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)[1] 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 through varying 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 (**Figure 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 glutathione (4) and fueling mitochondrial energy metabolism (12-14). Glutaminolysis generates tricarboxylic acid (TCA) cycle substrates (12) and supports the mitochondrial inner membrane potential ($\Delta\Psi$) required for PSC survival (15). A paradoxically high $\Delta\Psi$ in PSCs compared to PSC- differentiated progeny cells (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 (IF1), which prevents the ATP synthase from running as an ATP hydrolase (2). Since low $\Delta\Psi$ facilitates the induction of apoptotic pathways, enhanced apoptotic sensitivity of PSCs compared to PSC-differentiated progeny is surprising with comparatively heightened $\Delta\Psi$ 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

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[1] The abbreviations used are: i/h/PSC, induced/human pluripotent stem cell; OXPHOS, oxidative phosphorylation; TCA, tricarboxylic acid; $\Delta\Psi$, mitochondrial inner membrane potential; CPTF, core pluripotency transcription factor; TF, transcription factor; UCP2, uncoupling protein 2; HBP, hexosamine biosynthesis pathway; UDP-GlcNAc, UDP N-acetylglucosamine; OGT, O-GlcNAc transferase; O-GlcNAc, O-linked β-d-N-acetylglucosamine. OGA, O-GlcNAcase; SIRT1, sirtuin 1.

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 next section).

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 towards aerobic glycolysis or 'Warburg' metabolism (22). UCP2 functions as a carbon substrate transporter. In PSCs, UCP2 expels Carbon 4 (C4) intermediate metabolites including oxaloacetate, malate, and L-aspartate from the TCA cycle and mitochondrial matrix, thereby reducing electron-donating substrates for OXPHOS and ATP production (22). In cancer cells, UCP2 conversely promotes the incorporation of carbons from glutaminolysis into the TCA-cycle. Recent studies also show that glutamine supports the TCA cycle more robustly in PSCs than in differentiated cardiomyocyte progeny cells (12). Combined, these studies provide a model for PSCs in which UCP2 routes glucose-derived carbons into cytosolic biosynthetic pathways and glutamine-derived carbons into the TCA cycle to maintain $\Delta\Psi$ and low OXPHOS levels. This model is supported by a study that shows glucose provides metabolites only for the first steps (Ac-CoA, citrate, and *cis*-aconitate) of the TCA cycle whereas glutamine contributes metabolites to later TCA cycle steps as an anapleurotic fuel (12) (**Figure 2**).

Another potential carbon routing regulator in PSCs comes from cancer metabolism studies. Cancer cells show robust glucose import and augmented glycolysis to feed biosynthetic reactions. This activity blocks pyruvate oxidation to CO_2 in the mitochondria by repression of the mitochondrial pyruvate carrier (MPC) genes, *MPC1/2* (23). Pyruvate exclusion from mitochondrial oxidation may be a more general stem cell strategy beyond cancer cells that requires further study. Supporting this idea, repression of MPC levels occurs in intestinal and hair-follicle adult stem cells, while MPC levels increase with differentiation of intestinal crypt stem-like cells (24,25).

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 interlacing 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 Ser616 phosphorylation and activation of the mitochondrial fission regulator DRP1 by CDK1/cyclinB (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

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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 production 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 reveals metabolic roles in dedifferentiation. Changes in the expression of metabolic genes that shift OXPHOS to glycolysis precedes 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 O_2 tension promotes 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 HIF2α stabilization is deleterious during the last steps of iPSC generation by inducing tumor-necrosis-factor related apoptosis inducing ligand (TRAIL)-dependent (34), suggesting a stage-dependent role for HIF2α.

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 O_2 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 that neuronal fate by increase in regulating the activity of Lin28 (45). A synergistic combination of HIF1α and Notch signaling promotes hiPSC-derived NPC differentiation into astrocytes through DNA demethylation of the glial fibrillary acidic protein (GFAP) encoding gene (46). Overall, by promoting glycolysis and changing epigenome modifications associated with cell identity, HIF1α influences cell fate toward either pluripotency or differentiation depending on the environmental context. O_2 tension is an environmental driver that modifies metabolism to enable epigenome remodeling and changes in gene expression to influence cell fate.

