

Placental glycogen stores and fetal growth: insights from genetic mouse models

Simon J Tunster, Erica D Watson, Abigail L Fowden and Graham J Burton

Centre for Trophoblast Research, Department of Physiology, Development and Neuroscience, Physiology Building, Downing Site, Cambridge, UK

Correspondence should be addressed to S J Tunster; Email: slt95@cam.ac.uk

Abstract

The placenta performs a range of crucial functions that support fetal growth during pregnancy, including facilitating the supply of oxygen and nutrients to the fetus, removal of waste products from the fetus and the endocrine modulation of maternal physiology. The placenta also stores glucose in the form of glycogen, the function of which remains unknown. Aberrant placental glycogen storage in humans is associated with maternal diabetes during pregnancy and pre-eclampsia, thus linking placental glycogen storage and metabolism to pathological pregnancies. To understand the role of placental glycogen in normal and complicated pregnancies, we must turn to animal models. Over 40 targeted mutations in mice demonstrate the defects in placental cells that store glycogen and suggest that placental glycogen represents a source of readily mobilized glucose required during periods of high fetal demand. However, direct functional evidence is currently lacking. Here, we evaluate these genetic mouse models with placental phenotypes that implicate glycogen trophoblast cell differentiation and function to illuminate the common molecular pathways that emerge and to better understand the relationship between placental glycogen and fetal growth. We highlight the current limitations in exploring the key questions regarding placental glycogen storage and metabolism and define how to experimentally overcome these constraints.

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Introduction

The placenta is a unique organ that exists only during pregnancy to perform a diverse range of functions that collectively support optimal fetal growth while maintaining maternal well-being. Arguably, the principal role of the placenta is to mediate the supply of oxygen and nutrients from the mother to fetus (Burton & Fowden 2015). The placenta also removes waste products from the fetal circulation and forms a physical barrier that affords some protection against certain pathogens and toxins (Gude *et al.* 2004). Furthermore, the placenta also synthesizes and secretes hormones into the mother's blood to adapt maternal physiology and behavior, ultimately to ensure that the pregnancy is sustained and fetal growth is supported (Napso *et al.* 2018). In addition to facilitating glucose transport, the placenta metabolizes glucose for its own use and stores it in the form of the multi-branched polysaccharide glycogen. The purpose of placental glycogen stores in normal pregnancy remains unclear. The most widely accepted theory is that placental glycogen stores ensure that fetal glucose supply is maintained at times of maximal demand, such as during late gestation (Barash & Shafirir 1990, Coan *et al.* 2006). However, direct experimental evidence to support such a function is currently lacking.

Placental glycogen in humans

Despite the earliest reference to glycogen storage in the human placenta dating to the early twentieth century (Driessen 1907), understanding its role during normal or complicated pregnancies has remained an elusive goal. In the human placenta, glycogen is predominantly found in the cytotrophoblast cells (Wislocki & Bennett 1943), with the highest levels in the distal cytotrophoblast closest to the decidua (Georgiades *et al.* 2002). In uncomplicated pregnancies, placental glycogen content peaks toward the end of the first trimester before declining towards term (Villem 1953, Boyd 1959, Robb & Hytten 1976). Aberrant glycogen storage was reported in gestational diabetes (Heijkenskjold & Gemzell 1957, Gabbe *et al.* 1972, Diamant *et al.* 1982, Desoye *et al.* 1992, Gheorman *et al.* 2013) and preeclampsia (PE) (Arkwright *et al.* 1993, Tsoi *et al.* 2003), suggesting a possible role in the pathogenesis of these two common pregnancy complications. The relevance of aberrant glycogen storage in the context of human pregnancy complications has been reviewed elsewhere (Akison *et al.* 2017). However, one hypothesis suggests that, in diabetic pregnancies, the placenta stores excess glucose as glycogen to protect the fetus from hyperglycaemia, thus limiting fetal overgrowth (Desoye *et al.* 2002).

Considerable constraints limit our ability to explore placental glycogen function in humans, such as the lack of available tissue at the appropriate developmental stage. Accordingly, it is necessary to turn to the mouse model, which benefits from large litter sizes, a short gestation period that allows for the investigation of early pregnancy and a similar genome to humans that is easily manipulated. There are 47 known mouse models with targeted mutations that display phenotypes associated with the trophoblast cell subtype that stores glycogen. A common feature among these placental mutants is that fetal growth is co-ordinately affected. Therefore, the use of these mutant mouse lines will help to elucidate the normal physiological role of placental glycogen and may provide further insight to the relevance of placental glycogen in the human placenta during normal and complicated pregnancies.

Placental development in the mouse

The mouse is a particularly useful model for the human placenta, since they are both hemochorial, architecturally similar and express many of the same genes that regulate placental development and function (Rossant & Cross 2001). In particular, imprinted genes, which are characterized by expression derived wholly, or predominantly, from one or other parental allele, exert significant influence on placental development in both humans (Frost & Moore 2010) and mice (Tunster *et al.* 2013). Furthermore, the mouse placenta also accumulates glycogen stores in a specialized trophoblast cell subtype called the glycogen trophoblast (GlyT), some of which interact intimately with the maternal decidua (Rampon *et al.* 2005, Coan *et al.* 2006, Bouillot *et al.* 2006). For this reason, GlyT cells share similarities with human cytotrophoblast cells and establish the mouse as an ideal model in which to elucidate the function(s) of placental glycogen stores.

In the mouse, GlyT cells appear as clusters in the junctional zone (Jz) of the mature placenta, before a proportion of these cells invade the maternal decidua to congregate around maternal spiral arteries (Adamson *et al.* 2002). When considering how defects in placental glycogen storage and metabolism emerge, it is important to consider when GlyT first arise during placental development and whether defective GlyT differentiation is the primary cause of altered placental glycogen content. Development of the mouse placenta under normal circumstances has been extensively reviewed elsewhere (Rossant & Cross 2001, Watson & Cross 2005). Briefly, by implantation at embryonic day (E) 4.5, the mouse blastocyst comprises a layer of trophectoderm that surrounds the inner cell mass (ICM). The trophectoderm cells immediately adjacent to the ICM proliferate to give rise to two main trophoblast progenitor populations: the ectoplacental cone (EPC), which will differentiate to yield cells of the centrally

located Jz that is predominantly endocrine in function and the extraembryonic ectoderm (ExE), which will eventually give rise to the labyrinth zone (Lz) where, when vascularized by fetal capillaries, nutrient, gas and waste exchange between maternal and fetal blood circulations occurs (Fig. 1).

To date, nine trophoblast cell sub-types are known to differentiate from these progenitor populations. These include the spongiotrophoblast (SpT) and GlyT cells, which share a common EPC progenitor and together with parietal trophoblast giant cells (P-TGCs) comprise the mature Jz. SpT cells function predominantly in the production of hormones, including members of the *Prl* (prolactin/placental lactogen-related) and *Psg* (pregnancy specific glycoprotein) gene families. The GlyT lineage is named for the abundant stores of glycogen that they accumulate and metabolize during gestation. In total, five TGC sub-types have been identified. Based upon lineage tracing, gene-expression profiles and spatial localization within the placenta (Fig. 1), it is hypothesized that most of the TGCs also derive from the EPC (Simmons *et al.* 2007, Gasperowicz *et al.* 2013). TGCs associate with the maternal blood sinuses throughout the placenta and secrete hormones into the maternal circulation to modulate maternal physiology and placenta function. Sinusoidal-TGCs (S-TGCs) are located within the Lz, and together with a bilayer of syncytiotrophoblast (SynT-I and SynT-II) cells derived from the ExE, they create a trilaminar cellular arrangement that separates the maternal circulation from the extensively branched fetal vasculature (Adamson *et al.* 2002, Watson & Cross 2005, Simmons *et al.* 2008a).

