

Erythropoiesis in vertebrates: from ontogeny to clinical relevance

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1. ABSTRACT

Erythropoiesis is a complex process that starts in the course of embryo formation and it is maintained throughout the life of an organism. During the fetal development, erythropoiesis arises from different body sites and erythroblast maturation occurs in the fetal liver. After birth, erythropoiesis and erythroblast maturation take place exclusively in the bone marrow, generating a lifetime reservoir of red blood cells (RBCs), which are responsible for transporting oxygen through the bloodstream to tissues and organs. Several transcription factors and cytokines, such as GATA-1, GATA-2, FOG-1 and erythropoietin (EPO), constitute an elaborated molecular network that regulates erythropoiesis as they are involved in the differentiation and maturation of RBCs. The profound understanding of erythropoiesis is fundamental to avoid, treat or even soften the effects of erythropoietic clinical disorders and may be useful to improve patients' well-being.

2. INTRODUCTION

Erythropoiesis is a process by which hematopoietic stem cells (HSCs) proliferate and differentiate to produce mature red blood cells (RBCs). Because erythroid lineages are extensively studied at cellular and molecular levels, the knowledge on their phenotypic markers, regulating transcriptions factors and related erythroid diseases is well consolidated. Nevertheless, deeply understanding this complex process, especially in humans, may shed light on basic cellular biology and on the pathophysiology of various diseases including bone marrow failure, degenerative diseases and cancers (1).

3. ERYTHROPOIESIS

3.1. Fetal erythropoiesis

Erythropoiesis in the intrauterine stage is essential to support embryo survival, growth and development to fetus (2,3). During the intrauterine stage of development, erythropoiesis comprises three transient hematopoietic waves (2,3). The first erythropoietic wave takes place entirely in the yolk sac blood islands, generating all primitive erythrocytes-myeloid progenitors (3). At this stage, primitive erythroid cells emerge and remain predominantly in the bloodstream until a second wave arises, which produces definitive erythroid cells (4). In the course of the second erythropoietic wave, the maturation of erythroid precursors occurs in the bloodstream and in the liver, decreasing the number of precursors and increasing the presence of definitive erythroid cells in the blood (5,6). This erythropoietic wave in mice may correspond to the first hepatic colonization of erythroid progenitors in humans (7). During the third wave, HSCs emerge from the main arteries between the embryonic days 7.5-11.5 (E7.5-E11.5), residing in the aorta-gonad-mesonephros of the embryo, yolk sac and placenta, migrate to the fetal liver (E14.5 murine/day 23-27 humans), proliferate and accumulate in the bone marrow (E18.5 murine/10-11 weeks humans) (8,9). Concomitantly, burst forming unit-erythroid (BFU-E) arises from HSCs in the fetal liver originating mature erythroblasts (10,11). Towards the end of gestation, erythropoiesis moves from the liver to the bone marrow (4).

Mammal intrauterine erythropoiesis consists of primitive and definitive phases, both taking place in different sites of the embryo and fetus. Whereas primitive erythropoiesis occurs in the early formation

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of the embryo, close to E7.5 in mice and E17 in humans, definitive erythropoiesis begins during late fetal development, around E14 in mice and 7-8 weeks in humans (3,4). Primitive and definitive erythropoiesis involve cell trafficking through erythroid progenitors, erythroblast precursors, and RBCs compartments (3).

Erythroid progenitors originate from hemangioblasts (E7.5) and comprise two morphologically and developmentally distinct and temporally overlapping populations of erythroid lineages - primitive and definitive erythroid cells - which were firstly described more than a century ago (12-16). Primitive progenitors are nucleated cells that differentiate from mesodermal cells present in the yolk sac of the mammalian embryo during its early postimplantation development soon after the onset of gastrulation (E6.5) (3,4,17). They express adhesion molecules on their surface, so they are able to form colonies of maturing erythroid cells *in vitro* and may be found associated with endothelial cells *in vivo* (2,18). Definitive yolk sac erythropoiesis in mice and humans produces great amount of erythroid progenitors (E9.5) (3,7,19,20). The limited knowledge regarding primitive erythropoiesis in humans is mainly due to ethical issues concerning the isolation of embryonic stem cells and physical inaccessibility to early embryos. Nevertheless, it is suggested that this process happens in human embryos similarly to what occurs in mice (21). In human embryos, nucleated primitive erythroid cells appear in the fetal circulation during the first trimester (3). Primitive erythroblasts are the only circulating erythroid cells from 3 to 6 weeks of gestation. For instance, BFU-E are detected within 4-5 weeks gestation (22), after the second wave of colonization of the fetal liver by HSCs (4). Among many biological functions of erythrocyte progenitors during embryo growth and development, oxygen delivery, scavenge reactive oxygen species and vascular remodeling into mature blood vessels can be highlighted (23,24).

