Evolution of normal and neoplastic tissue stem cells: progress after Robert Hooke

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The appearance of stem cells coincides with the transition from single-celled organisms to metazoans. Stem cells are capable of self-renewal as well as differentiation. Each tissue is maintained by self-renewing tissue-specific stem cells. The accumulation of mutations that lead to preleukaemia are in the blood-forming stem cell, while the transition to leukaemia stem cells occurs in the clone at a progenitor stage. All leukaemia and cancer cells escape being removed by scavenger macrophages by expressing the ‘don’t eat me’ signal CD47. Blocking antibodies to CD47 are therapeutics for all cancers, and are currently being tested in clinical trials in the US and UK.

1. Introduction

Stem cells are now defined as cells, at the single-cell level, that both self-renew and differentiate to produce all cells of a particular tissue or organ or organism [1]. In vertebrate metazoans, the zygote goes through a set of divisions to form the blastula stage, called the blastocyst, before it implants into the uterus (in mammals) or in the early stages of development within the egg in non-mammals. After the blastocyst stage, the formation of the three major ‘germlayers’ of mesoderm, ectoderm and endoderm, plus the early germline progenitor cells, develop following gastrulation, and development progresses in the embryo to the neurula stage, which coincides with the beginning of formation of the adult type organs and tissues; this constitutes the transition from embryo to fetus. However, these early embryonic progenitors (e.g. the early endoderm, mesoderm and ectoderm germ layer cells) do not persist past development and there are no remnants of these cell types that exist in adults; they do not self-renew and are not stem cells. Thus stem cells are an invention of fetal development and its processes of tissue formation and organogenesis. Developmental and stem cell biologists have created laboratory artefacts of pluripotent stem cells in culture from pluripotent inner cell mass populations within the blastocyst, and these are useful for biological and developmental studies [2], but the existence of pluripotent stem cells in vivo has been claimed [3–10], but not verified by careful research [11,12]. Metazoan stem cells are like many single-celled organisms such as dictyostelium [13] and sporulating bacteria insofar as they can self-renew and differentiate, and it is conceivable that genetic programs for self-renewal versus differentiation will be shared, at least in part, in all living organisms.

Given that natural selection operates on units of organization, not just single genes within the units, it is appropriate to consider if not only individual metazoan organisms, and groups of organisms (such as individuals in a colonial organism [14], but also stem cell lineages could be units in natural selection [1]. That is the topic of this treatise.

2. Stem cell competitions

Colonial organisms such as the urochordate Botryllus schlosseri montereyi undergo life histories wherein the usual chordate stages of zygote — blastula — gastrula — neurula — fetus — new-born are followed by migration of the ‘tadpole’ new-born to a subtidal surface, and thence metamorphosis to an invertebrate stage via programmed cell death (PCD) and programmed cell removal (PrCR) of the chordate features of notochord, neural tube, segmented musculature, tail, etc. (figure 1) [14,15]. Within the tunic surrounding the metamorphosed ‘oozoid',
cells within the oozoid bud through the body wall to begin a two-week cycle of organogenesis and growth and form identical progeny called blastozooids; their development includes generation of a gastrointestinal system, gill slits, gonads and a two chambered heart with an intracorporeal blood vasculature connected to an extracorporeal vasculature in the tunic; and many diverse organs and blood cell types (figure 1) [14–18]. At the end of three weeks, the individuals die via PCD and PrCR, with linkage between death of the old and budding of the new [19]. None of the steps of organogenesis come from an embryonic set of events, and so this is akin to tissue and organ regeneration, although it occurs in new buds rather than repairing ageing resident organs [20]. The genome of the colony, therefore, outlives the lives of any of the individuals in the colony. In this way, as in other ways [20] the colony is a unit of natural selection, as is the tadpole that made it.