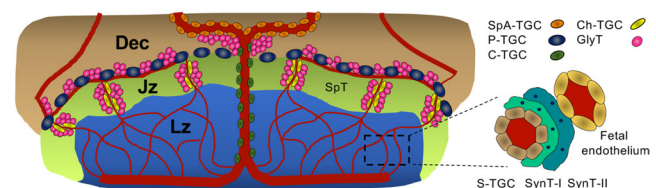


Figure 1 Structure and trophoblast lineages of the mature mouse placenta: The mature mouse placenta comprises three structurally and functionally distinct layers: the maternal decidua (Dec), junctional zone (Jz) and labyrinth zone (Lz). The junctional zone predominantly comprises the spongiotrophoblast (SpT) and non-migratory glycogen trophoblast (GlyT) cells. A proportion of GlyT migrate to the maternal decidua where they associate with maternal spiral arteries bringing maternal blood to the placenta. Five trophoblast giant cell sub-types have been described based on the localization on gene expression patterns: the parietal TGCs (P-TGCs) form a discontinuous cell layer at the boundary between the Jz and maternal decidua; spiral artery-associated TGCs (SpA-TGCs) line maternal spiral arteries through the decidua; canal-TGCs (C-TGCs) line maternal blood canals through the Jz and Lz; sinusoidal-TGCs (S-TGCs) replace the endothelial layer of maternal blood sinuses within the Lz and channel-TGCs (Ch-TGCs) surround the channels that traverse the Jz draining maternal blood from the placenta. Together with the S-TGCs, two layers of syncytiotrophoblast form the trilaminar structure of the murine labyrinth.

Based on lineage tracing experiments (Simmons & Cross 2005), GlyT cells share a common *Tpbpa*⁺ EPC progenitor with SpT cells and arise early in development. Periodic acid-Schiff (PAS) staining, which is a general staining method used to detect polysaccharides (e.g. glycogen) in addition to mucosubstances (e.g. glycoproteins and glycolipids), demonstrates that small quantities of glycogen are stored by GlyT from ~E5.5 (Tesser *et al.* 2010), suggesting that GlyT are specified soon after implantation. An early lineage split of the GlyT and SpT populations is further suggested by expression of the GlyT-specific marker genes *Pcdh12* and *Aldh1a3* in a subset of EPC cells from ~E7.5 and ~E8.5, respectively (Rampon *et al.* 2005, Bouillot *et al.* 2006, Outhwaite *et al.* 2015). GlyT number expands nearly 300-fold between E12.5 and E16.5 before declining ~60% by E18.5 (Coan *et al.* 2006). This expansion coincides with a marked increase in PAS staining from E12.5 (Adamson *et al.* 2002), which distinguishes GlyT from the adjacent SpT cells (Fig. 2A, B and C). By comparison, the SpT population increases less than four-fold during the same period, with a modest ~20% reduction by E18.5 (Coan *et al.* 2006). During this developmental time frame, placental

glycogen stores peak at ~E15.5 before declining by ~50% at E18.5 (Lopez *et al.* 1996) as the GlyT cell population diminishes. Even though both GlyT and SpT cells continue to express the Jz-marker gene *Tpbpa* in the mature placenta (Lescisin *et al.* 1988) (Fig. 2D and E), other GlyT-specific markers have been described, including the gap-junction genes *Gjb3* (*Cx31*) and *Gjb5* (*Cx31.1*), which are localised to GlyT cells from ~E12.5 (Coan *et al.* 2006) and E13.5 (Zheng-Fischhofer *et al.* 2007), respectively, alongside persistent expression of *Pcdh12* (Fig. 2F, G and H).

The putative role of placental glycogen

Studies in animal models have led to the hypothesis that placental glycogen stores provide a source of glucose to support fetal growth during late gestation (Coan *et al.* 2006). This hypothesis is supported by two observations: glycogen acts as the primary energy store in animals and placental glycogen diminishes toward the end of pregnancy coincident with a period of rapid fetal growth. However, little experimental evidence currently exists to directly support such a function. The location of GlyT cells next to maternal blood sinuses may provide some indication as to the ultimate destination of the glucose released from placental glycogen stores. For instance, from ~E12.5, some GlyT invade the decidua where they localize in close proximity to maternal spiral arteries and by E16.5 account for ~30% of the total GlyT population (Redline *et al.* 1993, Coan *et al.* 2006, Gasperowicz *et al.* 2013) (Fig. 1). Based on this association, it is possible that migratory GlyT cells metabolize glycogen into glucose for transport into the maternal blood entering the placenta for eventual fetal uptake. Indeed, large lacunae form in the decidua by E17.5 that are presumed to result from the lysis of multiple GlyT in the vicinity (Bouillot *et al.* 2006). In contrast, populations of non-migratory GlyT cells cluster in close proximity to channels in the Jz that drain maternal blood from the placenta (Gasperowicz *et al.* 2013) (Fig. 1). Whether these GlyT cells release glucose or other factors, such as hormones, into maternal blood to influence maternal physiology in preparation for parturition and lactation (Napso *et al.* 2018) to indirectly support fetal growth and well-being is yet to be determined. Beyond location, the migratory and non-migratory GlyT populations are distinguishable by expression of distinct *Prl* genes: migratory GlyT express *Prl7b1*, while non-migratory GlyT express *Prl6a1* (Simmons *et al.* 2008b). Further experiments are necessary to explore the functional differences between these GlyT sub-types. Simultaneously, it is also possible that placental glycogen stores might provide energy directly to the placenta, since it is a highly metabolic organ that consumes a considerable proportion of the glucose delivered to it (Hay 1995). Indeed, placental glycogen stores might fuel hormone production by the placenta (e.g. *Prl* and *Psg* gene family members), which

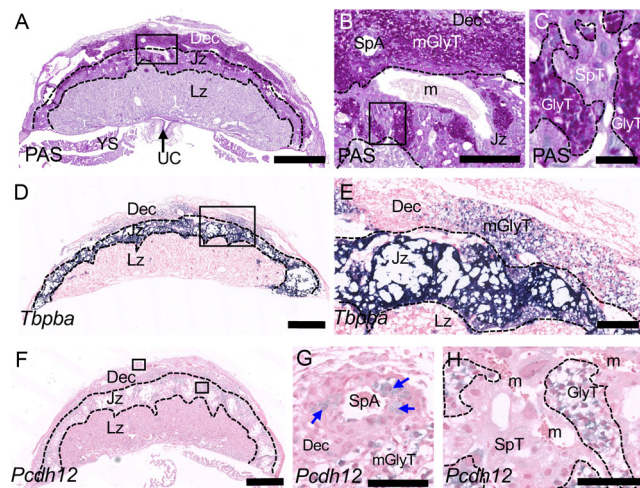


Figure 2 Histological methods for assessing glycogen trophoblast cells in the mouse placenta at E14.5. Histological sections of WT (C57BL/6J) mouse placentas at E14.5 stained using (A, B and C) Periodic acid-Schiff (PAS) stain (dark pink) that labels glycogen, glycoproteins and glycolipids, (D and E) *Tpbpa* RNA via an *in situ* hybridization probe (dark purple) that stains cells derived from the ectoplacental cone (e.g. spongiotrophoblast (SpT) and glycogen trophoblast (GlyT)) and (F, G and H) *Pcdh12* RNA via an *in situ* hybridization probe (dark purple) that stains GlyT. Nuclei are stained using (A, B and C) haematoxylin (blue) or (D, E, F, G, H) nuclear fast red (pink). Dec, maternal decidua; Jz, junctional zone; Lz, labyrinth zone; YS, yolk sac; UC, umbilicus (black arrow); SpA, spiral artery; m, maternal blood sinusoid; mGlyT, migratory GlyT (blue arrows). Dotted lines separate major placenta layers or trophoblast cell populations. Boxes represent regions shown in higher magnification to the right. Scale bars: A, D, F = 1 mm; B, E = 250 μ m; C = 50 μ m; G, H = 100 μ m.

increases dramatically toward the term (McLellan *et al.* 2005, Simmons *et al.* 2008b).

How placental glycogen is metabolized is not well understood. Glucagon might play a role in stimulating the release of glycogen stores from GlyT (Coan *et al.* 2006). Yet, placental glycogen content is unaltered in mice deficient for the glucagon receptor (Ouhilal *et al.* 2012), indicating that an alternative pathway might be involved. However, only a small number of glucagon-receptor mutants were examined at a single developmental time-point with no consideration of fetal sex. Fetal sex was shown to influence the placental glycogen content, at least in the spiny mouse (O'Connell *et al.* 2013). Therefore, a role for glucagon in regulating glycogen metabolism cannot currently be excluded. Additional models are required to more fully understand the enzymes that are important for glycogen metabolism in the mouse placenta.

