this observation, cell cycle analysis was performed on C2C12 myoblasts transfected with an Abcg2 overexpressing plasmid. Those cells that overexpressed Abcg2 and consequently effluxed Hoechst 33342 dye were arrested in G0/G1 phase of the cell cycle, consistent with the microarray results. To determine whether Abcg2 played a cytoprotective role I attempted to measure the viability of main population versus side population cells when exposed to the oxidative

compound menadione. These experiments were inconclusive, most likely due to limitations of the cell line used. To assess the regulation of Abcg2 I examined evolutionary conservation between the upstream regions of mouse and human Abcg2. Conserved regions were identified up to 11kb upstream of the mouse gene. In these regions, putative binding sites were discovered for transcription factors that are involved in stem and progenitor cell regulation. Present studies support that Abcg2 is a marker for stem and progenitor cells. Future studies will uncover additional functional roles of the transporter.

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## LIST OF ABBREVIATIONS

Abcg2: ATP binding cassette, subfamily G, member 2

AGM: Aorta-gonad-mesonephros

BCRP1: Breast cancer resistance protein

DMD: Duchenne muscular dystrophy

EGF: Epidermal growth factor

EGFP: Enhanced Green Fluorescent Protein

FACS: Fluorescence activated cell sorting

FTC: Fumitremorgin C

GFAP: Glial fibrillary acid protein

HSCs: Hematopoietic stem cells

KSL: c-Kit<sup>+</sup>, Sca-1<sup>+</sup>, Lin<sup>-</sup>

MDR: Multidrug resistance protein

MP: Main population

NSCs: Neural stem cells

PI: Propidium iodide

SP: Side population

SPOC: Skeletal-based precursors of cardiomyocytes

SSCs: Somatic stem cells

YFP: Yellow fluorescent protein

## **Introduction**

In the process of creating an organism, two cells fuse into one. This is then followed by the massive cell division that is required to create a complex multicellular creature. As the number of cells increase, numerous genetic programs are activated, transcribing proteins which differentiate these cells into endothelial, muscle, liver, and all the other cell types found in the adult organism. Pluripotent cells present in the early embryo, called embryonic stem cells, divide many times to produce the cells that will differentiate into the various cell types. The cells of the adult organism continue to function until they are injured or undergo apoptosis. One of the most widely studied questions in biology asks what cells present in the mature organism can replenish these cell populations. It is thought that most tissues of the body contain their own specific population of cells that divide and differentiate to replace the dead cells; these are called somatic stem cells (SSCs).

Somatic stem cells are defined by two criteria: proliferation, the ability to self-renew and plasticity, the ability to give rise to differentiated cells with a specific function. The fate of a given stem cell depends on whether it undergoes asymmetric or symmetric division. In asymmetric division, the multipotent stem cell divides, giving rise to one stem cell and one cell that will differentiate. In



symmetric division, both daughter cells will be the same type of cell, either both stem cells or both differentiating cells (Mayani 2003).

While stem cells provide a source of differentiated cells for their respective tissues, it is also thought that stem cells retain an inherent plasticity, or ability to differentiate into other cell types. There are two hypothesized methods of somatic stem cell plasticity: dedetermination and transdifferentiation. In the former, a stem cell would first have to revert to a more primitive stem cell that is less committed to a specific program, and then differentiate into cells of a different type. In the latter, a stem cell of one type would begin to follow the differentiation path of another type of cell, without first reverting to a primitive state (Mayani 2003). Whichever path a stem cell takes, another important distinction to make is differentiation vs. fusion. Some studies claim that transplanted cells have fused with endogenous tissue rather than assume a different cell fate (Terada 2002; Ying 2002; Wang 2003). For instance, Wang et. al. showed that the donor bone marrow cells that were responsible for repopulation of the liver had fused with endogenous hepatocytes, as evidenced by the resulting aneuploid karyotypes. Studies such as these illustrate that it is important to closely examine cell phenotypes when addressing the issue of plasticity. However, it may still be beneficial if cells fuse rather than differentiate if, through fusion, they are still able to contribute to the repair of the tissue. For instance, when satellite cells in skeletal

muscle are activated for repair, their mechanism of action is to fuse with existing myofibers (Hawke and Garry 2001).

Scientists have developed multiple strategies to address the question of differentiation vs. fusion. One strategy is to transplant a labeled stem cell, such as one expressing GFP or  $\beta$ -gal so that it can be traced, and examine the cells for tissue specific markers (Orlic 2001; Lagasse 2000). Another method includes injecting male cells into a female recipient and evaluating the tissue of interest for the presence of the Y chromosome in the new cells (Theise 2000). A third method is to inject cells that contain a tissue-specific promoter driving a transgene that will only be expressed if it transdifferentiates into the target tissue.

Although work is being undertaken to identify, characterize, and isolate stem cells in each tissue, much of it focuses on hematopoietic, skeletal muscle, epithelial, neural, and cardiac stem cells. In addition to identifying stem cells, scientists are also trying to discover the limits of each stem cell population's plasticity, and utilize this ability to treat disease and injury.