How does organogenesis occur in these animals, and what is the impact of their colonial organization on stem cell participation? The principal cells in the nascent bud are a mixture of germline and somatic stem cells [20,22]. Do these stem cells circulate or are they sessile? A peculiar feature of these colonial tunicates is that they are able to undergo allorecognition in the wild [23–25]. When two zooids or colonies abut on the same subtidal surface they extend blunt-ended ampullae of the blood vessels into the tunic of the other colony, and within a day this results in vascular anastomoses or rapid rejection. Fusion or rejection is controlled by a single, highly polymorphic locus (perhaps hundreds of alleles [24]) called Botryllus histocompatibility factor (BHF) [26]. Sharing a single allele at this locus allows anastomosis [24], usually between kin, and this results in the formation of natural chimeras [27]. In my laboratory, we have shown that these are somatic chimeras beginning with the next budding cycle [22], and more remarkably, itinerant germline stem cells not only can inhabit the testis or ovary of the anastomosed partner, but that heritable germline stem cell competitions usually result in all gonads of all individuals in the colony pair carrying only the germline of the ‘winner’ genotype [22,27]. This establishes a relatively common circumstance in the laboratory and in the wild that sibling oozoids give rise to anastomosed natural parasites wherein one animal’s body harbours a sibling’s germline [22,27]. The BHF-based immune rejection prevents both vascular anastomoses and chimera formations [26]. Therefore, the potential of germline stem cell competitions prevented by immune allorecognition effectively limits germline stem cell predation to kin, usually siblings, and provides a basis for maintaining diversity of this species [22,24]. Over 30 years ago, Buss...
[13] proposed that highly polymorphic histocompatibility genes derived from competitions for ‘germline’ niches, using as an example the formation of a ‘metazoan’ dictyostelium as a single amoeba coalesce to form a fruiting body colony wherein the stalk is topped by a spore-containing tissue, the spores (or cheaters) being the ‘germline’ equivalent. For us this represents two important aspects of metazoan evolution—stem cell competitions and mechanisms such as alleloimmunity to limit it to the extent that homogenization by successful germline predation does not occur [22,24].

It is within this framework that my lab re-approached the potential diversity of mouse germline [28] and somatic haematopoietic stem cells (HSCs) [29,30], and discovered stem cell competitions in both. In the germline of mice, four cells that form the germline [28] expand outside the embryo proper, then migrate to the incipient gonads of the genital ridge [31]. Although each developing seminiferous tubule contains a mixture of distinct immigrant germline stem cells, at a stage that just precedes the first meiotic division, the great majority of these cells undergo PCD (and presumably PrCR), and the non-culled stem cells give rise to groups of adjacent seminiferous tubules containing the clonal spermatogenic progeny from a single clonal survivor [28]. I proposed this could occur following endogenous transposon movements that would be natural mutagens, and that a process of competition leads to survivors versus those that are culled [28].

What about somatic stem cells? Prospective isolation of a somatic stem cell, the HSC, was first accomplished in 1988 [32], when it seemed clear that such cells should make up a homogeneous population of cells, each of which is capable of many cycles of self-renewal leading to production of all blood cell types for the life of the individual [32]. However, early studies on the differences between young mouse and old mouse HSCs revealed differences in outcome, analysing first their potency in transplanting lifelong haematopoiesis, their capability to home to haematopoietic sites on transplantation, and their burst size of production of more HSCs relative to the number of cells in the blood forming organ, bone marrow [30,33–35]. Cell intrinsic differences were found between old and young stem cells as a population [30]. Individual young mouse HSCs produced a balanced outcome of lymphoid committed progenitors (CLP) and myeloid committed progenitors (CMP) (figure 2), while old mouse [33] and old human [37] bone marrows were dominated by myeloid biased HSCs. This also proved to be cell intrinsic [30,37]. When a cell surface marker was found that distinguished myeloid biased from balanced HSCs, it became clear that what was changing between young and old was the frequency of predetermined HSCs that were mainly in the balanced or the myeloid biased category [30]. This could be explained by the maturation of young to old by epigenetic transitions, or by clonal competitions between HSC subsets predetermined to be one or the other type. Current evidence from ours and many other laboratories is for the clonal diversity hypothesis [30,38–41], but crucial in situ lineage tracing of a single HSC from young to old is not yet feasible.

