Metabolism in pluripotency: Both driver and passenger?

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Pluripotent stem cells (PSCs) are highly proliferative cells characterized by robust metabolic demands to power rapid division. For many years considered a passive component or “passenger” of cell-fate determination, cell metabolism is now starting to take center stage as a driver of cell fate outcomes. This review provides an update and analysis of our current understanding of PSC metabolism and its role in self-renewal, differentiation, and somatic cell reprogramming to pluripotency. Moreover, we present evidence on the active roles metabolism plays in shaping the epigenome to influence patterns of gene expression that may model key features of early embryonic development.

Most investigators view metabolism, which encompasses the synthesis and utilization of macromolecules and energy, as a passive supporter of self-renewal and rapid proliferation in pluripotent stem cells (PSCs) and their differentiated, slower dividing progeny. However, exciting recent studies are changing this perception by showing an active role for metabolism in PSC fate determination.

Metabolism in PSCs and somatic cells

Glycolysis and oxidative phosphorylation

Mammalian cells generate ATP by varying the ratios of glycolysis and oxidative phosphorylation (OXPHOS). Human and mouse PSCs produce energy mainly by the enzymatic conversion of glucose to lactate (1), which contrasts with resting somatic body cells that favor OXPHOS (Fig. 1) (2–5). This difference persists for PSCs made from blastocysts or by somatic cell reprogramming, independent of oxygen availability (6). We interpret this energetic difference as a possible programmed feature of cell state rather than a consequence of relative hypoxia in earliest embryo development. Despite a markedly lower ATP yield per glucose molecule, elevated glycolysis in PSCs, also seen in rapidly dividing cancer cells (Warburg effect), has several key advantages. Increased glycolytic flux fuels the biosynthesis of nucleotides, lipids, and reducing equivalents to support rapid cell replication. Maintaining embryonic integrity, or genomic stability during embryonic development, requires reducing genomic and mitochondrial DNA damage and protein and lipid oxidation from reactive oxygen species (ROS) produced by OXPHOS. A premium for embryonic integrity is also manifest as heightened apoptosis sensitivity in early embryos, germ cells, and PSCs (2, 7, 8). Favoring glycolysis reduces ROS, which, along with augmented antioxidant mechanisms, supports PSC self-renewal until differentiation is triggered with required OXPHOS and ROS elevations (9–11).

Glutamine

Glutamine supports PSC survival and expansion by increasing antioxidant GSH (4) and fueling mitochondrial energy metabolism (12–14). Glutaminolysis generates tricarboxylic acid (TCA) cycle substrates (12) and supports the mitochondrial inner membrane potential (∆Ψ) required for PSC survival (15). A paradoxically high ∆Ψ in PSCs compared with PSC-differentiated progeny (3, 16, 17), despite low OXPHOS in PSCs, may arise from the hydrolysis of glycolytic ATP by complex V ATP synthase. PSCs show low expression of inhibitory factor 1, which prevents ATP synthase from running as an ATP hydrolase (2). Because low ∆Ψ facilitates the induction of apoptotic pathways, enhanced apoptotic sensitivity of PSCs compared with PSC-differentiated progeny is surprising with comparatively heightened ∆Ψ in PSCs and requires further study.

Lipids

Similar to rapidly dividing cancer cells and antigen-activated lymphocytes, robust lipid biosynthesis occurs in PSCs to replenish membranes and organelles (16). Lipid production also supports somatic cell reprogramming to pluripotency (18, 19). Carbons for lipid building are siphoned from glycolysis and
glutaminolysis biochemical pathways (12, 14). Indeed, lipid anabolism promotes PSC identity, notably by regulating mitochondrial dynamics (see below).

**Regulation of PSC metabolism**

**Core pluripotency transcription factors**

In embryonic stem cells (ESCs), core pluripotency transcription factors (CPTFs), such as OCT4, interact with the promoters of genes encoding glycolytic enzymes hexokinase 2 and pyruvate kinase M2 (PKM2) to drive transcription and augment glycolytic flux (5, 20, 21). Metabolic coordination by CPTFs indicates an essential role for metabolism in pluripotency.

**Regulators of mitochondrial carbon routing**

Uncoupling protein 2 (UCP2) is a mitochondrial inner membrane protein expressed in PSCs that limits OXPHOS and ROS production (2). Aberrant re-expression of UCP2 in many types of cancer also inhibits OXPHOS to bias ATP production toward aerobic glycolysis (22). The metabolic coordination by CPTFs indicates an essential role for metabolism in pluripotency.