## **Hematopoietic Stem Cells**

Hematopoietic stem cells (HSCs) are perhaps the most widely studied stem cell population. They arise from the aorta-gonad-mesonephros (AGM) region in the mouse embryo around embryonic day 10 and are believed to colonize the fetal liver and bone marrow (de Bruijn 2000). The adult bone marrow is the main site of hematopoiesis where the HSCs give rise to all blood cell types, though they only comprise 0.005 - 0.01% of all bone marrow cells (Mayani 2003). Upon stimulation, HSCs differentiate to become granulocytes, monocytes, megacaryocytes, erythrocytes, and lymphocytes. This multipotency can be demonstrated through the use of the colony forming assay, in which unfractionated bone marrow is plated onto a semisolid media and allowed to form clonogenic colonies of the various myeloid and lymphoid lineages (Ogawa 2002).

Although there is not one specific marker for HSCs, there are ways of identifying populations of cells that are highly enriched in HSCs. Cells are identified using flow cytometry to detect the presence or absence of surface markers. Studies have shown that the most primitive HSCs have a  $CD34^{-}$ ,  $c\text{-Kit}^{+}$ ,  $Sca\text{-}1^{+}$ ,  $Lin^{-}$  phenotype, also known as  $CD34^{-}$  KSL (Smith 1991; Spangrude 1995; Osawa 1996; Uchida 1996). This population of cells has been demonstrated to contain single cells with the ability to reconstitute the hematopoietic system of lethally irradiated mice, but in only approximately 20% of

recipients (Osawa 1996). Recently, Matsuzaki et al. discovered a way to further purify HSCs that utilizes the ability of a population of cells, termed the side population, to efflux the DNA binding dye Hoechst. The CD34<sup>-</sup> KSL cells with the greatest dye efflux ability, or Tip-SP, exhibited multilineage, long-term competitive repopulation in over 90% of recipients (Matsuzaki 2004).

The ability to isolate and purify HSCs may offer a better therapy for alleviating or curing certain diseases that affect the blood and immune systems. In patients with cancer, the bone marrow can be extracted before treatment, purified, and injected back into the patient following treatment that destroys both cancerous and normal cells (Mayhall 2004). HSC transplant can also be used for autoimmune diseases such as multiple sclerosis and juvenile chronic arthritis. In cases such as these, the HSC transplant is used to rebuild the patient's immune system after ablative treatment (Wulffraat and Kuis 1999; Fassas 2002). Depending on the type of treatment, whether the HSCs are autologous – from the patient, or allogenic – from a matched donor, the symptoms of the disease can be alleviated or even be cured.

In addition to replacing the hematopoietic system, HSCs have also been shown to have the ability to become other cell types and repair damaged tissue. This has widespread implications in tissue repair, especially since bone marrow cells are more easily obtained than other stem cells. Some studies have shown that following injury,

bone marrow derived cells are present in the muscle of recipient mice (Camargo 2003; Corbel 2003). Other studies have shown that cells derived both from whole bone marrow and KSL purified HSCs can be found in the liver (Lagasse 2000; Theise 2000). Mezey et al. claim that cells derived from whole bone marrow can become neural cells by showing that donor cells from male mice are present in brain tissue and express the neural marker NeuN (Mezey 2000). In addition to becoming muscle, liver, and neural cells, studies have also claimed that bone marrow can regenerate injured heart and even become cardiomyocytes. Orlic et al. injected  $\text{lin}^- \text{c-kit}^+$  EGFP male bone marrow cells into the infarcted left ventricle of female mice and found repair in 40% of recipients (Orlic 2001). Another study utilized an *in vitro* method to establish a cardiomyogenic cell line. Bone marrow stromal cells were cultured in the presence of 5-azacytidine, which induced spontaneous beating, formation of branched myotubes, and expression of cardiomyocyte-specific genes, such as myosin, actinin, and desmin (Makino 1999).

However, there are also several studies that find that HSCs do not transdifferentiate (Bjornson 1999). Menthena et al. showed, through the use of double immunohistochemical and immunofluorescent labeling of both liver and bone marrow derived cells that, in their hands, liver progenitor/oval cells derive from liver tissue and not from the donor bone marrow (Menthena 2004). One study

replicated the methods of HSC isolation and transplantation used by Orlic et al. but used phenotypic and lineage markers instead of immunofluorescence staining to detect cells. That study did not find that bone marrow stem cells differentiated into cardiomyocytes in either normal or infarcted hearts or that they participated in tissue regeneration (Murry 2004). In addition, Wagers et al. used lethally irradiated mice engrafted with a single GFP<sup>+</sup> HSC that was c-kit<sup>+</sup> Thy1.1<sup>lo</sup> Lin<sup>-</sup> Sca-1<sup>+</sup> and examined various tissues 4-9 months after engraftment. The authors did not find any GFP<sup>+</sup> cells that either stained with tissue-specific markers, were negative for CD45, or exhibited a distinct morphology in kidney, skeletal or cardiac muscle, or lung tissues, and found only a few GFP<sup>+</sup> cells present in brain and liver (Wagers 2002).