Common functionality of genes involved in GlyT development and function

Of the 47 mutant mouse lines that are known to exhibit GlyT phenotypes (with or without aberrant glycogen storage), 38 different genes are represented. As the list lengthens, common genetic pathways and gene classifications have emerged as important players in GlyT formation and function. The majority of these genes can be assigned to at least one of three functional groups (Table 1): imprinted and X-linked genes, cell signalling genes and genes involved in transcriptional regulation.

Imprinted and X-linked genes

Imprinted genes represent an unusual class of autosomal gene that are characterized by complete or partial parental-allele-biased expression. This means that gene expression is derived wholly, or predominantly, from either the maternally inherited allele (i.e. maternally expressed) or paternally inherited allele (i.e. paternally expressed) in one or more tissues. In excess of 100 imprinted genes have been reported in the mouse, many of which are known to regulate placental development and function (Tunster *et al.* 2013). A broad role for imprinted genes in regulating the GlyT lineage has been reviewed previously (Lefebvre 2012), whereby four genes (*Ascl2*, *Cdkn1c*, *Igf2* and *Phlda2*) that reside within a ~1 Mb imprinted region on mouse distal chromosome 7 were discussed in detail. In addition to these genes, the paternally expressed *Dlk1*, *Peg3* and *Peg10* genes are also implicated in regulating the GlyT lineage and/or placental glycogen stores (Table 1), further emphasizing the importance of imprinted genes in regulating placental glycogen stores.

An special class of imprinted genes is the X-chromosome-linked genes. To ensure similar gene dosage between

males and females, one X chromosome in female cells is silenced. In extraembryonic lineages of female mouse conceptuses, the paternally inherited X-chromosome is preferentially silenced (Takagi & Sasaki 1975). A role for X-linked genes in regulating placental glycogen storage is demonstrated by mice that inherited only a single paternally inherited X chromosome (XpO) and display an expansion of the GlyT population (He *et al.* 2017). In support of this hypothesis, GlyT phenotypes were reported to varying degrees in loss-of-function models of four X-linked genes (i.e. *Plac1*, *Ldoc1*, *Wdr1* and *Esx1*) (Table 1). The functional convergence of imprinted and X-linked genes in regulating placental glycogen storage is consistent with the established role of imprinted genes in modulating fetal nutrient supply across the placenta (Angiolini *et al.* 2006, Tunster *et al.* 2013) and with the purported function of placental glycogen stores in providing an energy source to support fetal growth during late gestation. With the majority of imprinted genes exhibiting placental expression in the mouse, it will be of interest to explore whether other imprinted genes are involved in regulating placental glycogen storage.

Cell-cell signalling

Studies of mutant mouse lines that report glycogen storage defects that arise secondary to SpT phenotypes implicate a role for SpT-derived signals in the regulation of placental glycogen metabolism. For instance, genetic knockout or overexpression of the maternally expressed imprinted gene *Phlda2* causes an expansion or reduction of the SpT population, respectively (Tunster *et al.* 2010, 2014, 2015). Unaltered expression of the GlyT marker genes *Pcdh12* and *Gjb3* suggested that there was no overt effect on GlyT population size in either model. However, placental glycogen content closely paralleled the SpT phenotype, with a reduced SpT population leading to diminished glycogen content and an expanded SpT population associated with increased glycogen storage (Tunster *et al.* 2010, 2014, 2015). These studies implicate cell-to-cell signalling between SpT and GlyT, though the specific pathways that mediate this effect are unclear. A clue might lie within the *Crim1* knockout model. *Crim1* encodes for a transmembrane protein that mediates signal transduction by binding growth factors (e.g. vascular endothelial growth factor A; VEGF-A) to the cell surface. While *Crim1* mRNA expression is limited to SpT cells, the GlyT population expands in the absence of CRIM1 function (Pennisi *et al.* 2012). Therefore, CRIM1 might regulate a SpT-derived factor that signals to GlyT to regulate their proliferation (Pennisi *et al.* 2012).

Further evidence for a role of SpT-derived signals in modulating placental glycogen stores is provided by a comparison of *Phlda2* null conceptuses and their WT littermates with strain-matched control litters. Loss of

Table 1 Classification and expression of genes implicated in regulating GlyT differentiation and/or function.

Symbol	Gene name	Function	Spatial expression	GlyT differentiation [†]	Glycogen storage ^{††}	References
Imprinted and X-linked genes						
<i>Asc2</i>	<i>Achaete-scute complex homolog 2</i>	Maternally expressed basic helix-loop helix transcription factor	Highly expressed in both EPC and ExE during early development. Expression declines toward the term	✓	✓	Guillemot <i>et al.</i> (1994), Rossant <i>et al.</i> (1998)
<i>Cdkn1c</i>	<i>Cyclin-dependent kinase inhibitor 1C</i>	Maternally expressed cyclin-dependent kinase inhibitor	Widely expressed with high expression in GlyT	×	✓	Matsuoka <i>et al.</i> (1995), Georgiades <i>et al.</i> (2002), Coan <i>et al.</i> (2006)
<i>Dlk1</i>	<i>Delta-like homolog 1</i>	Paternally expressed transmembrane glycoprotein. Encodes the precursor to fetal antigen 1 (FA1) that functions as a Notch antagonist.	Expressed in endothelial cells lining the fetal vasculature of the Lz. Not expressed in any trophoblast lineage.	✓	n/a	Laborda (2000), Baladron <i>et al.</i> (2005), Yevtdiyenko & Schmidt (2006)
<i>Igf2</i>	<i>Insulin-like growth factor 2</i>	Paternally expressed insulin-like growth factor 2	Highly expressed in Jz and Lz between E9.5 and E12.5. Expression subsequently declines dramatically in the Lz and SpT but remains highly expressed in GlyT.	✓	✓	Redline <i>et al.</i> (1993), Carter <i>et al.</i> (2006)
<i>Peg3</i>	<i>Paternally expressed gene 3</i>	Paternally expressed zinc finger transcriptional repressor	Widely expressed in the developing placenta	✓	✓	Relaix <i>et al.</i> (1996)
<i>Peg10</i>	<i>Paternally expressed gene 10</i>	Paternally expressed retrotransposon-derived gene	Widely expressed in all trophoblast lineages	✓	n/a	Ono <i>et al.</i> (2006)
<i>Phlda2</i>	<i>Pleckstrin homology-like domain family A member 2</i>	Maternally expressed pleckstrin-homology domain protein that inhibits the AKT pathway by competing for PIP targets	Highly expressed in the EPC and ExE. Restricted to the chorionic plate and syncytiotrophoblast layers of the Lz by E10.5. Expression declines dramatically from E12.5. Very few PHLDA2-positive cells remain at E14.5	n/a	✓	Frank <i>et al.</i> (1999), Frank <i>et al.</i> (2002), Saxena <i>et al.</i> (2002)
<i>Esx1</i>	<i>Extraembryonic, spermatogenesis, homeobox 1</i>	X-linked paired-like homeobox domain protein	Expressed in the EPC and chorion before becoming restricted to the Lz by mid-gestation	✓	n/a	Li <i>et al.</i> (1997), Li & Behringer (1998)
<i>Plac1</i>	<i>Placental specific protein 1</i>	X-linked putative signal peptide	Placentaspecific expression from early to mid-gestation. EPC and TGCs at E7.5; P-TGCs, Jz and Lz, by E11.5; restricted to P-TGCs by E14.5	n/a	✓	Cocchia <i>et al.</i> (2000)
<i>Ldoc1</i>	<i>Regulator of NFKB signalling</i>	X-linked gene derived from long terminal repeat retrotransposon	Highly expressed in TGCs, EPC and ExE at E8.5. Restricted to non-migratory GlyT by E15.5 and absent by E18.5.	×	n/a	Naruse <i>et al.</i> (2014)
<i>Wdr13</i>	<i>WD repeat domain 13</i>	X-linked member of WD-repeat protein family	Expressed predominantly in the Lz. Lower expression in the SpT and decidua. Not expressed in GlyT	n/a	✓	Singh <i>et al.</i> (2015)
Cell-cell signalling						
<i>Akt1</i>	<i>Thymoma viral proto-oncogene 1</i>	Encodes protein kinase B α (PKB α), a downstream effector of the phosphatidylinositol 3-kinase (PI3K) signalling pathway	Widely expressed in all trophoblast lineages and fetal endothelium	n/a	✓	Yang <i>et al.</i> (2003)

(Continued)

Table 1 Continued.