**Mitochondrial network**

PSCs show punctate mitochondria with immature inner membrane cristae and evidence of reduced functionality with low OXPHOS (2, 4, 5) and ROS production (14, 26). A granular mitochondrial morphology contrasts with elongated mitochondrial networks in somatic cells and helps to sustain CPTF expression and prevent expression of differentiation genes (27). Conversely, the REX1 pluripotency-associated transcription factor (TF) causes Ser-616 phosphorylation and activation of the mitochondrial fission regulator DRP1 by CDK1/cyclin B (27). Also, repression of mitochondrial fusion proteins...
MFN1/2 during somatic cell reprogramming is linked to reduced p53 expression and increased proliferation (26). Together, these studies connect mitochondrial network dynamics with pluripotency and proliferation in PSCs.

Mitochondrial dynamics regulators may influence PSC metabolic flux. A granular mitochondrial morphology supports fatty acid (FA) biosynthesis and promotes glycolytic gene expression (14). Studies show that mitochondrial fission with an immature ultrastructure, rather than function of respiratory chain complexes, supports a glycolytic preference (2, 4, 5). In immortalized fibroblasts, mitochondrial dysfunction and a shift to glycolysis occurs with mitochondrial fission factor overexpression (28). Additionally, MFN1/2 depletion can augment the expression and stabilization of the glycolytic master up-regulator, hypoxia-inducible factor 1α (HIF1α) (26). These data suggest that network regulators influence both the cell cycle and metabolism in pluripotency. The potential for mitochondrial network morphology to affect the expression of cell fate and metabolism genes requires further investigation. New insights from recent studies on metabolic control of chromatin structure and gene expression (detailed later) provide a potential mechanism for this connection.

**Metabolism in pluripotent cell-fate transitions**

**Metabolic events during iPSC generation**

Reprogramming somatic body cells to induced pluripotent stem cells (iPSCs) is a model for cell-fate transitions. iPSC pro-
duction provides insight for how metabolism governs pluripotency and self-renewal or differentiation into highly specialized and functional cell types. Stimulating glycolytic flux by modulating pathway regulators or effectors promotes iPSC reprogramming efficiency, whereas impeding glycolysis has the opposite effect (21, 29, 30). Transcriptome and proteome analyses during reprogramming reveal metabolic roles in dedifferentiation. Changes in the expression of metabolic genes that shift OXPHOS to glycolysis precede the induction of pluripotency and self-renewal genes (21, 31–34). An early reprogramming hyper-energetic state, partly mediated by estrogen-related nuclear receptors, shows elevated OXPHOS and glycolysis, with increases in mitochondrial ATP production proteins and antioxidant enzymes (32, 35, 36). An early burst in OXPHOS increases ROS generation and leads to an increase in nuclear factor (erythroid-derived 2)-like 2 (NRF2) activity, which promotes a subsequent glycolytic shift through HIF activation (36). Together, these studies show a progression from a hyper-energetic state to glycolysis during the conversion to pluripotency.

**Hypoxia-related pathways in PSC fate transitions**

Inducing glycolysis and reducing OXPHOS by modulating p53 and HIFs can influence somatic cell dedifferentiation. p53 inactivation (37–40) and HIF stabilization in low O₂ tension promote reprogramming efficiency (34, 41) and reversible pluripotency re-entry during early differentiation (42). Early in reprogramming, HIF1α and HIF2α are stabilized in normoxia and are notably required for metabolic shift by facilitating the expression of glycolysis-enforcing genes such as the pyruvate dehydrogenase kinase 3 (34). However, enforced HIF2 stabilization is deleterious during the last steps of iPSC generation by inducing tumor necrosis factor–related apoptosis inducing ligand (TRAIL) (34).

Conversely, HIFs and hypoxia-related pathways are also effectors in driving early differentiation depending on environmental context. For instance, hypoxia promotes PSC differentiation into definitive endoderm and retinal or lung progenitors (43, 44). In the context of neurogenesis, low O₂ tension and HIFs propel a neural fate at the expense of other germ lineages in early differentiation of hPSCs. At later stages of neural specification from neural progenitor cells (NPCs), hypoxia promotes glial rather than neuronal fate by inducing ligand (TRAIL) (34).