## **Skeletal Muscle Stem Cells**

Among the tissues of the body, skeletal muscle has a tremendous ability to regenerate and repair itself. This regeneration is accomplished by muscle progenitor cells termed satellite cells, so named for their location in muscle. Satellite cells are defined by their position adjacent to myofibers and surrounded by the basal lamina (Schultz and McCormick 1994). They can also be visually distinguished by their higher nuclear-to-cytoplasmic ratio and smaller nuclei when compared to myotubes (Schultz and McCormick 1994). In addition to visual distinctions, satellite cells are also characterized by several molecular markers. C-met, a receptor tyrosine kinase, was found to be expressed in all satellite cells, in both quiescent cells and cells that were in the period of activation and differentiation (Cornelison and Wold 1997). Although vascular cell adhesion molecule-1 (VCAM-1) is present during embryological development and is down-regulated in adult myotubes, it was shown to retain its expression in satellite cells (Jesse 1998). Another marker of satellite cells is an isoform of the winged helix transcription factor myocyte nuclear factor, FoxK1 $\beta$ . This isoform is predominantly expressed in satellite cells, and is downregulated as the satellite cells proliferate and differentiate (Garry 2000). The paired box transcription factor Pax7, another marker of satellite cells, is required for satellite cell specification (Seale 2000). While these and other proteins are markers for satellite cells, many are

also expressed in other tissues. It may be best to use a combination of these markers when identifying satellite cells.

Satellite cells facilitate repair and regeneration in response to muscle injury, whether caused by exercise, toxins, or disease. Once injury occurs, satellite cells become activated, begin to proliferate, and move to the injured area by chemotaxis (Schultz and McCormick 1994). At the site of injury, the activated satellite cells can then fuse to the damaged myofiber to repair it or fuse with each other to form new myofibers, while others satellite cells undergo self-renewal (Schultz and McCormick 1994). Satellite cells are able to repair and renew repeatedly, but eventually they lose this ability due to aging of the organism and disease (Jejurikar 2003). This loss of proliferative capacity is particularly seen in diseases such as Duchenne muscular dystrophy (DMD), an X-linked recessive disease caused by a null mutation at the dystrophin locus (Burghes 1987). Normally dystrophin binds to actin to link it to the sarcolemma. In DMD, dystrophin is absent in the skeletal muscle and therefore actin is not able to associate with the sarcolemma membrane, resulting in delicate myofibers that are more susceptible to injury (Rybakova 2000). Satellite cells are activated to repair the damaged tissue, but as the cells are repeatedly activated, their ability to proliferate and repair injured muscle is exhausted (Cossu 2000).



In addition to satellite cells, muscle also contains a pluripotent stem cell population termed the side population, or SP. Dual-wavelength flow cytometry is used to detect the cells based on their ability to efflux the DNA-binding dye Hoechst 33342 (Goodell 1996; Asakura 2002). Like HSCs, muscle SP are sca-1<sup>+</sup> lin<sup>-</sup>, but they appear to be different from bone marrow SP in that they do not express c-kit and CD45 (Gussoni 1999). Studies have suggested that these cells can give rise to hematopoietic cells, satellite cells, and can contribute to myofiber formation (Gussoni 1999; Jackson 1999; Asakura 2002).

It has also been suggested that there is a population of skeletal muscle cells that can differentiate into cardiomyocytes. In this study, nonadherent cells were isolated from murine skeletal muscle and termed skeletal-based precursors of cardiomyocytes (SPOC). SPOC cells are CD34<sup>-</sup> CD45<sup>-</sup> and c-kit<sup>-</sup> and begin spontaneously beating in culture in the presence of epidermal growth factor (EGF). When injected into the peripheral circulation of mice with myocardial infarct, the GFP<sup>+</sup> SPOC cells were able to migrate to the infarct and 8% became cardiomyocytes that expressed phosphorylated cardiac myosin regulatory light chain (Winitsky 2005).

## Epithelial Stem Cells

Epithelial cells are located in many areas of the body and are characterized by the speed at which they turn over. Rapidly self-renewing epithelial cells tend to act as a protective barrier and are located in the skin, intestine, and eye. Persistent epithelial cells do not turn over rapidly and are located in the liver, kidney, and mammary gland (Rizvi 2005). Each of these populations has its own stem cell compartment, consisting of quiescent stem cells and the proliferative transient amplifying daughter cells that become the differentiated epithelial cells (Rizvi 2005). While stem cell markers for epithelial cells are not well defined, in the rapidly self-renewing populations, stem cells can be identified by their ability to retain the DNA labels [3H]thymidine and BrdU (Mackenzie 1985; Morris 1985; Braun 2003). A recent study suggested that  $\alpha 6$  integrin<sup>bright</sup> CD71<sup>dim</sup> cells may represent putative stem cells in the skin (Webb 2004). Although it is more difficult to locate stem cells in the persistent epithelium, studies have claimed to have identified BrdU label-retaining stem cells in kidney (Maeshima 2003).

Epithelial skin cells have been demonstrated to be multipotent. Juvenile or adult mouse tissue was cultured in epidermal growth factor and fibroblast growth factor and small floating spheres of cells were collected. They were then incubated in neural differentiating conditions and the cells began to express neural markers, including nestin,  $\beta$ III-

tubulin, neurofilament-M, NeuN, and a neuron-specific T $\alpha$ 1  $\alpha$ -tubulin:nlacZ transgene. Some of the floating cells also began expressing glial markers GFAP and CNPase, or an oligodendrocyte precursor marker A2B5 (Toma 2001).

Skin stem cells are already being used in therapy. In burn patients, keratinocytes are extracted from a non-injured area, expanded in culture, and then grafted onto the burned areas. By using autologous cells, the danger of rejection is removed (Alonso 2003). Epithelial stem cells may be promising for use in other therapies as well. If stem cells can be coaxed to become other cell types, such as neural cells, then they can be readily obtained from the host and used to treat neurodegenerative disorders without the complications of graft vs. host disease.