Symbol	Gene name	Function	Spatial expression	GlyT differentiation†	Glycogen storage††	References
<i>Crim1</i>	Cysteine rich transmembrane BMP regulator 1	Transmembrane protein that binds growth factors such as VEGF-A to the cell surface	Primarily expressed in SpT. Low expression in P-, C- and syncytiotrophoblast	n/a	×	Pennisi et al. (2007), Wilkinson et al. (2007), Pennisi et al. (2012)
<i>Csf2</i>	Colony stimulating factor 2 (granulocyte-macrophage factor 2)	Encodes the cytokine granulocyte-macrophage colony-stimulating factor 2	Expressed in the decidua and Jz	✓	n/a	Kanzaki et al. (1991), Robertson et al. (1999)
<i>Egfr</i>	Epidermal growth factor receptor	Encodes epidermal growth factor receptor (EGFR)	Expressed in Jz and Lz at E18.5	✓	✓	Dackor et al. (2007)
<i>Htra1</i>	Htra serine peptidase 1	Serine protease that functions as an antagonist of TGF-β signalling	Expressed in P-TGCs at E7.5. Expression is barely detectable by E13.5.	×	×	Oka et al. (2004), Nie et al. (2005), Hasan et al. (2015)
<i>Hectd1</i>	HECT domain E3 ubiquitin protein ligase 1	Ubiquitin ligase that functions as a negative regulator of Wnt signalling	Widely expressed in all regions of the placenta between E7.5 and E13.5.	✓	✓	Tran et al. (2013), Sarkar et al. (2014)
<i>Igf1bp1</i>	Insulin-like growth factor binding protein 1	Carrier protein for insulin-like growth factors	Strongly expressed in the yolk sac endoderm but not expressed in trophoblast lineages	✓	n/a	Hwa et al. (1999), Carter et al. (2006)
<i>Pcdh12</i>	Protocadherin 12	Member of the protocadherin subgroup of the cadherin family of transmembrane calcium-dependent cell–adhesion proteins	Expressed exclusively in GlyT lineage throughout gestation	n/a	✓	Rampon et al. (2005)
<i>Pgf</i>	Placental growth factor	Encodes the pro-angiogenic placental growth factor (PlGF)	Widely expressed in the placenta at E10.5	✓	✓	Achen et al. (1997), Tayade et al. (2007)
<i>Pik3ca</i>	Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha	Encodes the ubiquitously expressed PI3-kinase catalytic subunit p110α	Ubiquitously expressed	n/a	✓	Foukas et al. (2006)
<i>Pr17d1</i>	Prolactin family 7, subfamily d, member 1	Member of the prolactin/placental lactogen (Pr/Pl) gene family	Widely expressed in all trophoblast subtypes; highest expression in GlyT	✓	✓	Simmons et al. (2008a)
<i>Ptp4a2</i>	Protein tyrosine phosphatase 4a2	Protein phosphatase	Widely expressed in all trophoblast lineages	✓	✓	Dong et al. (2012)
<i>Pthlh</i>	Parathyroid hormone-like peptide	Encodes the constitutively expressed parathyroid hormone-related peptide (PTHrP)	Constitutively expressed	n/a	✓	Wysolmerski & Stewart (1998), Duval et al. (2017)
<i>sFlt-1</i>	Soluble fms related receptor tyrosine kinase 1	An anti-angiogenic factor that sequesters placental growth factor (PGF) and vascular endothelial growth factor (VEGF)	Expressed in the EPC and later the Jz	✓	n/a	Kendall & Thomas (1993), Breier et al. (1995), Levine et al. (2006)
Transcriptional regulators						
<i>Arnt</i>	Aryl hydrocarbon receptor nuclear translocator	Encodes the HIF1β subunit of the heterodimeric transcription factor hypoxia inducible factor (HIF)	Constitutively expressed	✓	n/a	Adelman et al. (2000)

<i>Bahd1</i>	<i>Bromo adjacent homology domain containing 1</i>	Chromatin modifier that mediates heterochromatin-associated gene silencing. Implicated in the silencing of <i>IGF2</i> in humans	Not reported	n/a	✓	Bierme <i>et al.</i> (2009)
<i>Cited2</i>	<i>Chp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2</i>	Transcriptional co-factor	Expressed in all trophoblast lineages.	✓	n/a	Dunwoodie <i>et al.</i> (1998), Withington <i>et al.</i> (2006) Kozak <i>et al.</i> (1997), Cowden Dahl <i>et al.</i> (2005)
<i>Hif1a</i>	<i>Hypoxia inducible factor 1, alpha subunit</i>	Encodes the HIF1 α subunit of the heterodimeric transcription factor hypoxia inducible factor (HIF)	Constitutively expressed but HIF1A protein is degraded in normoxia.	✓	n/a	Wang <i>et al.</i> (2008), Sharma <i>et al.</i> (2019) Mould <i>et al.</i> (2012)
<i>miR-126a</i>	<i>microRNA 126a</i>	Endothelial-specific microRNA	Widely expressed in fetal endothelium of Lz, syncytiotrophoblast, P-TGC, SpT and GlyT.	✓	✓	Kuckenber <i>et al.</i> (2010) Kruger <i>et al.</i> (2007)
<i>Prdm1</i>	<i>PR domain containing 1, with ZNF domain</i>	Zinc-finger transcriptional repressor	Expressed in GlyT progenitors at E7.5. Highly expressed in SpA-TGCs.	n/a	n/a	Hemberger <i>et al.</i> (2000), Deussing <i>et al.</i> (2002)
<i>Tfap2c</i>	<i>Transcription factor AP-2, gamma</i>	Transcription Factor AP-2 Gamma	Expressed in the trophoctoderm at E4.5. Restricted to Jz and TGCs by E11.5.	✓	✓	Nakayama & Nakayama (2006), Nishiyama <i>et al.</i> (2015), Zheng <i>et al.</i> (2016)
<i>Sp1 & Sp3</i>	<i>Trans-acting transcription factor 1 & 3</i>	Zinc-finger transcription factors	Ubiquitously expressed	n/a	n/a	Liu <i>et al.</i> (1999), Wang <i>et al.</i> (2004)
Miscellaneous						Celebi <i>et al.</i> (2012), Reichmann <i>et al.</i> (2013)
<i>Cts7</i>	<i>Cathepsin 7</i>	Placenta-specific papain-like cysteine cathepsin protease that functions in lysosomal proteolysis	Highly expressed in TGCs at E7.5; expression declines and is restricted to the Lz by E15.5	✓	n/a	
<i>Fbx12</i>	<i>F-box and leucine-rich repeat protein 12</i>	Member of the F-box family of proteins, which function as the substrate recognition component in E3 ubiquitin ligase complexes	Jz specific at E15.5	n/a	✓	
<i>Pdcd5</i>	<i>Programmed cell death 5</i>	Promoter of both apoptotic and the non-apoptotic programmed cell death pathway (paraptosis)	Not reported	✓	✓	
<i>Tex19.1</i>	<i>Testis expressed gene 19.1</i>	Mammalian-specific hypomethylation-sensitive genome-defence gene	Widely expressed in the EPC and Jz; some patchy expression in Lz	✓	n/a	

[†]Changes in GlyT abundance or maturation implied an effect in GlyT differentiation. ^{††}Altered regulation of glycogen stores is suggested by an effect on total placental glycogen content (see Tables 2, 3, 4 and 5 for details and references).
 E, embryonic day; EPC, ectoplacental cone; ExE, extraembryonic ectoderm; GlyT, glycogen trophoblast cells; Jz, junctional zone; Lz, labyrinth zone; n/a, data not available; P, postnatal day; PAS, Periodic Acid Schiff stain; Syn I-II, syncytiotrophoblast cell layer I; TGC sub-types: C-TGC, canal TGC; P-TGC, parietal TGC; S-TGC, sinusoidal TGC; SpA-TGC, spiral artery associated TGC; TGC, trophoblast giant cell.

function of *Phlda2* results in expansion of the Jz (Frank *et al.* 2002), which is attributable to a disproportionate increase in the SpT population (Tunster *et al.* 2015). While there was no overt effect on GlyT cell number, an accumulation of glycogen in placentas from *Phlda2* null their WT littermates was apparent at E18.5. One explanation might be that the entire litter was exposed to an enhanced endocrine-signalling environment caused by SpT expansion in *Phlda2* null placentas resulting in excessive placental glycogen storage that potentially deprives the fetuses of nutrients (Tunster *et al.* 2015). However, it is not possible to exclude a role for broader effects on maternal physiology in impairing fetal growth in this model.