Metabolic in pluripotency exit and early differentiation

**Metabolic remodeling during PSC differentiation**

Spontaneous nondirected hPSC differentiation shows an opposite metabolic shift compared with somatic cell reprogramming. A gradual increase in lactate production associates with an increase in O₂ consumption, mitochondrial biogenesis, and ROS accumulation (2, 11, 49). This progressive metabolic remodeling is partly mediated by UCP2 repression, which enables complete mitochondrial oxidation of pyruvate leading to an increase in OXPHOS (2). An increase in ROS is a direct consequence of increased OXPHOS and is enforced by repression of major antioxidant defenses (11, 49), suggesting a role for oxidative stress in PSC differentiation. Support for this idea comes from mouse ESC (mESC) cardiac differentiation studies that show ROS augmentation through activation of mitogen-activated protein kinase (MAPK) signaling pathways (9, 10, 50). OXPHOS and ROS are also driven by proteins orchestrating mitochondrial dynamics through REX1 repression (27) and the requirement for MFN2 and OPAL expression during cardiomyocyte differentiation from mESCs (51).

**Metabolites supporting pluripotency exit**

Although PSCs and cancer cells have a shared metabolic hallmark, aerobic glycolysis or the Warburg effect, a unique mechanism for how this metabolic shift supports pluripotency exit has recently been proposed. A critical point of divergence is that PSCs strategically utilize glycolysis to produce both lactate and cytosolic Ac-CoA by siphoning glucose-derived citrate from the TCA cycle (Fig. 2). Inhibition or promotion of glycolytic Ac-CoA enhances or delays differentiation, respectively, suggesting that Ac-CoA has a key role during the glycolytic switch in pluripotency exit (52). In PSCs, glycolytic Ac-CoA production is through ATP citrate lyase enzyme activity and may consequently fuel histone acetylation. However, in the 1st h of spontaneous differentiation, repression of this enzyme may assist exit-associated epigenome remodeling by reducing substrate for histone acetylases (52).
Metabolic shift kinetics linked with cell fate

In vitro modeling of embryonic tri-lineage differentiation provides insight for metabolic events during early lineage commitment. Substantially diminished glycolytic flux does not occur for all lineages. Sustained high aerobic glycolytic flux is necessary for early ectoderm lineage commitment and expression of ectoderm-specific differentiation genes (53). Conversely, a metabolic shift toward OXPHOS has recently been observed in early mesoderm and endoderm lineage cells and is consistent with an elevated OXPHOS requirement for PSC generation of cardiomyocytes (54). The utilization of other carbon sources and pathway fluxes beyond glucose in early fate outcome remains unexplored.

Hexosamine biosynthesis and fate transitions

The hexosamine biosynthesis pathway (HBP) is a nutrient-sensing pathway that depends on glucose, glutamine, and cytosolic Ac-CoA levels (Fig. 2). HBP branches from glycolysis to produce UDP-GlcNAc as an end product. UDP-GlcNAc is a substrate of O-GlcNAcase (OGA) counteracts OGT activity, and this dynamic cycling of protein GlcNAcylation regulates numerous cell processes such as cell cycle, signaling pathways, transcription, and organelle and chromatin dynamics (55).

During development and general differentiation processes, GlcNAcylation is implicated in the regulation of pluripotency and gene silencing (56–62). Manipulation of O-GlcNAcylation to elevate O-GlcNAc motifs delays mESC differentiation and subsequent generation of cardiomyocytes (56–61). Conversely, a decrease in O-GlcNAcylation disrupts self-renewal and reprogramming (57) but promotes differentiation in neuronal cells (63–65). Moreover, CPTFs such as OCT4 and SOX2 harbor an O-GlcNAcylation motif that is quickly erased upon differentiation (57). Together, these studies suggest that a high rate of O-GlcNAcylation is involved in the maintenance and acquisition of pluripotency, whereas its reduction is linked to pluripotency exit and differentiation. Elevated glucose, glutamine, and Ac-CoA production in PSCs could support enhanced HBP flux to provide substrate for OGT (Fig. 3). CPTF promoter occupancy at the OGA-encoding gene (66, 67) implies a role for protein O-GlcNAcylation dynamics in pluripotency. This suggestion is supported by in vivo studies showing roles for OGT and OGA during embryogenesis (68–70). Remarkably, high-level O-GlcNAcylation was linked with perturbation in glucose homeostasis and neural tube defects in the fetus of diabetic mice (71). Thus, HBP constitutes a direct link between metabolism and protein O-GlcNAcylation, with a suggested role in regulating pluripotency dynamics and cell-fate acquisition by regulating TFs and the epigenome remodeling machinery, but this idea requires further study.

Metabolism modulates epigenetic remodeling

Metabolism has key roles for inducing, maintaining, and exiting pluripotency. It is remarkable that major metabolic pathways can influence the activity of multiple epigenome-
modifying enzymes, providing an exciting potential connection to cell-fate plasticity.