As the embryo develops, its vascular network, yolk sac and placenta links to each other, connecting the circulatory system and initiating the heart beating. The large size of erythroblasts precursors may create shear forces that correlate with the embryo vascular remodeling (7,23). Prior to the second wave of erythropoiesis, erythroid progenitors produced in the yolk sac lose adhesion molecules and secrete metalloproteases, facilitating their entry into the bloodstream (25). Active circulation starts at E9 (26).

In primitive erythropoiesis, progenitor cells differentiate into erythroblast precursors in the bloodstream (E9.5-E17.5) (24,27), although signals that induce this phenomenon remain unclear (26,28). Throughout definitive erythropoiesis, progenitor cells migrate to the fetal liver (E9.5) and accumulate into blood islands, which contain macrophages surrounded by

differentiating progenitors and newly formed precursor cells at various stages of maturation (E9.5-E12.5) (29). The intimate contact of macrophages with erythroblasts allows phagocytosis and destruction of the expelled nuclei from erythroid precursors by macrophages. Besides that, macrophages promote erythroblast proliferation under stress conditions, as it happens in hypoxia (30-32). In this way, macrophage activity in the blood islands is essential for erythroblast maturation and proliferation (33). Therefore, the fetal liver provides a suitable microenvironment for the expansion and differentiation of definitive erythroid cells (25,33). This organ also acts as a niche for the expansion and differentiation of definitive HSCs, generating definitive erythroid cells that differentiate through a hierarchy of progenitors (5,6).

Erythroblast precursors (proerythroblasts, basophilic, polychromatophilic and orthochromatic erythroblasts) are nucleated cells found and matured either in the bloodstream (primitive erythropoiesis) or liver (definitive erythropoiesis). These cells differ from each other according to morphological changes that occur during their development. Losses of nucleoli (E9.5-10.5), nuclei condensation (E10.5), cytoskeleton remodeling accompanied by a decrease in cell size (E10.5-E11.5), enucleation of orthochromatic erythroblasts (E12.5), intracellular hemoglobin (Hb) accumulation and organelle clearance are reflected by changes in cytoplasmic staining of these cells as they mature (24,34-37). Similarly to what happens to mice, human erythroblasts enucleate *in vivo* as they interact with macrophages within the placenta (38). Enucleation results in formation of pyrenocytes and reticulocytes and may favor primitive RBCs to acquire a more hydrodynamic shape that is useful for their transit through the bloodstream. At least, reticulocytes will mature into RBCs (37,39-42).

During RBCs maturation, their progenitor loses surface area and cytoplasmic volume (E14.5-17.5) (42). Circulating reticulocytes and mature RBCs compose the third erythropoietic compartment. The production and release of reticulocytes into the bloodstream is responsible for the maintenance of RBC levels in the blood during homeostasis (43). Definitive erythropoiesis begins in the yolk sac of mice and human embryos, originating the first circulating definitive RBCs that emerge from the liver (E11.5-12.5). Later in the fetal development, this initial transient phase is replaced by a life-lasting erythropoietic system that uses HSCs as a cell source for erythropoiesis (44). Erythroid-myeloid progenitors definitive erythropoiesis acts as a developmental transition between primitive and HSC-derived erythropoiesis (5). In mammals, definitive RBCs circulate as smaller and anucleated cells through fetal and postnatal life.