We have further identified fourteen genes that encode for specific components of cell-signalling pathways that might help to establish the importance of cell-cell signalling in the regulation of placental glycogen content (Table 1). These genes include signalling molecules such as cytokines (*Csf2*), hormones (*Pthlh*, *Prl7d1*) and growth factors (*Pgf*), receptors (*Egfr*) and downstream effectors, such as kinases (*Akt1*, *Pik3ca*) and phosphatases (*Ptp4a2*). Some of these genes encode for key intermediates in a diverse range of signalling pathways, namely VEGF (e.g. *Crim1*), epidermal growth factor (EGF) (e.g. *Egfr*) and transforming growth factor (TGF) (e.g. *Htra1*) pathways.

In particular, aberrant AKT signalling is implicated in GlyT phenotypes associated with genetic knockouts of *Ptp4a2*, *Tfap2c*, *Igf2* or *Phlda2* (Frank *et al.* 1999, Saxena *et al.* 2002, Dong *et al.* 2012, Takao *et al.* 2012, Sharma *et al.* 2016, Sferruzzi-Perri *et al.* 2017). This, combined with the fact that loss of function of *Akt1* itself impairs placental glycogen storage (Yang *et al.* 2003), indicates that the AKT pathway is key to this process. AKT signalling is known to regulate specific cellular processes including growth, proliferation, metabolism and survival (Yu & Cui 2016, Hermida *et al.* 2017, Manning & Toker 2017). Specific to its role in glycogen storage, AKT also regulates glycogenesis through the inhibition of glycogen synthase kinase 3 (GSK3), a negative regulator of glycogen synthase (Cross *et al.* 1995, Diehl *et al.* 1998). Other models that show changes in the expression of *Igf2* or *Phlda2* (e.g. *Pcdh12* knockout (Rampon *et al.* 2008)) might also implicate AKT-signalling defects in their GlyT phenotypes. While aberrant AKT signalling was reported in the placentas of human FGR infants (Yung *et al.* 2008), placental glycogen storage has not yet been investigated in the context of human FGR to date.

Ablation of *Akt1*, which encodes for protein kinase B α (PKB α), causes fetal and placental growth restriction (Yang *et al.* 2003). A near complete loss of glycogen-containing trophoblast cells was reported (Yang *et al.* 2003), though this result was based solely on examination of PAS-stained placenta sections. The absence of PAS staining is

more likely to indicate a failure to accumulate glycogen, rather than ablation of the GlyT lineage. Therefore, this model should be revisited for a more detailed analysis of the GlyT phenotype, including determination of spatiotemporal expression of markers such as *Pcdh12* (Bouillot *et al.* 2006), *Gjb3* (Coan *et al.* 2006), *Aldh1a3* (Outhwaite *et al.* 2015) and biochemical analysis of glycogen content (Lo *et al.* 1970). Regardless, the result is consistent with the role of AKT in regulating GSK3 and, indirectly, glycogen synthase (Yang *et al.* 2003).

Upstream regulators of AKT signalling include PRL2 and IGF2, both of which have been implicated in placental development. The *Ptp4a2* gene encodes for the protein phosphatase PRL2 and, when knocked out, the placentas were small in size due to a substantially reduced Jz defined by a near complete loss of SpT with only a few non-migratory GlyT remaining (Dong *et al.* 2012). While PAS staining was reduced, placental glycogen content was not directly quantified (Dong *et al.* 2012). *Ptp4a2*^{-/-} placentas also exhibited reduced AKT phosphorylation (Dong *et al.* 2012), indicating that PRL2 is important for this process. The associated *Ptp4a2*^{-/-} fetuses were growth restricted at E16.5. In fetal tissues, AKT and MAPK (mitogen activated protein kinase) pathways are activated via IGF2 signalling mediated primarily through binding IGF1R (insulin-like growth factor 1 receptor) (Forbes & Westwood 2008, Sferruzzi-Perri *et al.* 2017). However, the absence of a placental phenotype in *Igf1r* null mice suggests that IGF2 acts through an alternative, unknown receptor in the placenta (Baker *et al.* 1993, Efstratiadis 1998). Whether IGF2 activates AKT signalling in the placenta is unclear, and a detailed assessment of AKT signalling in the placenta of *Igf2* mutants is required. Additionally, further work is warranted to explore the broad role of AKT signalling in regulating the placental glycogen stores by utilizing mouse models with known GlyT phenotypes.

Transcriptional regulators

The GlyT population is highly dynamic, with the number of GlyT cells increasing by nearly 300-fold between E12.5 and E16.5, and switching from an apparently glycogenic state to a glycogenolytic state (Lopez *et al.* 1996). These changes implicate major shifts in transcriptional regulation to modulate placental glycogen metabolism. A broad role for transcriptional regulators in modulating placental glycogen storage and/or the GlyT lineage has not been previously recognized. We identified eight genes encoding specific transcriptional regulators that are implicated in the development and/or function of the GlyT lineage (Table 1). One example is the endothelial-specific microRNA *miR-126a* (*miR-126*), which when ablated leads to global hypermethylation associated with dysregulated expression of placenta-

specific genes (e.g. *Prl6a1*, *Pcdh12* and *Tpbpa*) and imprinted genes (e.g. *Igf2*, *Phlda2* and *Cdkn1c*) (Sharma *et al.* 2019). Genetic ablation of *miR-126a* results in Jz hyperplasia, attributable to a specific expansion of the GlyT population, without a change in SpT abundance. Consequently *miR-126a*^{-/-} placentas accumulated ~50% more glycogen than controls and were associated with fetal growth restriction at E15.5 (Sharma *et al.* 2019). The specific targets of *miR-126a* are yet to be determined. Further work is required to fully elucidate the transcriptional networks involved in regulating the GlyT lineage and glycogen storage.

Using genetic mouse models to understand the function of placental glycogen

The association of altered placental glycogen storage with human pregnancy complications supports an important role for glycogen in achieving a successful pregnancy outcome (reviewed in Akison *et al.* 2017). The majority of mouse models with GlyT phenotypes show evidence of fetal growth restriction (FGR), which is consistent with the putative role of placental glycogen in supporting fetal growth (Tables 2 and 3). In contrast, the remaining models showed GlyT phenotypes that were either associated with normal, enhanced or undetermined effects on fetal growth (Table 4) or embryonic lethality around mid-gestation (Table 5) that precluded a meaningful assessment of fetal growth.

In our evaluation of the literature, we observed that the extent to which GlyT phenotypes are characterized varies considerably between studies. Indeed, only a minority of these models were assessed using a direct biochemical determination of placental glycogen content. Instead, reduced glycogen storage or mobilization was inferred from one or more of the following methods: reduced (or absent) PAS staining; reduced GlyT abundance as determined by histology and/or reduced genetic marker expression for GlyT cells and mislocalization of GlyT within the Lz or a failure of GlyT cells to migrate to the decidua. As a result, there is a need for established criteria in describing GlyT phenotypes and glycogen storage and metabolic defects. We identified four key parameters for characterizing GlyT phenotypes: (1.) GlyT lineage specification and differentiation by assessing lineage marker expression, (2.) GlyT cell number, (3.) GlyT localization and degree of migration into the decidua and (4.) quantification of total placental glycogen content using a biochemical assay (Lo *et al.* 1970). A collective evaluation of these genetic mutants using these criteria will help to separate GlyT developmental defects from metabolic/storage defects and improve our understanding of how placental glycogen stores support growth.