**TCA cycle–derived metabolites**

hPSCs produce cytosolic Ac-CoA from glycolysis, but rapidly lose this activity in early differentiation, which parallels reduced histone acetylation and expression of pluripotency markers coinciding with the expression of early differentiation genes (52). The simultaneous occurrence of these temporal events suggests that a metabolic shift could drive changes in gene expression patterns and cell fate by modulating histone acetylation. A complementary question could be whether metabolism also affects the dynamics of epigenome methylation. One possible connection could be via the TCA cycle metabolites α-ketoglutarate (α-KG) and succinate, respective cofactor and inhibitor for epigenome demethylase remodeling enzymes. α-KG, made from either glucose or glutamine, is a cofactor for Jumonji C-domain containing histone demethylases (JHDM) and ten-eleven–translocase (TET) DNA demethylases that sustain the naïve pluripotent state in mESCs (72). Yet, in the context of early differentiation, increased α-KG levels enhance ectoderm lineage commitment (73), suggesting that metabolism influences chromatin dynamics contextually in pluripotency maintenance or exit.

**O-GlcNAcylation**

HBP is another potential link between metabolism and epigenome remodeling (Fig. 2). OGT influences DNA methylation and histone modifications by regulating the stabilization, localization, or substrate specificity for specific sets of genes. OGT modifies the epigenome machinery, including TET family enzymes and polycomb group proteins, which are transcriptional repressors that regulate gene expression patterns during embryonic development and differentiation (59). In ESCs, by physically interacting with these proteins, OGT is directed toward the chromatin to influence histone methylation, including H3K4 tri-methylation (H3K4me3), DNA methylation through TET1 interactions, and recruitment of TFs to specific target genes (56–61). Enriched GlcNAc motifs in the catalytic subunit of polycomb complex PRC1 represses neural differentiation genes, whereas this motif is absent on stemness-associated genes, including cell cycle genes (74). Moreover, O-GlcNAcylation may be implicated in neural and neuronal cell-fate determination through epigenetic modulation by the association of OGT with TET3, resulting in recruitment of NeuroD1 to brain-specific target genes (64). O-GlcNAcylation modifications appear to influence the determination of specific neuronal identity. During mESC differentiation, OGA co-localizes with the histone acetyltransferase p300 on the neuropeptide-encoding gene orexin in orexin neurons, whereas OGT co-localizes with histone deacetylase sirtuin 1 (SIRT1) in non-orexin-expressing cells (65). Because of the direct link between HBP and O-GlcNAcylation, we propose that metabolic fluctuations induced by specific microenvironmental differentiation drivers, such as hypoxia, could participate in establishing distinct epigenome patterns associated with cell fate and function acquisitions and maintenance.

*S-Adenosylmethionine (SAM)*

Methyltransferases for histones and DNA depend on the levels of SAM and threonine, which are required for pluripotency. Extracellular threonine in mESCs or methionine in hPSCs are the only amino acids critical for pluripotency and used for SAM production (75, 76). PSCs use internal regulatory systems to maintain intracellular SAM levels that involve p53 and p38 cell cycle and apoptosis regulators (8, 76). mESCs or hPSCs grown in reduced threonine/methionine show spontaneous differentiation and slowed growth (82, 83). Threonine depletion decreases SAM production and influences H3K4me3 levels, suggesting a possible mechanism for how threonine and SAM levels regulate pluripotent cell fate (75).

**Ascorbate**

Another regulator of histone modifications is ascorbate, the principal form of vitamin C at physiological pH. Ascorbate is an epigenomic regulator of DNA methylation and a modulator of iPSC reprogramming efficiency (77, 78). It is also a cofactor for TET enzymes that catalyze the oxidation of 5-methylcytosine to 5-hydroxymethylcytosine. By contributing to the demethylation of both DNA and histones, ascorbate appears to augment the erasure of epigenetic memory, and in this manner, it enhances stem cell reprogramming (77). Increased ascorbate enhances iPSC generation, which parallels TET1 deficiency in improving reprogramming efficiency. Conversely, TET1 over-expression impairs reprogramming (76). Although TET1 in the absence of ascorbate remains functional, the addition of ascorbate is critical for the epithelial-to-mesenchymal transition during reprogramming to pluripotency (79).

**NAD**

Cellular NAD level is directly impacted by the metabolic state, such as glycolytic flux, and regulates the activity of NAD⁺-dependent histone deacetylase sirtuins (Fig. 2), including SIRT1, which is induced in hPSCs (80). SIRT1 controls cell fate by regulating p53-dependent homeobox protein transcription factor NANOG (homeobox protein transcription factor) expression and transcriptional repression of differentiation genes in hPSCs (8, 80, 81). During hESC differentiation, SIRT1 is repressed, leading to acetylation and reactivation of multiple differentiation genes, including PAX6, TBX3, and DLL (80). Further investigations are required to understand how distinct metabolic shifts during cell-fate conversions influence the NAD⁺/NADH ratio and, subsequently, how NAD levels impact histone acetylation remodeling events specifically through sirtuin activities.