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Transcriptional regulators play an important role in erythropoiesis as they drive lineage-specific cellular development and maturation. Primitive and definitive erythroid cells have particular requirements for transcriptional and soluble factors, expressing endless gene signatures according to their stage of maturation (24,25,45). Therefore, gene expression studies are extremely important as they enrich the knowledge on the biology of primitive and definitive erythropoiesis. Many authors have investigated erythroid cells at transcriptional, posttranscriptional, and epigenetic levels (44,46-51). A transcriptional roadmap for primitive erythropoiesis can be found online at Gene Expression Omnibus (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24127>). Besides that, gene expression profile in morphologically comparable states of primitive and definitive erythroid precursors is also available online (<http://www.cbil.upenn.edu/ErythronDB>).

3.2. Adult erythropoiesis

Erythropoiesis is tightly regulated by cytokines, such as erythropoietin (EPO), transcription factors, such as GATA-1, GATA-2, FOG-1, and micronutrients, such as iron and vitamin B12 (52,53). During early stages of erythropoiesis, HSCs give rise to common myeloid progenitors, megakaryocyte-erythrocyte progenitors, colony forming unit-erythroid (CFU-E) cells and BFU-E (54). During late stages (also referred as *terminal erythroid differentiation*), morphologically recognizable proerythroblasts undergo mitosis to produce basophilic, polychromatic, and orthochromatic erythroblasts. Orthochromatic erythroblasts expel their nuclei to generate reticulocytes. Finally, reticulocytes mature in the bone marrow, losing their intracellular organelles, such as mitochondria (55,56) and ribosomes, and undergo extensive membrane remodeling, generating RBCs that enter the bloodstream (29,54).

BFU-E and CFU-E cells have been traditionally defined by colony assays (57, 58). BFU-E is characterized by CD45⁺GPA⁺IL-3R⁻CD34⁺CD36⁻CD71^{low} phenotype and CFU-E is characterized by CD45⁺GPA⁺IL-3R⁻CD34⁻CD36⁺CD71^{high} phenotype. Whereas the BFU-E colony-forming ability of CD45⁺GPA⁺IL-3R⁻CD34⁺CD36⁻CD71^{low} cells requires stem cells factor (SCF) and EPO, the CFU-E colony-forming ability of CD45⁺GPA⁺IL-3R⁻CD34⁻CD36⁺CD71^{high} cells requires only EPO, demonstrating specific requirements related to the development of RBCs. Techniques that ensure the isolation of highly pure human BFU-E and CFU-E progenitors are extremely useful to study disordered erythropoiesis in inherited and acquired hematological diseases (54).

BFU-E-derived colonies require 14 days in human systems to form mature colonies that typically contain more than a thousand erythroid cells. In contrast, CFU-E progenitors require only 7 days to form mature

colonies consisted of only 16–32 cells. Thus, CFU-E are only 4–5 cell divisions upstream of mature RBCs (3).

Lately, researchers have been focused on elucidating how erythroid differentiation is regulated. Recent discoveries have clarified that lineage-specific transcription factor networks are essential for proper differentiation of erythroid cells, being GATA-1 and GATA-2 important transcription factors involved in the regulation of erythroid gene expression (52).

GATA transcription factor family is composed of six members in mammals, showing a highly conserved expression pattern in vertebrates. GATA-1, GATA-2 and GATA-3 are classified into the hematopoietic GATA subfamily based on their expression profiles and domain structures (59,60). Several advanced experimental approaches have further revealed the importance of GATA-1 in adult hematopoiesis, especially for erythropoiesis. Friend of GATA (FOG-1), as the name implies, is a very close interacting partner of GATA-1 (51). It is a large nine zinc finger-containing protein, which does not bind directly to DNA. Four of the FOG-1 zinc fingers contribute to its interactions with GATA-1 (61). FOG-1 is highly expressed in erythroid cells and megakaryocytes, mirroring expression of GATA-1 in these lineages. The phenotype of the FOG-1 gene knockout is very similar to that of the GATA-1 knockout as it results in mid embryonic lethality due to severe anemia (62).