Reduced placental glycogen content is frequently associated with fetal growth restriction

Several mouse models that demonstrate a glycogen storage deficit are also associated with FGR (Table 2). It is well known that IGF2 is an important regulator of fetal and placental growth (DeChiara *et al.* 1990, Constância *et al.* 2005). *Igf2* mRNA is highly expressed in the GlyT lineage (Redline *et al.* 1993, Georgiades *et al.* 2002, Coan *et al.* 2006), and constitutive deletion of *Igf2* results in reduced GlyT abundance and placental glycogen content (Lopez *et al.* 1996). Deletion of the placenta-specific *Igf2* transcript (*Igf2P0*) results in a similar reduction of GlyT cell number (Sferruzzi-Perri *et al.* 2011), even though the *Igf2P0* transcript accounts for only 10% of total placental *Igf2* (Moore *et al.* 1997). While constitutive deletion of *Igf2* results in a 50% reduction in fetal weight (DeChiara *et al.* 1990), *Igf2P0* mutants are 25% lighter than controls (Constância *et al.* 2005), at least partially attributing FGR to a placental defect. However, the contribution of placental glycogen is unclear, as glycogen content was not directly assessed in the *Igf2P0* mutants.

Human placentas exhibiting elevated expression of *PHLDA2* are frequently linked with FGR (reviewed in Jensen *et al.* 2014), although placental glycogen stores have not been investigated in these placentas. Analysis of a mouse model with overexpression of *Phlda2* demonstrates that placental glycogen content is reduced by 50% of controls. However, the effect on glycogen storage is likely secondary to a reduction in the *Prl8a8*⁺ SpT population, since there was no overt effect on expression of the GlyT markers *Pcdh12* or *Cjb3* (Tunster *et al.* 2010, 2014, 2015). The effect on fetal growth in the *Phlda2* overexpression model is complex and dependent upon the genetic background of the mouse, even though similar placental defects are apparent between strains. For instance, fetal growth was asymmetrically restricted when on the 129S2/SvHsd background (Salas *et al.* 2004, Tunster *et al.* 2010), but was unaffected on the C57BL/6 background (Tunster *et al.* 2014). Since genetically WT placentas on the C57BL/6 background naturally accumulate more than twice the glycogen content of 129S2/SvHsd placentas (Tunster *et al.* 2012), fetal growth might be protected on the C57BL/6 background.

Even though GlyT are important for fetal growth, these cells are not essential to fetal survival. GlyT cells were absent in mutant mouse lines, whereby the expression of *Ascl2* was at ~50% of endogenous levels (*Ascl2*^{lacZ/Del7Al} or *Del7Al*^{+/+} mutants). Placentas either demonstrated a lack of PAS stain and/or *Pcdh12* expression at E15.5. The associated fetuses survived to term, albeit exhibiting growth restriction of 15–20% (Lefebvre *et al.* 2009, Oh-McGinnis *et al.* 2011, Bogutz *et al.* 2018). In contrast, *Ascl2* null placentas lack the EPC progenitor cells that give rise to the SpT and GlyT resulting in embryonic

Table 2 Genetic mouse models with fetal growth restriction and placentas with reduced glycogen content and/or GlyT phenotypes.

Mouse Model	Characteristics	Fetal weight or size	Placental weight	Glycogen content	GlyT number	GlyT markers	GlyT localization	Lz phenotype	References
<i>Akt^{-/-}</i>	Knockout	↓ (E14.5, E16.5)	↓ (E14.5, E16.5)	↓ PAS	n/a	n/a	n/a	Reduced Lz size	Yang et al. (2003)
<i>Def^{+/+}</i>	Ascl2 expressed reduced by 40%	↓ (P0)	↓ (E15.5)	n/a	↓↓↓ (E15.5)	↓ <i>Tpbp</i> ↓↓↓	n/a	Disorganized structure	LeFebvre et al. (2009), Oh-McGinnis et al. (2011)
<i>Ascl2^{lacZ/Def1M}</i>	Ascl2 expressed reduced by 60%	↓ (E15.5)	↓ (E15.5)	↓↓↓↓ PAS	↓↓↓ (E15.5)	↓ <i>Tpbp</i> ↓↓↓	n/a	Disorganized structure	Bogutz et al. (2018)
<i>Bahd1^{-/-}</i>	Knockout	↓ (E18.5)	n/a (↓ circumference and area at E18.5)	↓ PAS	n/a	n/a	n/a	Reduced Lz size	Lakisic et al. (2016)
<i>Csf2^{-/-}</i>	Mixed 129/Sv x C57BL/6 background	↓ (E16.5)	Normal (E16.5)	n/a	↓	n/a	n/a	Reduced Lz size	Kanzaki et al. (1991), Robertson et al. (1999)
<i>Dlk1^{-/-}</i>	Knockout*	↓ (E18.5, P7)	Normal (E12.5, E14.5, E16.5)	n/a	↑ progenitors ↓ mature GlyT	n/a	n/a	Reduced Lz size; vascularization defect	Yevtdiyenko & Schmidt (2006), Appelbe et al. (2013), Cleaton et al. (2016)
<i>Egfr^{-/-}</i>	Knockout	↓ (from E13.5)	↓ (from E11.5)	n/a	n/a	↓ <i>Tpbp</i> (E13.5)	n/a	n/a	Sibilia & Wagner (1995)
<i>Egfr^{mut2}</i>	<i>Egfr</i> hypomorph	↓ (E18.5) (Effects are genetic background dependent)	↓ (variable, E15.5, E18.5)	↓ PAS	n/a	↓ <i>Tpbp</i> ↓ <i>Pcdh12</i>	n/a	Increased expression of <i>Ccm1</i> , <i>Dlx3</i> , <i>Tcf7b</i>	Dackor et al. (2009b)
<i>Fbx12^{-/-}</i>	Knockout	↓ (E17.5)	↓↓↓ (E17.5)	↓ PAS	n/a	↓ <i>Tpbp</i> ↓ <i>Pcdh12</i> ↓ <i>Gjfb3</i>	n/a	Vascularization defect	Nishiyama et al. (2015)
<i>hIGFBP1-Tg</i>	Over-expression of human <i>IGFBP1</i>	↓ (E11.5)	↑ (E11.5)	n/a	↓ GlyT:SpT ratio (in females)	n/a	n/a	Increased Lz size	Crossey et al. (2002)
<i>HtrA1^{-/-}</i>	Knockout	↓ (E14.5)	↓ (E14.5)	n/a	n/a	↓ <i>Tpbp</i>	Mislocalization of <i>Tpbp</i> ⁺ ; PAS ⁻ cells within Lz	n/a	Nie et al. (2005), Hasan et al. (2015)
<i>Igf2^{-/-}</i> or <i>Igf2^{+/-}</i>	Fetal and placental knockout*	↓ (E16.0)	↓↓ (E15.5) ↓ (E18.5)	↓↓ glycogen (E15.5, E18.5)	↓↓ (E15.5, E18.5)	n/a	n/a	n/a	DeChiara et al. (1990), Redline et al. (1993), Lopez et al. (1996), Carter et al. (2006)
<i>Igf2P0</i>	Loss of placental-specific <i>Igf2</i> transcripts*	↓ (from E16.5)	↓ (E13.5) ↓ (E15.5, E18.5)	n/a	↓ (E15.5)	n/a	n/a	Reduced Lz size, increased trophoblast barrier thickness, reduced diffusional capacity	Sibley et al. (2004), Constância et al. (2005), Sferuzzi-Perri et al. (2011)
<i>Lv-hsFLT-1</i>	Overexpression of human <i>sFLT-1</i>	↓ (E18.5)	↓ (E18.5)	n/a	↓ GlyT proportion of Lz	n/a	n/a	Reduced Lz size	Kuhnel et al. (2017)
<i>Peg3^{+/-}</i>	Knockout*	↓ (E17.5) ↓ (P0)	↓ (E14.5, E17.5)	↓ glycogen (E14.5)	↓ (males more affected than females)	↓ <i>Tpbp</i> (in males only) <i>Pcdh12</i> and <i>Gjfb3</i>	n/a	n/a	Kuroiwa et al. (1996), Relaix et al. (1999), Curley et al. (2004), Thiaville et al. (2013), Lee et al. (2015), He et al. (2016), Tunster et al. (2018)