Lipid metabolism and mitochondrial dynamics in somatic cell reprogramming

Compared with differentiated cells, iPSCs undergo rewiring of energetic and biosynthetic programs as illustrated by the reduction of mitochondrial oxidative stress pathways and rapid lipogenesis (19). For instance, somatic cell reprogramming efficiency is promoted by increase in key lipogenic enzymes, such as Ac-CoA carboxylase (ACC) and FA synthase (18,19).

De novo FA biosynthesis controls reprogramming and pluripotency through shifts in mitochondrial dynamics. Equilibrium toward mitochondrial fission is driven by lipogenic enzyme (ACC1) inhibition of mitochondrial fission factor (FIS1), ubiquitin–proteasome degradation, and the lipid generation (14). Mitochondrial dynamics is further

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supported by reduction of MFN1/2, and an increase of the mitochondrial A-kinase anchoring protein RAB32 involved in mitochondrial fission synchronization (26,47). Genetic or pharmacological perturbation of MFN1/2 endorses HIF1α stabilization though ROS production and promotes iPSC generation by indirectly favoring a metabolic transition from OXPHOS to glycolysis (26,48). These findings hint at an interconnected mechanism triangulating lipid metabolism, mitochondrial fission, and a metabolic shift to glycolysis that favors the PSC state (**Figure 1**).

Metabolism in Pluripotency Exit and Early Differentiation

Metabolic remodeling during PSC differentiation

Spontaneous non-directed hPSC differentiation shows an opposite metabolic shift compared to somatic cell reprogramming. A gradual increase in lactate production associates with an increase in O_2 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 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 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 OPA1 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 (**Figure 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 (ACLY) enzyme activity and may consequently fuel histone acetylation. However, in the first hour 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 & fate transitions

The hexosamine biosynthesis pathway (HBP) is a nutrient-sensing pathway that depends on glucose, glutamine, and cytosolic Ac-CoA levels (**Figure 2**). HBP branches from glycolysis to produce UDP N-acetylglucosamine (UDP-GlcNAc) as an-end product. UDP-GlcNAc is a substrate of O-GlcNAc transferase (OGT) for post-translational protein modification by O-GlcNAcylation with addition of O-linked β-d-*N*-acetylglucosamine (O-GlcNAc). The removal of O-GlcNAc by 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

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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, while 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 (**Figure 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 suggest 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 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 (JmjC)-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 (**Figure 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, while 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, while OGT co-localizes with histone deacetylase sirtuin 1

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(SIRT1) in non-orexin expressing cells (65). Due to 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-adenosyl methionine

Methyltransferases for histones and DNA depend on the levels of S-adenosyl methionine (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, enhances stem cell reprogramming (77). Increased ascorbate enhances iPSC generation, which parallels TET1 deficiency in improving reprogramming efficiency. Conversely, TET1 overexpression 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 (**Figure 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 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). While the inner cell mass of pre- and post-implantation blastocysts yield 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 chimeric 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 dependency in the primed state, despite having functionally mature mitochondria (86). The coordination of TFs Zic3 and Esrrb regulates bivalent metabolism observed in naive PSCs (87). Naïve PSCs also have a greater glycolytic output compared to 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 metabolite rate modification arising from dissimilar metabolic profiles between primed and naïve PSCs is implicated in distinct transcriptional patterns and

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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 in the next sections

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 (**Figure 2**), sustains the naïve state in mESCs by global hypo-methylation (72). Additionally, as previously mentioned, HBP couples macromolecular metabolism to O-GlcNAc modifications in proteins, including epigenetic modifiers (**Figure 3**) (94). Cycling of these post-translational modifications by OGT and OGA are required for naïve and primed state induction, maintenance, and differentiation (95,96). OGT interacts with TET1 enzymes preferentially at transcription start sites, thereby influencing gene expression (58). This may implicate OGT in globally regulating the DNA hypo-methylation profile in naïve compared to primed PSCs. As such, the O-GlcNAcylation cycle could have a role in the observed differences of X-chromosome inactivation (XCI) in primed state female ESCs (97). Thus, a potential link between OGT and XCI may have functional relevance in the context of naïve and primed PSCs (94).