FOG-1 is an essential coregulator of GATA-1 during hematopoiesis, mediating both transcriptional activation and repression (62,63). The importance of FOG-1 is underscored by the finding that FOG-1-deficient mice die from anemia with defects resembling loss of GATA-1 (62-64).

In contrast, GATA-2 is necessary for maintaining storage pools of hematopoietic stem and progenitor cells. Both, GATA-1 and GATA-2 expression is dynamically changed during erythroid differentiation and have particularly functions, which remain to be clarified (52). Further *in vitro* and *in vivo* studies focusing on transcription factors may provide valuable understanding regarding molecular mechanisms that regulate erythropoiesis.

3.3. Hemoglobin, role of erythropoietin in erythropoiesis and the iron metabolism

Hb is the main oxygen and carbon dioxide carrier present in erythroid cells and is responsible for oxygen delivery to body tissues (65).

During gestation, a sequential activation of genes responsible for the production of globin chains occurs, leading to the formation of different types of embryonic and fetal Hb that differ from each other according to their constitutive chains (66). These newly synthesized chains are capable of binding to heme and iron, forming the Hb molecule.

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Embryonic Hb is found exclusively during the first 10 to 12 weeks of gestation and is synthesized by primitive erythroblasts in hematopoietic centers of the mesenteric onfalo-channel (67). Two ζ (zeta) and two ϵ (epsilon) chains, two α (alpha) and two ϵ chains, and two ζ chains and two γ (gamma) chains respectively form Gower 1 Hb, Gower 2 Hb and Portland Hb (68). Embryonic Hb has a high affinity to oxygen, hampering the release of oxygen at tissue level (69). During the third trimester of pregnancy, the production of ϵ chains decreases as β (beta) chains gradually replace them, resulting in the production of fetal Hb (HbF) (70). This phenomenon facilitates the release of oxygen to tissues in a more efficient manner than embryonic Hb (71,72).

In healthy newborns, two thirds of Hb are type A (Adult Hb) and one third belongs to the HbF (73). Adult Hb is a tetramer composed of both alpha and beta like polypeptide subunits ($\alpha_2\beta_2$), called HbA. A normal variant of HbA (HbA2) consisting of two alpha and two delta chains ($\alpha_2\delta_2$) can be found at low levels in normal human blood. The composition of these subunits varies over the course of ontogeny, leading to assembly of Hb molecules with different physiologic properties. In humans, two developmental switches take place for the production of the β -like subunits of the hemoglobin molecule. This switch is known as the primitive to definitive Hb switch at the β -globin locus (45). Kruppel-like factor 1 (KLF1) and B-cell CLL/lymphoma 11A (BCL11A) are two transcription factors with key roles in the developmental regulation of Hb expression. In particular, KLF1 activates β -globin and BCL11A, which in turn represses γ -globin expression (74).

The constant blood Hb concentration is maintained by EPO. Synergistically to EPO signaling effects, Stem cell Factor (SCF) signaling pathway also plays an essential role in erythroid cell development. SCF receptor is a member of the type III subfamily of receptor tyrosine kinase, which also includes the receptor for macrophage colony-stimulating factor (M-CSF) and platelet-derived growth factor (PDGF) (75). Similarly, interleukin-3 (IL-3) can also interact with EPO to stimulate more immature erythroid progenitors (76). EPO is a 30.4 kD acidic glycoprotein with 165 amino acids that acts as a hormone, cytokine and growth factor (77,78). It affects not only erythroid cells, but also other blood cell lines, such as myeloid cells, lymphocytes and megakaryocytes. Thus, EPO is able to enhance phagocytes function of polymorph nuclear cells and reduce the activation of macrophages, modulating the inflammatory process (79).

EPO is primarily expressed by hepatocytes during the fetal stage (78). It is an important cytokine that is required for the growth, survival and differentiation of red blood progenitor cells, exerting its physiological role by binding to its specific cell surface receptor (EpoR), which is predominantly found on erythroid precursor cells (80,81). In this way, EPO plays a central role in

the regulation of erythropoiesis by blocking apoptosis in erythroid progenitors and enhancing proliferation and differentiation of their progenies. Additionally, it has been reported that EPO contributes to the expansion of multipotent hematopoietic progenitors (82). Mice lacking EPO or EpoR are embryonic lethal *in utero* due to severe anemia, suggesting EPO primary role in the regulation of red cell production (81).