## **Neural Stem Cells**

Neural stem cells (NSCs) can give rise to three different major cell types: neurons, astrocytes, and oligodendrocytes (McKay 1997). Unlike hematopoietic and muscle stem cells, NSCs are isolated mainly based on clonal proliferation rather than cell markers. Cells are isolated from tissue and exposed to mitogens such as epidermal growth factor and fibroblast growth factor 2 in serum-deficient culture and NSCs are identified as small proliferative colonies (Vescovi 1993; Palmer 1995). However, there are markers to distinguish between the more differentiated cell types. Markers for the three major neural types include TUJ1 for neurons, glial fibrillary acid protein (GFAP) for astrocytes, and GalC for oligodendrocytes (Gage 2000). Scientists are beginning to use progenitor cell-selective reporter gene expression and surface antigen-based sorting to purify cells (Goldman 2005).

There are a variety of diseases affecting the central nervous system that may be treated with NSCs. One study showed that both fetal and adult human oligodendrocyte progenitor cells can develop into astrocytes and myelinating oligodendrocytes in a demyelinated mouse model (Windrem 2004). Studies like these may one day result in therapies for demyelinating diseases such as Tay-Sachs, adrenoleukodystrophy, and multiple sclerosis (Goldman 2005).

Like other stem cells, neural stem cells have been demonstrated to become other cell types. In a study by Bjornson, NSCs were

isolated from embryonic or adult forebrain of ROSA26 mice and cultured in epidermal growth factor and fibroblast growth factor 2. The cells were then injected into sublethally irradiated Balb/c mice and after 5-12 months analyzed for the presence of the lacZ gene. They detected a strong signal in mice injected with either embryonic, adult, or clonally derived NSCs. They also used clonogenic analysis and immunocytochemistry to determine whether the NSCs displayed hematopoietic characteristics and found that bone marrow isolated from NSC recipients displayed the ROSA26 specific antigen H-2K<sup>b</sup> and formed granulocyte, macrophage, and B cell colonies (Bjornson 1999).

## Cardiac Stem Cells

Until recently it was thought that a resident cardiac progenitor cell population might not exist. One reason for this was due to a seeming lack of regenerative capacity, especially after cardiac injury. However, the past few years have seen an increasing number of reports that claim to be able to isolate a cardiac progenitor population that can give rise to beating cardiomyocytes. Matsuura et al. purified a population of Sca-1<sup>+</sup> cells from adult murine heart that began spontaneously beating and expressed cardiac genes, including Nkx2.5, Gata4, and cardiac  $\alpha$ -actin, after treatment with oxytocin (Matsuura 2004). Beltrami et al. identified a cardiac population that was Lin<sup>-</sup> c-kit<sup>+</sup> and expressed Gata4, Nkx2.5, and Mef2. In differentiation medium, clones from an individual cell produced cells that expressed markers for three cardiac lineages: myocytes, endothelial cells, and smooth muscle cells. They also took GFP labeled precursors and injected them into the border region of infarcted heart and identified a band of new myocardium expressing GFP (Beltrami 2003). A third study isolated a population of cells that were Sca-1<sup>+</sup> and negative for Lin, c-kit, Flk-1, CD45, and CD34. They infused Sca-1<sup>+</sup> cells that contained an  $\alpha$ MHC-Cre transgene into mice containing a floxed lacZ gene. After two weeks they saw Cre<sup>+</sup> cells, indicative of differentiation. Half of the Cre<sup>+</sup> cells were also positive for lacZ, suggesting fusion of donor cells with resident myocytes (Oh 2004).

The heart, like most other tissues, also contains a side population of cells (Hierlihy 2002; Martin 2004; Pfister 2005). These cells were shown to be positive for sca-1 and negative for c-kit, CD34, CD45, and CD31 (Martin 2004), although Pfister et al. also identified a CD31<sup>+</sup> SP fraction. CD31<sup>+</sup> cells occupied a distinct portion of the SP arm from the CD31<sup>-</sup> fraction, although the CD31<sup>+</sup> cells were shown to lack the ability to differentiate into cardiomyocytes (Pfister 2005). All three studies utilized a co-culture method to demonstrate differentiation ability. GFP<sup>+</sup> SP cells were co-cultured with wild type cardiac cells and after incubation were examined for markers of cardiac differentiation. This assessment showed that GFP<sup>+</sup> cells were positive for connexin 43 (Hierlihy 2002; Pfister 2005), alpha-actinin (Martin 2004), Gata4 and MEF2C, and 10% began spontaneously beating at a low frequency (Pfister 2005).

While it appears that cardiac SP cells are able to differentiate into cardiomyocytes, it is unclear whether they are also able to differentiate into other cell types. Martin et al. plated cardiac SP cells in methylcellulose media and found that they were able to form hematopoietic colonies (Martin 2004). However, Hierlihy et al. found that myocardial cell suspensions formed limited hematopoietic colonies in methylcellulose. In addition, while cardiac SP cells could contribute to myotubes by fusing to co-cultured primary-derived skeletal muscle myoblasts, SP cells driving a skeletal muscle specific myf5/lacZ

transgene did not express  $\beta$ -gal or myogenin when co-cultured with C2C12 myoblasts (Hierlihy 2002).