### 3. Stem cell competitions in the organismal evolution of cancer stem cells

Cancers are made up of cells derived from tissues and organs which contain normal stem cells, progenitors and lineage committed cells, e.g. the blood system (figure 2). Having nearly the complete roadmap of quantal transitions from HSC through multipotent progenitors lacking self-renewal (short term-HSC and multipotent progenitors (MPP) [42]) in mice, to CMP in mice [43] and humans [44], and CLP [45], and downstream from them ever more committed progenitors (e.g. granulocyte–macrophage progenitor (GMP) and megakaryocyte/erythroid progenitor (MEP) [43,46]), allowed me and my colleagues to look at mouse and human myelogenous leukaemias to attempt to understand where in the lineage tree the leukaemias emerged. The starting point was producing a strain of mice wherein PCD via two pathways was blocked in haematopoietic cells [47]. About 15% of the mice developed acute myelogenous leukaemia (AML), and their leukaemias could be transferred to other mice only with GMP cells. My colleagues and I could infer that the progression to leukaemia required at least five to seven rare events, either genetic or epigenetic. Most of these events could not confer self-renewal, and so must have occurred in self-renewing cells to persist sufficiently to form a clone that was leukaemic [48]. In 2000, we analysed AML patients’ bone marrows taken from a repository at Hiroshima Hospital. The patients analysed were known to have a chromosomal translocation (8 : 21) to form a fusion gene, aml 1:eto, which occurs in many patients with AML. Because we could isolate HSCs from MPP, from CMP and from GMP, we found the cells in the leukaemia that would make leukaemic cells in vitro [49] and would transfer the leukaemias to immunodeficient mice [50]. These leukaemia stem cells (LSC) were at the MPP stage, and neither HSCs nor myeloid lineage large (blast) cells from them transferred the leukaemia [50,51]. The particular breakpoint of the translocation produced a clonal tracer for that leukaemia, and in every case, the MPP–LSC translocation was found in otherwise normal HSCs in the same patient, and at a frequency that could only be explained by expansion from a single cell to hundreds of thousands of ‘preleukaemia’ cells [49]. This clearly implied that normal HSCs harboured the initiating event and were expanding, but that more events would be required before the preleukaemic and marked HSCs could give rise to the leukaemic MPP-LSC [48]. What we did not realize is that the preleukaemic stem cells were expanding at the expense of normal HSCs, not adding to normal HSCs.

This latter point became clear when my laboratory studied several cases of blood diseases, which can progress to AML. Chronic myelogenous leukaemia (CML) is the precursor to blast crisis acute leukaemia, which is usually in the myeloid lineage (MBC). Fialkow [52] had shown that in the chronic phase, the myeloproliferative clone was not only limited to the increased frequency granulocyte lineage, but also dominated progeny of erythroid, monocytic, megakaryocytic and B lymphoid cells. Nowell et al. [53] and Rowley et al. [54] showed later that CML resulted from a prototypic chromosomal translocation, 9 : 22, to produce a bcr:abl fusion oncogene. My colleagues and I showed that the translocation was in HSCs, and that the bcr:abl HSC clone expanded at the expense of normal HSCs, without measurably increasing the total frequency of HSC phenotype cells [51,55,56]. The disease appeared to be a strong myeloid bias of the bcr:abl HSCs rather than an uncontrolled self-renewal of these HSCs [51]. The transition of CML to MBC CML led to dramatically expanded GMP stage cells which could transfer the tumour in vivo and give leukaemic colonies in vitro [51]. The GMP LSC had activated the wnt/β-catenin pathway...
[51], a necessary event for their self-renewal related proliferation [56]. In four of seven patients this involved GMP-specific missplicing of GSK3β, the enzymatic inhibitor of β-catenin protein, which lost its kinase domain. This misspliced loss of exon 8, which encodes the kinase domain, only occurred in the GMP LSC, which are approximately 5% of the marrow, and is hardly seen if one examines whole marrow instead of purified GMP LSC [56]. This makes the point that epigenetic analysis of heterogeneous populations is too crude to identify cell stage specific changes in gene expression; enrichment or purification is required to know which cells expressed or silenced or spliced which genes.

Other myeloid proliferative disorders follow the same pattern: clones with preleukaemic mutations in genes such as Jak2 [57], calreticulin [58] and the various genes resulting in myelodysplastic syndrome (MDS) [55] allow expansion of the disease or preleukaemic clone at the expense of normal HSCs in the patient, and in the cases tested, upon HSC transplantation into immune deficient mice [53]. To test the hypothesis that HSCs are the cell stage of clonal progression of preleukaemia, resulting in ever more competitive HSC clones, we sequenced the exomes of many AML samples to define each of these, to escape the stem cell frequency dictated by virtual and/or structural niche interactions, the last, proliferative and self-renewing event probably would occur at the stage of a downstream progenitor [48].