Genotype	Phenotype	Time	Glycogen	Migration	Cellular	Pathway	Reference
<i>Phlda2</i> ^{+/+;BAC1} or <i>Phlda2</i> ^{+/+;BAC3}	2–4-fold overexpression of <i>Phlda2</i>	↓ (variable, from E12.5)	↓↓ glycogen ↓ PAS	n/a	n/a	Impaired migration of PAS ⁺ cells to decidua	Tunster et al. (2010), Tunster et al. (2014)
<i>Plk3ca</i> ^{+/+} or <i>Plk3ca</i> ^{-/-}	Knockout	↓ (E15.5)	↓↓ glycogen (if dam is <i>Plk3ca</i> ^{+/+})	n/a	n/a	Reduction in Lz size, fetal capillary volume, exchange surface area and diffusion capacity dependent upon maternal genotype	Foukas et al. (2006), Sferuzzi-Perri et al. (2016)
<i>Pip4a2</i> ^{-/-}	Knockout	↓ (E16.5)	↓ PAS	↓ Non-migratory GlyT ↓↓↓ Migratory GlyT	↓ <i>Tpbp</i>	Failure of <i>Tpbp</i> ⁺ cells to migrate to decidua	Dong et al. (2012)
<i>Pthlh</i> ^{-/-}	Knockout	↓ (from E16.5)	↓ glycogen (E12.5, E14.5, E18.5) normal glycogen (E16.5)	n/a	↓ <i>Tpbp</i>	Reduced Lz size, reduced transport capacity	Duval et al. (2017)
<i>Ldoc1</i> ^{+/+} or <i>Ldoc1</i> ^{-/-}	Knockout	↓ (E16.5) Normal (E18.5)	n/a	Normal	<i>Pcdh12</i> normal	Mislocalization of <i>Prl6a1</i> ⁺ cells in Lz	Naruse et al. (2014)
<i>Sp1</i> ^{+/+} , <i>Sp3</i> ^{-/-}	Embryonic lethal between E16.5 and birth	↓↓ (E16.5)	n/a	n/a	↓ <i>Tpbp</i> ↓ <i>Pcdh12</i>	Disorganized structure	Kruger et al. (2007)
<i>Tex19.1</i> ^{-/-}	Knockout	↓ (E18.5)	n/a	↓↓↓ (E18.5)	↓ <i>Tpbp</i> ↓ <i>Pcdh12</i> ↓ <i>Cjfb3</i>	Fewer S-TGCs	Celebi et al. (2012), Reichmann et al. (2013)
<i>Tfap2c</i> ^{-/-}	Knockout	↓ (E14.5) ↓ (E18.5)	n/a	n/a	n/a	Mislocalization of PAS ⁺ cells within Lz	Kuckenberg et al. (2010), Kaiser et al. (2015)
<i>Cre-Tpbp</i> : <i>Tfap2c</i> ^{-/-}	Conditional knockout of <i>Tfap2c</i> in <i>Tpbp</i> ⁺ cells	↓ (from E16.5)	↓↓ glycogen (E14.5)	↓↓↓ (E16.5)	↓ <i>Tpbp</i> (E12.5) ↓↓↓ <i>Tpbp</i> (E16.5) ↓ <i>Cjfb3</i>	n/a	Sharma et al. (2016)
<i>Wdr13</i> ^{+/+}	Knockout*	↓ (from E17.5)	↓ PAS staining	n/a	n/a	Reduced Lz size, fewer S-TGCs, Increased MBS	Singh et al. (2015)

Developmental stages in brackets is the time assessed. Total placental glycogen content quantified by biochemical or enzymatic methods or estimated from comparison of PAS (Periodic Acid Schiff) staining.

* denotes imprinted or X-linked gene; heterozygous inheritance of a null allele from the normally active parental lineage effectively ablates gene expression. ↓ = <20% reduction; ↓↓ = 20–50% reduction; ↓↓↓ = >50% reduction; ↓↓↓↓ = undetected; ↑ = <20% increase; ↑↑ = 20–50% increase; ↑↑↑ = >50% increase. E, embryonic day; GlyT, glycogen trophoblast cells; Jz, junctional zone; MBS, maternal blood sinusoids; P, postnatal day; n/a, not available; SpT, spongiotrophoblast cells; S-TGCs, sinusoidal trophoblast giant cells; Tg, transgenic.

Table 3 Genetic mouse models with fetal growth restriction and increased placental glycogen content and/or GlyT phenotypes.

Mouse Model	Characteristics	Fetal weight or size	Placental weight	Glycogen content†	GlyT number	GlyT markers	GlyT localization	Lz phenotype	References
<i>Ascl2</i> ^{-/-} Tg	<i>Ascl2</i> over-expression	↓ (E18.5)	↓ (E12.5, E14.5) Normal (E16.5, E18.5)	↑↑ glycogen (E16.5) ↑↑↑ glycogen (E18.5)	n/a	↓↓↓ <i>Tpbpa</i> ↑↑ <i>Plhl7b1</i> Normal <i>Pcdh12</i> Normal <i>Gjb3</i>	Mislocalisation of <i>Tpbpa</i> ⁺ ; PAS ⁺ cells within Lz	n/a	Tunster <i>et al.</i> (2016)
<i>Crim1</i> ^{KST264/KST264}	Hypomorphic gene-trap insertion	↓ (E17.5)	↓ (from E13.5)	Normal PAS	n/a	↑ <i>Pcdh12</i> ⁺ cell area	n/a	Fewer S-TGCs	Pennisi <i>et al.</i> (2007), Pennisi <i>et al.</i> (2012)
<i>Csf2</i> ^{-/-}	C57BL/6 background	↓ (E14.5) Normal (E17.5)	↓ (E17.5)	n/a	↑↑↑	↑ <i>Tpbpa</i>	n/a	n/a	Sferruzzi-Perri <i>et al.</i> (2009)
<i>Esx1</i> ^{+/-} or <i>Esx1</i> ^{-/-}	Knockout*	↓↓ (P0)	↑↑↑ (E14.5) ↑↑ (E18.5)	n/a	↑	↑ <i>Tpbpa</i>	n/a	Vascularization defect. Failure of SynT-II formation	Li <i>et al.</i> (1997), Li & Behringer (1998)
<i>miR-126a</i> ^{-/-}	Knockout, embryonic lethal (from E15.5)	↓ (E15.5)	Normal (E12.5, E15.5)	↑↑↑ glycogen (E15.5)	↑ (E13.5, E15.5)	↑ <i>Tpbpa</i> ↑ <i>Cdkn1c</i> (E15.5)	n/a	Increased Jz:Lz ratio (no effect on gross Lz size)	Sharma <i>et al.</i> (2019)
<i>Pcdh12</i> ^{-/-}	Knockout	↓ (E12.5, E17.5)	↓ (E17.5)	↑↑↑ glycogen (E12.5) ↑↑ glycogen (E17.5) ↑ PAS	n/a	n/a	Mislocalization of PAS ⁺ cells within Lz	Reduced cell density	Rampon <i>et al.</i> (2005), Rampon <i>et al.</i> (2008)
<i>Plac1</i> ^{+/-} or <i>Plac1</i> ^{-/-}	Knockout*	↓ (E16.5)	↑↑↑ (E16.5)	↑ PAS	n/a	n/a	n/a	n/a	Cocchia <i>et al.</i> (2000), Jackman <i>et al.</i> (2012)
<i>Phlda2</i> ^{+/-}	Knockout*	Normal (vs <i>Phlda2</i> ^{+/-} littermates) ↓ (vs WT litters)	↑↑ (from E12.5)	↑↑ glycogen	n/a	↑↑ <i>Tpbpa</i> Normal <i>Pcdh12</i> Normal <i>Gjb3</i>	n/a	n/a	Frank <i>et al.</i> 1999, 2002, Tunster <i>et al.</i> (2015)
<i>Plhl7d1</i> ^{-/-}	Knockout	↓ (E12.5)	↓ (E12.5 in males)	↑↑↑ PAS (males only)	↑↑ (males only)	n/a	n/a	Increased Jz:Lz ratio. impaired remodelling of maternal spiral arteries.	Zhang <i>et al.</i> (2019)
<i>Plhl7h</i> ^{-/-}	Knockout	↓ (from E16.5)	Normal	↓ glycogen (E12.5, E14.5) Normal glycogen (E16.5) ↑ glycogen (E18.5)	n/a	↓ <i>Tpbpa</i>	n/a	Reduced Lz size, reduced transport capacity	Duval <i>et al.</i> (2017)

Developmental stage in brackets is the time assessed.