Cardiovascular disease is the leading cause of death in the United States. In 2002, there were 928,000 deaths from cardiovascular disease, 1.6 times more than deaths from cancer (American Heart Association 2005). One of the main factors contributing to failure after injury is the loss of cardiomyocytes (Smits 2005). Currently scientists are focusing on the promise of stem cell transplant to regenerate the injured tissue by looking at both cardiac progenitor cells and stem cells from other tissues that appear to have the ability to contribute to cardiac repair (Makino 1999; Orlic 2001; Winitsky 2005).



## **Abcg2**

In 1996 Margaret Goodell isolated a new population of cells from bone marrow. Whole bone marrow had been stained with the DNA binding dye Hoechst 33342 and FACS sorted using red and blue emission wavelengths. They observed a group of cells that was Hoechst<sup>low</sup> and created a side arm of cells branching off of a main population of brightly staining cells. These cells were enriched for hematopoietic stem cell activity and could be eliminated after incubation with verapamil, an inhibitor of the multidrug resistance protein (MDR), which had been shown to efflux dyes from cells (Goodell 1996). Side population cells have since been found in many adult tissues, including skeletal muscle, brain, mammary tissue, liver, and lung, and appear to represent a progenitor cell population (Asakura 2002; Murayama 2002; Alvi 2003; Summer 2003; Wulf 2003).

MDR is a member of the ATP binding cassette (ABC) family of membrane transporters. These transporters use energy from binding ATP to transport various substances across the plasma membrane, endoplasmic reticulum, and mitochondrial membrane (Dean 2001). The 49 members of the ABC family transport sterols, peptides, bile salt, drugs, and other toxins (Dean 2001). One of the most recently discovered ABC transporters is Abcg2, also known as breast cancer resistance protein (BCRP1). Abcg2 was first discovered in the human MCF-7 breast cancer line through its ability to confer resistance to

drugs such as doxorubicin, daunorubicin, and mitoxantrone (Doyle 1998). Abcg2, unlike most other members of the ABC transporter family, is a half-transporter with six transmembrane domains and functions as a homodimer (Doyle 1998).

The ability of cells to efflux Hoechst dye is conferred by Abcg2, and was demonstrated by overexpressing the protein in both bone marrow and skeletal muscle. The presence of side population cells could be reversed by adding either the broad inhibitor reserpine, or the Abcg2 specific inhibitor fumitremorgin C (FTC) (Zhou 2001; Martin 2004).

Several studies have suggested that Abcg2 expression may be a marker for stem or progenitor cells. SP cells isolated from bone marrow have been shown to be able to reconstitute lethally irradiated mice (Goodell 1996), regenerate muscle in the mdx mouse (Gussoni 1999), and regenerate cardiomyocytes (Jackson 2001). Based on these studies and preliminary data, I undertook experiments to further evaluate the functional role and regulation of Abcg2 in stem cells.

The preliminary data for my studies came from a microarray performed on main and side population cells. To generate these populations, C2C12 myoblasts were transfected with either empty vector or constitutively active Abcg2. The cells were then sorted by dual-wavelength FACS and the Hoechst<sup>low</sup> SP and Hoechst<sup>bright</sup> MP cells were collected. RNA from these cells was isolated, labeled, and

hybridized to an Affymetrix gene chip containing over 20,000 genes.

The resulting microarray data showed Abcg2 overexpressing cells have a greater than 2-fold increase in mRNA levels of many genes that are important in cytoprotection and cell cycle control.

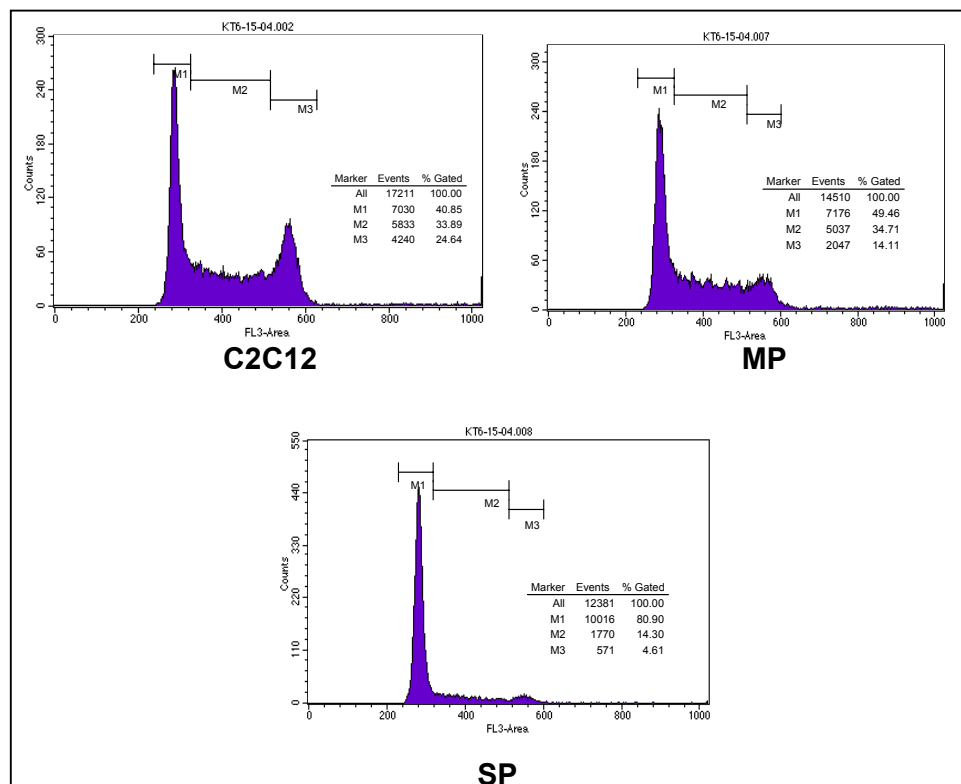
Unigene name	GP signal strength	Fold Change	MP signal strength
<b>Upregulated in SP cells</b>			
activating transcription factor 3	1665.8	9.19	132.5
GRO1 oncogene	660.6	6.96	91.6
proliferin 2	7272.4	5.66	854.7
N-myc downstream regulated 1	3291.1	5.28	574.5
cyclin-dependent kinase inhibitor 1A (P21)	1254.1	4.92	261.4
glutathione S-transferase, alpha 2 (Yc2)	551.2	4.29	121.3
glutathione S-transferase, alpha 4	1086.7	4.00	252.3
serine protease inhibitor 13	303.5	4.00	60.1
Metallothionein 2	4775.7	3.03	1478.6
cyclin G2	303.8	2.14	144.5
<b>Downregulated in SP cells</b>			
cell division cycle 6 homolog ( <i>S. cerevisiae</i> )	177.2	-2.00	510.4