The general principle that emerges is that most initiating and early mutations in these clones are of genes that regulate epigenetic programmes, and themselves are not directly active in self-renewing cell divisions [59]. It is unlikely that they could have been perpetuated had they occurred in a non-stem cell. The final mutations in this entire series, biased for patients with Flt3 internal tandem repeat activating events and ras mutations, occurs in the MPP progeny of the preleukaemic clone [60]. The malignant MPP are no longer under control for their population size and niche location, and can be found in all bone marrow sites sampled [60].

These events occur in the myelogenous leukaemias. I proposed that similar premalignant progression occur in all tissues in which resident stem cells are required for tissue maintenance [48]. Thus, I expect that mutations and malignant epigenetic events will be found in mammary stem cells giving rise to breast cancers, CNS stem cells [61] giving rise to malignant brain tumours [62], intestinal stem cells [63] giving rise to colorectal cancers [64] and so on. In each of these, to escape the stem cell frequency dictated by virtual and/or structural niche interactions, the last, proliferative and self-renewing event probably would occur at the stage of a downstream progenitor [48].

4. Stem cell competitions, migration and metastasis

Within at least chordate metazoans, some cell populations required migration to land in sites required for their
Figure 3. Single-cell analysis determines the sequence of mutations acquired in preleukaemic HSCs in acute myeloid leukaemia. Each row depicts the proposed clonal evolution of leukaemia in each of three patients. Adapted from [59]. (Online version in colour.)

function. These migrations can occur within an organ, but in the case of blood and blood forming cells, migrations are required between organs via the blood vasculature. My laboratory and others, for example, have defined several homing receptors, chemokine receptors, cell surface adhesins and endothelial addressins to allow various naive, activated and memory T and B lymphocytes to give site-appropriate and whole body protection against various microbial pathogens, toxins and even emergent malignant cells [65–67]. Malignant lymphomas can use these homing receptors for site-specific metastases [68–70], and tumours such as malignant lymphomas can use these homing receptors for genets, toxins and even emergent malignant cells [65–67].

Successful migration of cells past macrophages occurs if the cells do not express ‘eat me’ markers on their surface, or if they express dominant ‘don’t eat me’ markers, to counteract the ‘eat me’ signals [84]. For example, granulocytes in mice have a 1–2 day lifespan, and this is controlled by both PCD and PrCR [85]. New-born granulocytes express no ‘eat me’ signals, but 12–24 h later, normally just after the initiation of PCD but before the cells burst, they express ‘eat me’ signals that signal macrophages to phagocytose them [85]. Even granulocytes deprived of PCD by enforced expression of the anti-PCD molecule bcl2 express the ‘eat me’ signal at the time their dying counterparts without bcl2 express it, and homeostasis is assured by PrCR by macrophages with receptors for the ‘eat me’ signals [85]. I proposed that events leading to cell death trigger the independent pathways of PCD and PrCR [48,84,85]. These events could be intrinsic clocks, like in neutrophils, DNA damage, mutations, unfolded protein response, inflammation, intracellular infection, over-proliferation and at least some mutations in the progression to cancer [84]. When my colleagues and I compared the gene expression profiles of LSC and their normal haematopoietic counterparts in mouse [47,86] and human [50], one of the highly overexpressed genes was CD47. Oldenborg et al. [87] had shown in 2000 that CD47 was the predominant determinant of mouse red blood cell intravascular lifespan. They further showed that it was a ‘don’t eat me’ signal for macrophages, acting as a ligand for macrophage SIRPα, a receptor tyrosine phosphatase acting via its cytoplasmic ITIM motif to activate SHP1 to block phagocytosis [87]. Towards the end of the red cell life, the balance of ‘eat me’ to CD47 signals allows phagocytosis in the marrow, splenic and liver sinuosoids by macrophages (for review, see Chao et al. [84]). We showed that CD47 was expressed at low levels in quiescent bone...
isolated human fetal brain CNS stem cells transplant into immune-deficient mouse brains successfully, become restricted to the CNS zones of the subventricular zones of the lateral ventricle and the dentate gyrus (DG) of the hippocampus [61], where for the life of the host show site-appropriate neurogenesis, self-renewal, migration and differentiation to progeny cells at distant sites [61,110]. This continued cycle of proliferation, self-renewal, migration and differentiation probably occurs at lower rates than haematopoiesis or intestinal cell turnover, but is similarly susceptible to mutations and epigenetic change. It is clear from the discussion of progression to leukaemic malignancy above that the same will apply to neurogenesis, e.g. for the development of glioblastoma, and that should be testable when downstream oligolineage progenitors in neural lineages get to the point of having progressively isolated intermediates from human or mouse neural stem cells. A curiosity is the many cases of neurodegenerative disease that derive from germline-inherited mutations, but do not manifest as disease until far later. Perhaps other functions of the brain that have both structural and even ‘mind’ functions should similarly be open to mutations and/or heritable epigenetic changes that alter functions such as migration, with consequences that result in disease. Kemperman, Gage and co-workers [111,112] opened the possibility that hippocampal DG neurogenesis plays a role in the mind functions of types of short-term memory. Dendritic and axonal connections that result from DG neurogenesis probably mediate the rapid acquisition of short-term memory, and insofar as that type of memory gets transferred via circuitry to cortical foci, feedback and feed-forward events could be involved.