Moreover, naive to primed epigenetic transitions are partly mediated by nicotinamide N-methyltransferase (NNMT), which decreases H3K27me3. By consuming SAM and upregulating 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 have been shown to enhance naive state acquisition by increasing TET expression and catalysis (99). In contrast, high ratios of L-proline to ascorbate prevents naive state maintenance, although the mechanism(s) by which L-proline induces epigenetic changes is yet to be elucidated (100). 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.

Conflict of Interest Statement

The authors declare that they have no conflicts of interest with the contents of this article.

Author Contributions

Conceptualization by PD and MAT. Manuscript research, writing and figures preparation by PD, VL, RMTN, SALK, and MAT. Editing by PD, VL, and MAT.

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Figure Legends

Figure 1: Metabolic transitions between pluripotency and differentiation. The primed pluripotent state is characterized by elevated glycolysis, which associates with a fragmented mitochondrial network. Glycolytic metabolism fuels rapid proliferation and self-renewal while maintaining molecular integrity from decreased oxidative stress. PSC metabolism appears to favor a relatively high level of protein O-GlcNAcylated motifs, particularly on SOX2 and OCT4, that are quickly erased upon differentiation. These modifications could also regulate other transcription factors and epigenome remodelers upon pluripotency exit. During PSC-derived generation of somatic cells, such as cardiomyocytes, oxidative metabolism is upregulated by mitochondrial dynamics via REX1 repression and MFN2 and OPA1 expression. This supports efficient mitochondrial energy production at the expense of macromolecular biosynthesis. The consequence of increased OXPHOS is increased ROS production and oxidative stress, which may serve regulatory roles in differentiation. Conversely, the reprogramming of somatic cells toward pluripotency depends on an early glycolytic shift and mitochondrial morphology remodeling facilitated by RAB32 kinase and lipid biosynthesis induced FIS1 stabilization. The downregulation of proteins driving MFN1/2 can promote a glycolytic shift through HIF1α stabilization.

Figure 2: Influence of metabolism on the epigenome in the maintenance of pluripotency. Glycolytic flux regulates the NAD+/NADH ratio, which controls the activities of sirtuin (SIRT) histone deacetylases. TCA cycle intermediates exported from the mitochondria include citrate and α-KG. Conversion of cytosolic

citrate to Ac-CoA provides a donor for HAT-mediated histone acetylation. α-KG is a cofactor for histone and DNA demethylation reactions by JHDM and TET enzymes, respectively. By-products of glucose and glutamine catabolism supply reactants for O-GlcNAc modifications of epigenetic remodeling proteins through the hexosamine biosynthesis pathway (HBP). Highlighted in red, blue, and green are the metabolic pathways associated with pluripotency, their contribution to TCA cycle metabolite production, and their subsequent influence on the epigenome (solid lines). Another potential mechanism for how metabolism can shape transcriptional patterns could be by fueling HBP-derived O-GlcNAcylation of proteins driving epigenome remodeling (dashed line).