Figure 1. Disregulated genes in C2C12 SP cells

These genes include glutathione S-transferase and metallothionein 2, which reduce hydroperoxides and regulate zinc homeostasis in response to nitrosative stress, respectively, and cyclin G2, which is a negative regulator of cell cycle progression.

Since stem cells are a reserve for adult tissues and only need to divide to replace dead cells, they spend most of their time in the G0, or quiescent stage of the cell cycle. Finding upregulated genes that play a negative role in cell cycle progression prompted me to examine the

cell cycle of SP cells. C2C12 myoblasts were transfected with empty vector or Abcg2, and MP and SP cells were isolated by FACS. Cells were stained with the DNA binding dye propidium iodide (PI) and analyzed by flow cytometry. Cells that are in S or G2/M phases of the cell cycle have more DNA and therefore will bind more PI, resulting in a brighter signal. 40-50% of cells transfected with empty vector or main population cells were in G0/G1 phase of the cell cycle, whereas 80% of cells overexpressing Abcg2 were in G0/G1. Therefore it appears that SP cells, like stem cells, are quiescent.



**Figure 2. Cell cycle analysis of C2C12 cells either mock treated or transfected with GFP or Abcg2**

Since array data identified several genes involved in oxidative stress reduction and cytoprotection, I attempted to determine whether cells that overexpressed Abcg2 were less susceptible to oxidative stress.

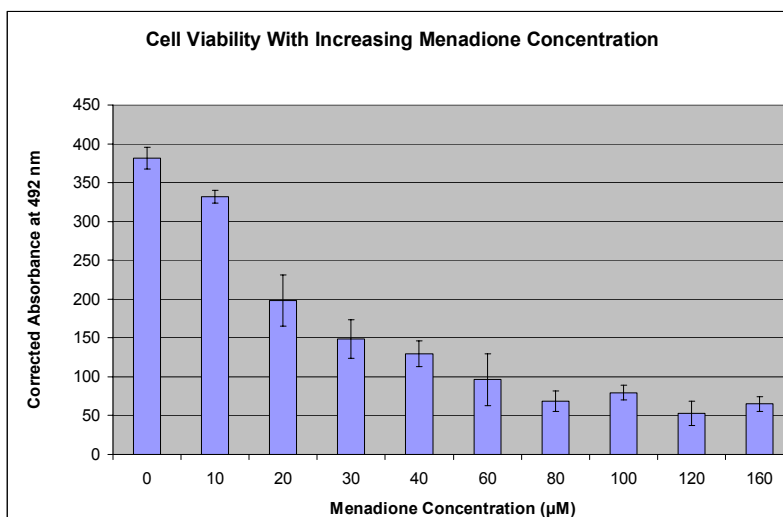


Figure 3. Cell viability of C2C12 cells with increasing menadione concentration

To do this, I first established a concentration of menadione at which there would be 50% cell death in C2C12 myoblasts. Menadione is a compound that produces the oxidative products  $O_2^-$ , hydroxyl radicals ( $OH\cdot$ ) and hydrogen peroxide during its metabolism. To test the viability I used a tetrazolium salt reagent that is reduced into a red formazan product by mitochondrial dehydrogenases of viable cells. The absorbance of the media is proportional to the number of viable cells. I then mock treated or transfected either GFP or Abcg2 into

C2C12 myoblasts, collected C2C12, GFP<sup>-</sup>, GFP<sup>+</sup>, MP and SP fractions, and exposed them to 20  $\mu$ M menadione for 1 hour.