After birth, EPO is mainly produced by peritubular interstitial fibroblasts in the renal cortex (83-85), although its mRNA may be detectable in the liver, spleen, bone marrow, lung and brain (86). Hepatic EPO is produced by hepatocytes and contributes about 10% of the plasma EPO (87). The secretion of EPO into the circulation and its plasma concentrations (6-32 UI/L) are determined by the transcription rate of the EPO gene (in chromosome 7), which plays a key role in controlling cellular oxygen concentration (78,88, 89). In this way, plasmatic EPO is inversely related to the oxygen content in the blood.

Hypoxia is the main regulator of EPO levels (90). Although several transcription factors are involved, hypoxia inducible factors (HIFs) are key regulators of the hypoxic response pathway. The three members of the HIF transcription factor family are known as HIF-1, -2 and -3. HIF-1a was first identified as a mediator of EPO induction in response to hypoxia *in vitro*. However, HIF-2 has now been identified as the primary transcription factor that controls EPO synthesis. All HIF transcription factors interact with HIF-1b to regulate the genes involved in erythropoiesis, including the Epo gene, as well as in iron metabolism, which is essential for tissue oxygen delivery (91-93). The HIFs are inactivated in normoxia by enzymatic hydroxylation of their α -subunits (94-96). Acute exposure of mammals - including humans - to hypoxia conditions, such as those found at high altitudes, enhances plasma EPO in more than 10-fold (90). Although the ratio of oxygen delivery to oxygen requirements is the primary physiologic regulator of EPO production, anabolic and androgenic steroids also can stimulate EPO production by an unknown mechanism (97-100).

HIFs play a central role in control of both iron metabolism and erythropoiesis. Interestingly, hepatocyte-derived HIF-2 is also involved in the regulation of iron metabolism genes, supporting a role for HIF-2 in the coordination of EPO synthesis with iron homeostasis (92).

Erythropoietic tissue is the major body consumer of iron, which is essential for erythropoiesis especially for heme and Hb synthesis by maturing erythroblasts (101,102). Most of the iron in the body is in Hb of red cells, which contain about 1 mg of iron per mL of erythrocytes. In contrast, transferrin, the plasma iron carrier that is the exclusive source of iron for erythropoiesis, carries 2-3 mg of iron in all blood plasma (103,104).

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Approximately 20%-30% of body iron is stored within polymers of ferritin in hepatocytes and in macrophages (105). Erythropoiesis requires approximately 30 mg of iron per day, mainly provided by the recycled iron from macrophages, which ingest senescent erythrocytes and release iron (105). A minimal amount of iron is provided by intestinal iron absorption through the mediation of specific transport proteins (101). The most important transport protein for iron systemic regulation is ferroportin-1 (FPN1), which in association with the plasma ferroxidase ceruloplasmin, allows the transport of iron into the plasma across the membrane of absorptive enterocytes, macrophages and hepatocytes (105-108). Cellular iron uptake primarily occurs by the endocytic pathway, in which iron is transported into the circulation by transferrin and released to erythroblasts by the interaction of diferric transferrin with the transferrin receptor (109-111).

The key regulator of systemic iron homeostasis is hepcidin, a small antimicrobial peptide synthesized by the liver, which regulates intestinal iron absorption, plasma iron concentrations and tissue iron distribution due its ability to bind FPN1 on cellular surface blocking its iron transport activity, and to increase FPN1 degradation (103,112). Hepcidin is upregulated by both increased iron stores and inflammation. On the other hand, hepcidin secretion is reduced in response to signals that cause an increase in iron release from cells, such as iron deprivation, and stimulus to erythropoiesis (105,113-115).

A large amount of literature is available regarding iron transporting through membranes, intracellular iron trafficking and the relationship between iron and erythropoiesis (105-113).

3.4. Clinical relevance of erythropoiesis disorders

Erythroid development is a refined regulated process that requires a continual replacement of cells as mature blood cells have limited lifespans. Dysregulation of this process may cause hematological malignancies (116).