Two examples of diseases of the mind could be relevant: in senile dementias such as Alzheimer’s disease (AD), the first signs are loss of short-term memory [113]. AD phenotype mice develop amyloid plaques [114], thought by many to be the toxic cause of loss of hippocampal neurogenesis [115]. However, transplantation of normal human fetal CNS stem cell derived neurosphere cells into the DG region of AD immune-deficient mice shows healthy neurogenesis in apposition to plaques, implying that cell intrinsic toxicity rather than β-amylloid induced toxicity is important (figure 4; N Uchida, A Tsukamoto-Weissman, IL Weissman, G Carlson 2003 unpublished data). This could result from germline heritable mutations as initiating events, only to become pathogenic later in life with the acquisition of dominant CNS SC mutations or epigenetic changes. The second example is schizophrenia. My colleagues and I have written elsewhere [116] that the initial sign of this disease is usually reported as auditory hallucinations, or ‘voices in the brain’. PET scans of patients with this disease show focal prefrontal or temporal active foci of increased glucose uptake in concert with the voices. Spontaneous discharges from focal areas of brain can result in epileptic seizures when in the motor cortex. We proposed that this could begin with hippocampal neurogenesis, and result from unregulated circuitry, e.g. in areas not surrounded by adult Gaba-ergic inhibitory neurons. The manifestations of voices, later attributed to persona, could be the result of disease progression. The finding that a group of patients from a Scottish family had heritable disease linked to the gene disc-1 allowed Ming, Song et al. [117] to test the role of disc-1 in hippocampal neurogenesis. New-born DG neurons with disc-1 knockout mis-migrated to regions in and around the DG lacking surrounding neurons, including Gaba-ergic neurons. Because these CNS stem cell clones are derived over a lifetime...
from self-renewing cells, it is conceivable that genetic or somatic variations in a dominant CNS SC clone could eventually connect with a circuitry transferred to the part of the brain responsible for generating voices, or stories. This kind of hypothesis leads to the potential for basic and clinical experiments to connect the biology of neurogenesis and the properties described above of stem cells to the development of these kinds of diseases.

In conclusion, with the appearance of metazoans and the tissue and organ segregation of functions, a class of cells, stem cells, retain the property of self-renewal to maintain homeostasis. The stem cell functions of self-renewal, migration and regulated differentiation to non-self-renewing progeny have resulted in diversity of tissue stem cells within an individual in order for clonal selection to allow maximal fitness of tissue homeostasis throughout the changing internal events in long-lived organisms. Clonal selection also operates in the stem cell competitions between tissue stem cells within an organ, and on germline stem cells, which can be units of natural selection between individuals in a species. Selection can be based on the variations also occurring with mutations or unscheduled epigenetic alterations, and the progeny that are more competitive are on a path to cancer and/or tissue or organ degenerative diseases, in part controlled by the events of PCD and PrCR. Studying the biology, developmental biology and stem cell biology of stem cell systems may seem like opening the pages of a book already read, but can also offer clues for disease pathogenesis and functions of the brain.

Competing interests. I declare I have no competing interests.

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Endnote

‘There are colonies of pelagic tunicates which have taken shape like the finger of a glove. Each member of the colony is an individual animal, but the colony is another individual animal, not like the sum of its individuals... So a man of individualistic reason, if he must ask, ‘Which is the animal?’ must abandon his particular kind of reason and say, ‘Why, it’s two animals and they aren’t alike any more than the cells of my body are like me. I am much more than the sum of my cells, and, for all I know, they are much more than the division of me’ [21].

References


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