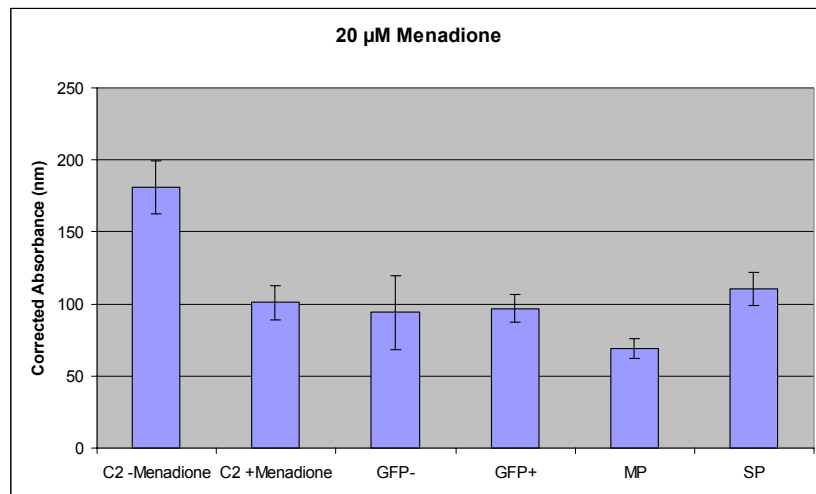


Figure 4. Cell viability of C2C12 cells either mock treated or transfected with GFP or Abcg2 with the addition of 20  $\mu$ M menadione

From this data, Abcg2 is not protective against menadione-induced oxidative stress, but there should also be GFP, MP, and SP controls that were not exposed to menadione. The lack of cytoprotection seen in this assay may be due to limitations of C2C12 cells. Through personal communication I learned that C2C12 is not the best cell line to use in cell death studies due to variability in the death process. It was suggested that using hydrogen peroxide on mouse embryonic fibroblasts would be a better alternative and those studies are in progress.

To assess the regulation of *Abcg2*, I examined evolutionary conservation between the upstream regions of human and mouse *Abcg2*. Using the UCSC genome browser I identified conserved regions up to 11kb upstream of the mouse *Abcg2* gene. I selected these regions in which to analyze conserved transcription factor binding sites that may play a role in regulating *Abcg2* expression.

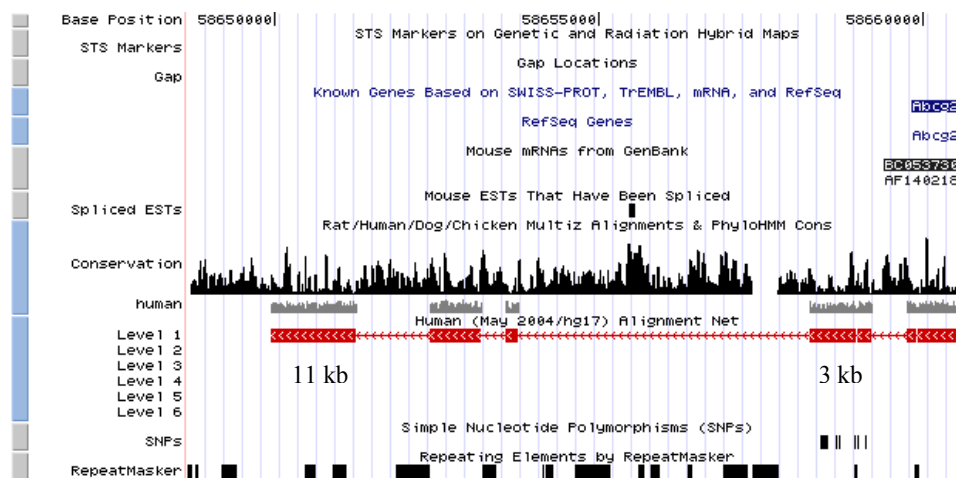


Figure 5. Evolutionary conservation of 11kb upstream of *Abcg2* between mouse and human

Using the programs Consite and rVista, I identified conserved putative transcription factor binding sites. Many of these transcription factors are involved in stem and progenitor cell regulation. For example, *aml-1* (*runx-1*) is required for definitive hematopoiesis in the fetus, is critical for normal hematopoiesis in the adult mouse, and can act as a transcriptional activator or repressor (Yamagata 2004; Growney 2005). *HFH2* (*FoxD3*) is required for the maintenance of progenitor cells in the embryo (Hanna 2002) and is expressed in neural crest cells and

motorneuron progenitors in the developing spinal cord (Labosky 1998). Stat5a is required during the terminal stages of myeloid differentiation (Kieslinger 2000) and has been shown to activate transcription of Bcl-X(L) in erythroid cells to reduce apoptosis (Socolovsky 1999). Sox factors are also implicated in stem and progenitor cell regulation. Sox2 has been suggested to play a role in neural precursor proliferation and neural stem cell maintenance (Episkopou 2005), while Sox5 is

Kb upstream	Transcription Factor	Kb upstream	Transcription Factor
10	hfh1	7.4	aml-1
	broadcomplex 4		athb-1
	sox 5		hfh2
	sox 17		
9.8	agl3	6.8	tbp
9.6	stat5a	2.4-1.5	hfh-2
	cap		hunchback
	sox 17		e74a
	hfh3		c-fos
9.4	sox 5		freac-4
	c-fos		bzip910
8	hnf3-beta	1	hnf3-beta
	athb-1		aml-1
	athb5		cf2-ll
	sox 17		agl3
	broadcomplex-4		freac-4
	hunchback		sox-17
7.8	stat5a		sox 5
	cdxa		
	athb-1		
	nrf-2		
	e74a		
	freac-4		

Figure 6. Evolutionarily conserved transcription factors and their approximate location in the 11kb upstream region of Abcg2

important in chondrocyte differentiation and cartilage formation (Lefebvre 2001).