Figure 3: Nutrient-sensing hexosamine biosynthesis pathway (HBP) regulates pluripotency and differentiation. A branch of glycolysis fuels the HBP to produce UDP-N-acetylglucosamine (UDP-GlcNAc). Pathway flux depends on levels of macromolecular metabolism, including carbohydrate, lipid, nucleotide, and amino acid biosynthesis. UDP-GlcNAc is a key intermediate for posttranslational modification of Ser and Thr residues. The catalytic activity of O-GlcNAc transferase (OGT) and O-GlcNAcase (OGA) determines the level of protein O-GlcNAcylation. This modification influences pluripotency and differentiation gene networks via transcriptional and epigenetic machinery.
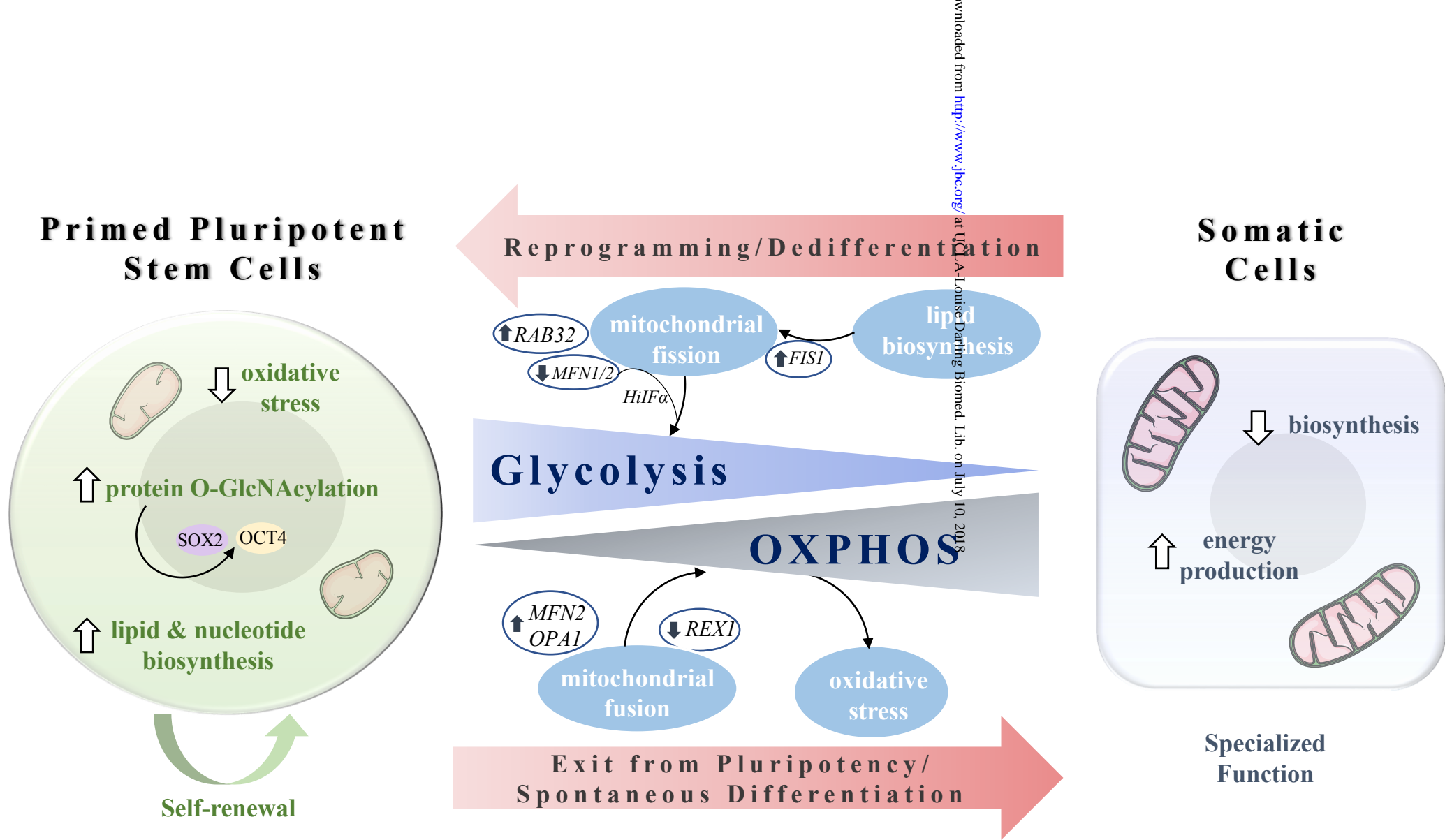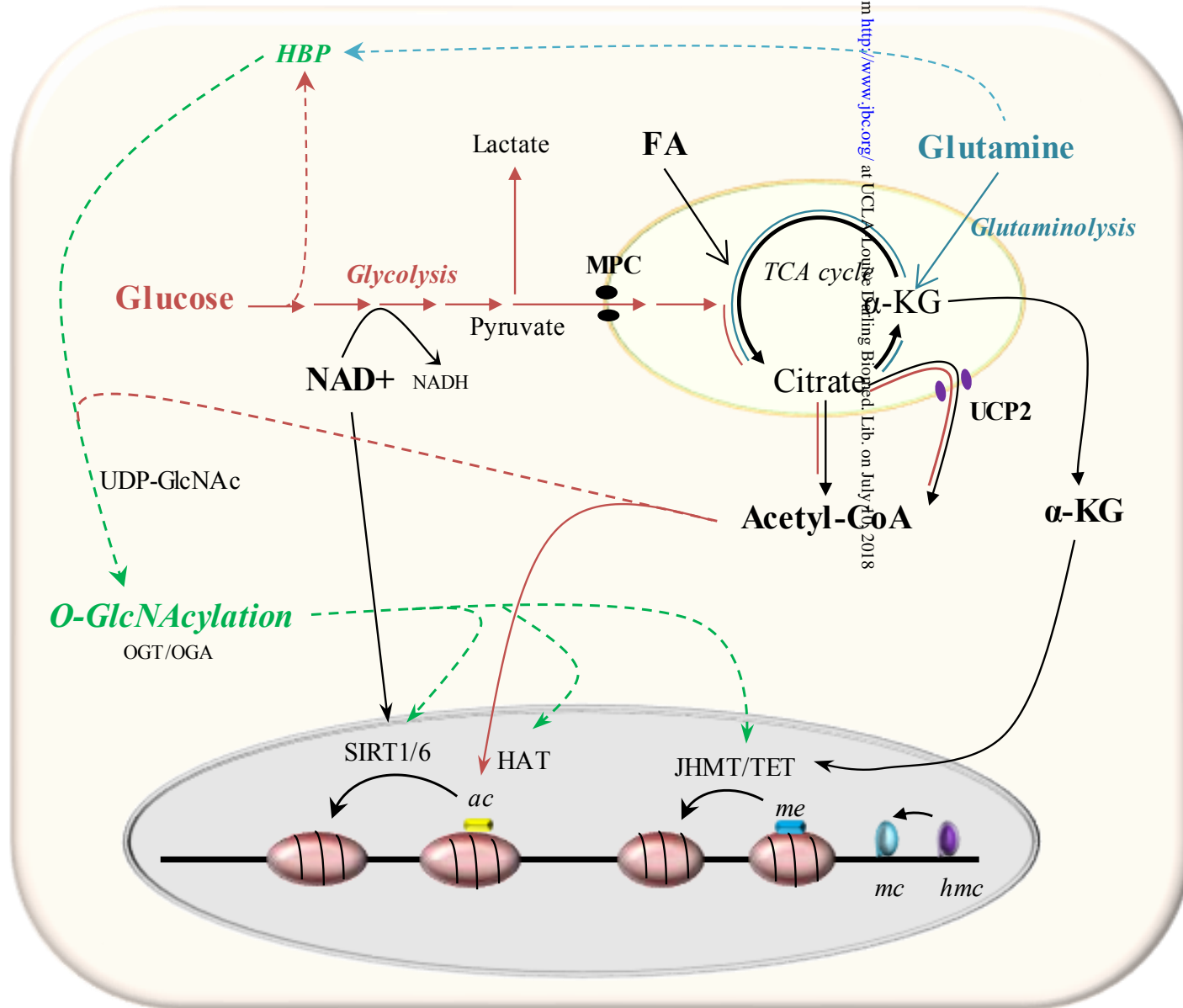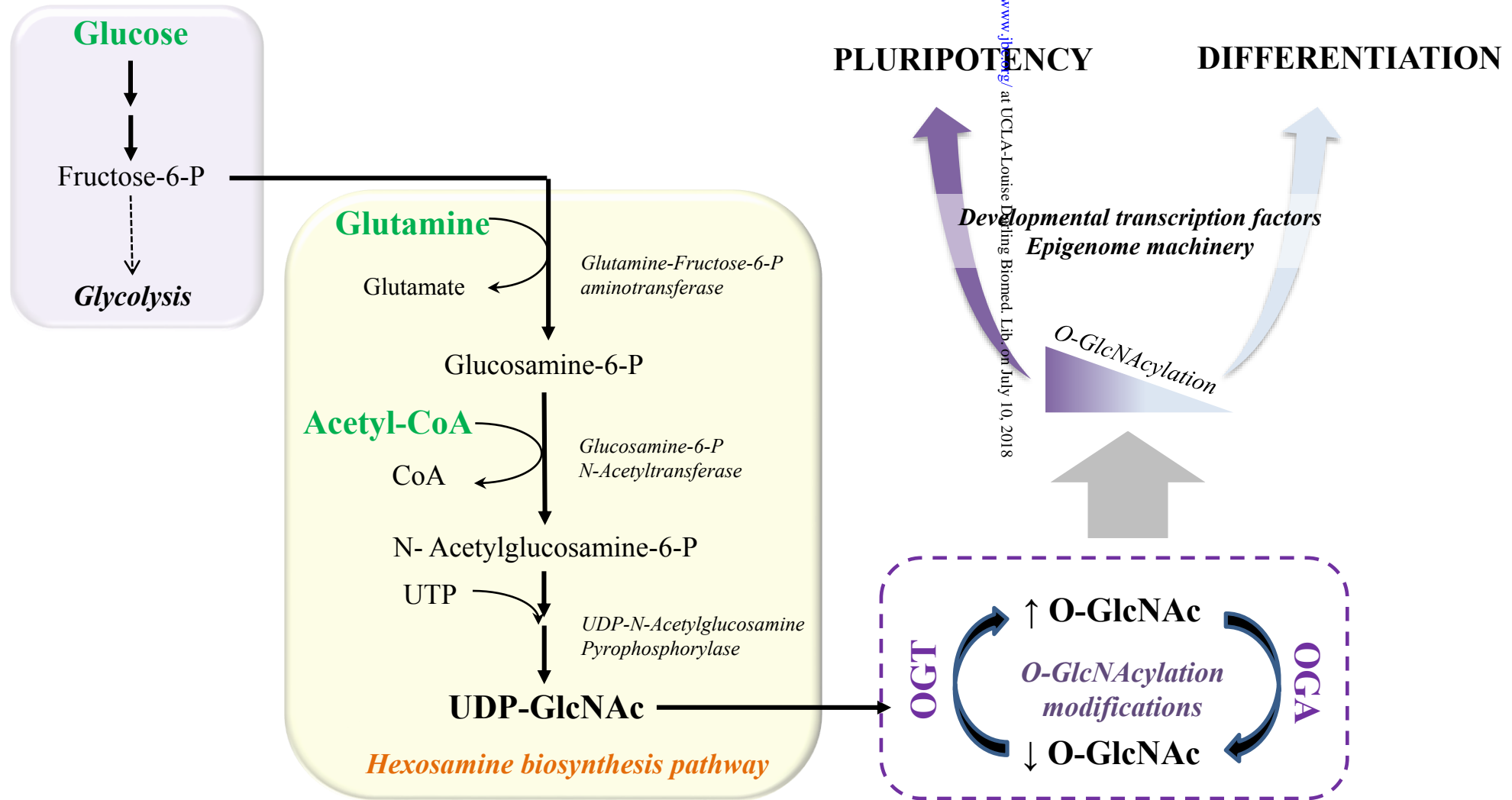
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Fig 1

Fig 2

Fig 3

Metabolism in pluripotency: Both driver and passenger?

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