Several diseases that are related to erythropoietic disorders have been documented over the years. Among them, anemia appears in higher frequency in consequence of diverse pathologic states such as neoplasias, inflammation, hemolysis, acute bleeding, marrow damage and cell maturation disorders. Anemia may be developed as a consequence of three main factors: 1) blood loss, 2) decrease in RBCs production and 3) increase of RBCs breakdown (117). Blood loss usually involves a bleeding trauma. Whereas the decrease in RBCs production often occurs in response to iron deficiency, lack of folate and/or vitamin B12, thalassemia, bone marrow neoplasms and others, the increase RBCs breakdown is a consequence of genetic

disorders and environmental conditions that may lead to infections (118,119).

Megaloblastic anemia is usually associated with lack of vitamin B12 and results in the inhibition of DNA synthesis during RBCs production and can cause important neurological manifestations (120). Another type of megaloblastic anemia is derived from folate deficiency, essential for RBCs formation and to growth (121). However, among the micronutrients-related anemia, iron deficiency is the most common (122). Iron anemia is a result of a prolonged negative iron balance due a chronic and prolonged iron loss or by inefficient iron absorption or by a nutrition iron deficiency. Iron anemia results in body iron storage depletion and can be distinguished from functional or relative iron deficiency, which are defined as a response to intravenous iron with an increase in Hb or a decrease in erythropoiesis-stimulating agent requirement, respectively (123).

Thalassemia is another erythropoietic syndrome that results from the imbalance of α - or β -globin chain production. This imbalance leads to an impaired RBC synthesis and more erythroid progenitors in the bloodstream, correlating to an imbalance of the proper erythropoiesis and the iron metabolism (124). The neoplasms, such as bone marrow neoplasms and solid tumors, particularly gastric, breast, and lung cancers are related to the decreased production of RBCs (125), and also the aplastic anemia which is characterized by the by peripheral blood pancytopenia in response to the fatty replacement and decreased hematopoietic precursors of the bone marrow immune-mediated (126). In addition to bone marrow neoplasms, acute erythroid leukemias may be derived from abnormal erythroid hyperplasia in bone marrow (127).

As previously mentioned, RBCs breakdown is usually caused by genetic disorders and detrimental environmental conditions, causing hemolytic anemia, such as sickle cell anemia, G6PD deficiency, abnormalities of the erythrocyte membrane, autoimmune anemia, exposure to certain chemicals, drugs, and toxins as well as infections. Other causes are blood clots in small blood vessels and transfusion of blood from a donor with a blood type that does not match yours (130-132).

Iron deficiency anemia may be related to nutritional deficiency and/or blood loss. Nevertheless, this type of anemia remains the most common treatable anemia in the world, and despite of the low frequency of inherited erythropoietic syndromes, anemia as a blood disorder still deserves attention, due to its incidence in patients with cancer, as a result of the malignancy nature of the tumor and/or the cytotoxic effects of chemotherapy on the hematopoietic cells. Therefore, the management of cancer-associated anemia is one of the key issues to improve life quality and reducing morbidity in cancer patients (128).

4. SUMMARY

Although much is known about the erythropoiesis regulation as several factors involved in this process much still remains to be studied. However, the current knowledge ranging from the generation of RBCs and factors involved in this process can act in preventive and reparative ways providing benefits to those whom are committed by some RBC disorder.

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Abbreviations: RBCs: red blood cells; EPO: erythropoietin; HSCs: hematopoietic stem cells; E: embryonic days; BFU-E: burst forming unit-erythroid; CFU-E: colony forming unit-erythroid; Hb: haemoglobin; CFU-E: colony forming unit-erythroid; SCF: stem cells factor; KLF1: Kruppel-like factor 1; IL-3: Interleukin-3; EpoR: erythropoietin receptor; FPN1: ferroportin-1; HIFs: hypoxia inducible factors

Key Words: Fetus, Adult, Erythropoiesis, Hemoglobin, Erythropoietin, Iron metabolism, Erythropoietic disorders, Review

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