Based on transcription factor conservation data, I then undertook transcriptional analysis of the Abcg2 promoter utilizing the transcription factors sox2, sox5, and runx1. Two different promoter



fragments, extending from +165 bp to either 2.7 kb or 5.5 kb upstream, which I referred to as 3 Kb and 6 KB respectively, were cloned into the PGL3-Basic luciferase vector. The selection of these two fragments was made based on sequence conservation and ease of cloning. 100 ng of the promoter-luciferase construct was co-transfected with increasing concentrations of a plasmid containing the constitutively active transcription factor. Empty PGL3-Basic vector was co-transfected with each transcription factor as a control. Following a 24 hour incubation period, the cells were lysed and the extracts analyzed for a change in luciferase expression, indicating whether the transcription factor was able to activate or repress expression, or whether it had no effect. Unfortunately, the results from these experiments were uninterpretable because the background luciferase expression was very high. One interesting observation from these experiments was that in each case, the expression of the 6 kb promoter plasmid was reduced compared to the 3 kb plasmid of PGL3-Basic control. This could be due to either the large length of the inserted fragment or to a repressive element located somewhere between 2.7 and 5.5 kb upstream of the translational start site.

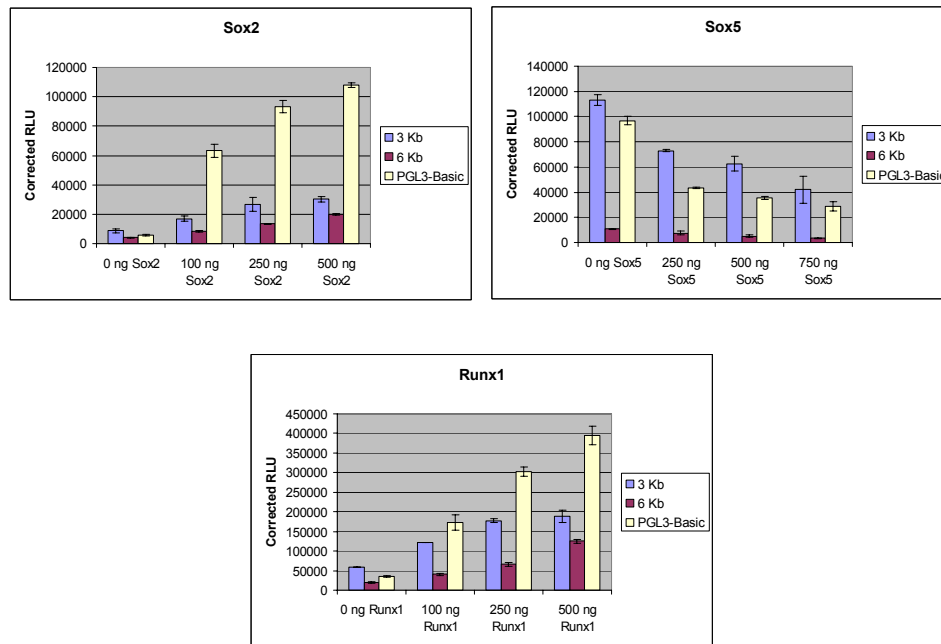


Figure 7. Transcriptional assays of C2C12 cells transfected with Abcg2 and either Sox2, Sox5 or Runx1

In addition to using transcriptional analysis to examine regulation of Abcg2, I am also creating constructs to use in the making of transgenic animals. I will have two mouse lines, with either an 11 kb or the 3 kb promoter fragment driving the expression of a yellow fluorescent protein (YFP). To examine whether there is expression of the transgene, I will mate male founders with wild type females and analyze the embryos and yolk sacs for fluorescent expression. I will look at the yolk sac because previous studies have shown that Abcg2 expression is strong in the yolk sac, so there should be a good chance that I should see expression of my transgene. The aim is to evaluate the upstream fragment of the Abcg2 gene that directs expression in

side population cells. Once identified, this promoter sequence can be used to drive a tetracycline-dependent transactivator that can activate a gene that is lethal to cells (Gallagher 2003). At points during development or after injury tetracycline can be administered and development or regeneration in the absence of side population cells can be examined. In addition, mice with fluorescent expression in side population cells could be mated to *Abcg2* <sup>-/-</sup> mice. This would allow cells that would normally express *Abcg2* to still be identified, since without *Abcg2* the cells are not able to efflux the Hoechst dye and the side population cells can not be identified. These cells could then be examined for stem or progenitor cell ability in the absence of *Abcg2*.

Based on present studies, it appears that *Abcg2* can be used as a marker for progenitor cell populations, which may be useful in therapeutic studies. What remains to be seen is exactly what kind of functional role *Abcg2* plays. Studies have shown that *Abcg2* is capable of effluxing chemotherapeutic drugs from cells, suggesting a protective role against xenotoxins (Burger 2004; Elkind 2005). Another study also suggests that *Abcg2* can efflux porphyrins, a heme precursor (Jonker 2002). Future studies should elucidate whether *Abcg2* plays an active role against oxidative stress, and whether it has any additional functions.

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