**Metabolism in naïve and primed pluripotency**

The pre-implantation blastocyst retains a developmentally unrestricted cell population that differs from its post-implantation counterpart (82). Although the inner cell mass of pre- and post-implantation blastocysts yields ESCs for growth *in vitro* (83, 84), pre-implantation ESCs exist in a naïve or ground pluripotent state, whereas post-implantation ESCs exist in a primed state. Naïve PSCs introduced in the pre-implantation blastocyst can contribute to a chimera mouse (85), whereas
primed PSCs cannot, discerning their distinct developmental potential. Another distinguishing characteristic between these two PSC states is how metabolism fuels the requirements for self-renewal and proliferation. Pre-implantation blastocyst-derived naïve PSCs utilize glycolysis and OXPHOS and then transition to glycolysis dependence in the primed state, despite having functionally mature mitochondria (86). The coordination of TFS Zic3 and Esrβ regulates bivalent metabolism observed in naïve PSCs (87). Naïve PSCs also have a greater glycolytic output compared with primed PSCs (88). Yet, different patterns of glycolysis and OXPHOS could play additional roles beyond supporting higher proliferation in naïve ESCs (89, 90). For instance, an open question is whether dissimilar metabolic profiles between primed and naïve PSCs is implicated in distinct transcriptional patterns and chromatin organization, ultimately influencing respective developmental potentials. This issue will most likely be a relevant topic in the coming years for the field, as illustrated by the studies conveyed below.

**Metabolism and the naïve PSC epigenome**

Naïve and primed PSCs show structural changes in chromatin structure, including histone and DNA modifications, that have functional consequences in regard to developmental potential through TF expression and suppression of lineage-restrictive genes (91). Although naïve hESCs with properties similar to mESCs have been claimed (85, 89, 90, 92), these cells show some differences in pluripotency markers and functions that probably require more optimized culture and nutrient conditions to improve consistency between species. There is increasing evidence for interactions between the metabolome and epigenome to sustain a global hypo-methylated profile associated with naïve PSCs (93). Mechanistically, glucose- and glutamine-derived TCA cycle metabolite α-KG, acting as a cofactor for JHMD and TET proteins (Fig. 2), sustains the naïve state in mESCs by global hypo-methylation (72). Additionally, as mentioned previously, HBP couples macromolecular metabolism to O-GlcNAc modifications in proteins, including epigenetic modifiers (Fig. 3) (94). Cycling of these post-translational modifications by OGT and OGA are required for naïve and primed state induction, maintenance, and differentiation (56, 95). OGT interacts with TET1 enzymes preferentially at transcription start sites, thereby influencing gene expression (58). This may implicate OGT in globally regulating the DNA hypomethylation profile in naïve compared with primed PSCs. As such, the O-GlcNAcylation cycle could have a role in the observed differences of X-chromosome inactivation in primed state female ESCS (97). Thus, a potential link between OGT and X-chromosome inactivation may have functional relevance in the context of naïve and primed PSCs (94).

Moreover, naïve to primed epigenetic transitions are partly mediated by nicotinamide N-methyltransferase (NNMT), which decreases H3K27me3. By consuming SAM and up-regulating Wnt signaling, NNMT prevents histone methylation in the naïve state (98). In addition to the role of ascorbate in reprogramming (84, 85), a combination of ascorbate and retinol has been shown to enhance naïve state acquisition by increasing TET expression and catalysis (99). In contrast, high ratios of l-proline to ascorbate prevents naïve state maintenance, although the mechanism(s) by which l-proline induces epigenetic changes has yet to be elucidated (96). Collectively, these studies suggest a role for metabolism in influencing naïve versus primed pluripotency dynamics by facilitating chromatin remodeling through multiple specific metabolites.

**Conclusions**

Accumulating evidence illustrates the influence of metabolism on differentiation plasticity by regulating the epigenetic machinery. Our current understanding provides a foundation for further investigations into links between environmental stimuli and subsequent metabolic adaptations that orchestrate epigenome remodeling events, which ultimately drive cell fate. A key open question is what recruits epigenome remodelers, co-factors, and substrates to specific loci to influence patterns of pluripotent and somatic cell gene expression. Here, we suggest that HBP may have a role by acting at crucial nodes connecting metabolism and epigenome remodeling. Answers to fundamental questions raised here will provide a deeper basis for generating safe and accessible PSC-derived cells for use in regenerative medicine, disease modeling, and drug screening applications in the future.

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