†Total placental glycogen content quantified by biochemical or enzymatic methods or estimated from comparison of PAS (Periodic Acid Schiff) staining. * denotes imprinted or X-linked gene; heterozygous inheritance of a null allele from the normally active parental lineage effectively ablates gene expression.

↓ = <20% reduction; ↓↓ = 20–50% reduction; ↓↓↓ = >50% reduction; ↑ = <20% increase; ↑↑ = 20–50% increase; ↑↑↑ = >50% increase. E, embryonic day; GlyT, glycogen trophoblast cells; Lz, labyrinth zone; P, postnatal day; n/a, not available; S-TGCs, sinusoidal trophoblast giant cells; SynT-II, syncytiotrophoblast cell layer II; Tg, transgenic.

Table 4 Genetic mouse models with normal or enhanced fetal growth and increased placental glycogen content and/or GlyT phenotypes.

Mouse Model	Characteristics	Fetal weight or size	Placental weight	Glycogen content [†]	GlyT number	GlyT markers	GlyT localization	Lz phenotype	References
<i>Cdkn1c</i> ^{+/+}	Knockout*	↑ (E15.5, E18.5) = (P0)	↑↑↑ (from E13.5)	↓↓ glycogen (E15.5, E18.5)	Normal	↓ <i>Tpba</i> ↓ <i>Gib3</i> <i>Pcdh12</i> normal	n/a	Increased Lz cell number, fewer S-TGCs	Takahashi et al. (2000), Georgiades et al. (2002), Coan et al. (2006), Tunster et al. (2011)
<i>Cts7</i> ^{Tg}	<i>Cts7</i> over-expression	n/a	n/a	n/a	↓↓ (E12.5)	↓ <i>Tpba</i> (E10.5, E12.5)	n/a	Fewer S-TGCs	Hemberger et al. (2000), Screen et al. (2008)
<i>Egfr</i> ^{Dsk5}	<i>Egfr</i> hypomorph	Normal (E15.5)	↑ to ↑↑↑ (variable, E15.5) Genetic background dependent	↑ PAS	↑	↑ <i>Tpba</i> ↑ <i>Pcdh12</i>	n/a	↓ <i>Gcm1</i> ↓ <i>Dlk3</i>	Dackor et al. (2007), Dackor et al. (2009b)
<i>H19</i> ^{-/-}	Knockout*	↑ (from E15.5)	↑ (E15.5, E18.5)	↑ glycogen (E15.5)	↑↑ (E15.5)	n/a	n/a	n/a	Leighton et al. (1995), Esquiliano et al. (2009)
<i>Pgf</i> ^{-/-}	Knockout	Normal (P0)	↑ (P0)	↑↑ glycogen ↑ Best's Carmine staining	↑	n/a	n/a	Reduced Lz size	Achen et al. (1997), Tayade et al. (2007), Parchem et al. (2018)

Developmental stage in brackets is the time assessed.

[†]Total placental glycogen content quantified by biochemical or enzymatic methods or estimated from comparison of PAS (Periodic Acid Schiff) staining. * denotes imprinted or X-linked gene; heterozygous inheritance of a null allele from the normally active parental lineage effectively ablates gene expression.

↓ = <20% reduction; ↓↓ = 20–50% reduction; ↓↓↓ = >50% reduction; ↑ = <20% increase; ↑↑ = 20–50% increase; ↑↑↑ = >50% increase. E, embryonic day; GlyT, glycogen trophoblast cells; Lz, labyrinth zone; n/a, not available; P, postnatal day; S-TGCs, sinusoidal trophoblast giant cells; Tg, transgenic.

Table 5 Genetic mouse models with glycogen content or GlyT phenotypes associated with embryonic lethality at mid-gestation.

Mouse model	Characteristics	Stage of embryonic lethality	Placental weight	Glycogen content†	GlyT number	GlyT markers	GlyT localization	Lz phenotype	References
<i>Arnt</i> ^{-/-}	Knockout	By E10.5	n/a	n/a	↓↓↓ progenitors (E9.5)	↓↓↓ <i>Tpbpa</i> (E9.5)	n/a	Reduced Lz size, Labyrinth trophoblast defect, decreased VEGF expression	Kozak et al. (1997), Maltepe et al. (1997), Adelman et al. (2000), Watson & Cross (2005)
<i>Asc12</i> ^{-/-} or <i>Asc12</i> ^{+/-}	Knockout*	By E10.5	n/a	n/a	↓↓↓ progenitors (E8.5)	↓↓↓ <i>Tpbpa</i> (E8.5)	n/a	Vascularization defect	Guillemot et al. (1994), Guillemot et al. (1995), Rossant et al. (1998)
<i>Cited2</i> ^{-/-}	Knockout; associated with congenital malformations (e.g. NTD)	By E13.5	↓↓ (E12.5)	n/a	↓ Migratory GlyT	↓ <i>Tpbpa</i>	Impaired migration to decidua	Vascularization defect	Dunwoodie et al. (1998), Yin et al. (2002), Withington et al. (2006), Barbera et al. (2002)
<i>Hectd1</i> ^{-/-}	Knockout; associated with congenital malformations (e.g. heart defects)	By E12.5	↓ (incomplete penetrance)	↓↓ glycogen	↓	↓ <i>Tpbpa</i> ↓ PAS	n/a	Disrupted structure, Vascularization defect	Sarkar et al. (2014), Sarkar et al. (2016)
<i>Hif1a</i> ^{-/-}	Knockout; associated with congenital malformations (e.g. NTD, heart defects)	By E10.5	n/a	n/a	↓↓↓ progenitors	↓ <i>Tpbpa</i>	n/a	Impaired vascularization of chorion	Kozak et al. (1997), Compennolle et al. (2003), Cowden Dahl et al. (2005)
<i>Pdcd5</i> ^{-/-}	Knockout; associated with congenital malformations (e.g. heart defects)	By E13.5	n/a	↓↓↓ PAS (E13.5)	↓↓↓ (E13.5)	n/a	n/a	Disorganized structure, Necrotic and hemorrhagic	Li et al. (2017)
<i>Peg10</i> ^{+/-}	Knockout*	By E10.5	n/a	n/a	↓↓↓ progenitors (E9.5)	↓↓↓ <i>Tpbpa</i> (E9.5)	n/a	Impaired development	Ono et al. (2006)
<i>Prdm1</i> ^{-/-}	Knockout; associated with congenital malformations (e.g. heart defects)	By E10.5	n/a	n/a	n/a	Normal <i>Tpbpa</i>	Failure to migrate to decidua	Disrupted structure	Vincent et al. (2005), Mould et al. (2012)

Developmental stage in brackets is the time assessed.

†Total placental glycogen content quantified by biochemical or enzymatic methods or estimated from comparison of PAS (Periodic Acid Schiff) staining. *Denotes imprinted or X-linked gene; heterozygous inheritance of a null allele from the normally active parental lineage effectively ablates gene expression.

↓ = <20% reduction; ↓↓ = 20–50% reduction; ↓↓↓ = >50% reduction; ↓↓↓↓ = undetected; E, embryonic day; GlyT, glycogen trophoblast cells; Lz, labyrinth zone; n/a, not available.

lethality at mid-gestation (Guillemot *et al.* 1994). Therefore, *Ascl2* is likely required for the formation of GlyT cells and might also be associated with glycogen storage or metabolism.

Beyond GlyT differentiation, several mouse strains demonstrate abnormal localization of GlyT (Table 2). Normally, GlyT are present in the Jz with a subpopulation of GlyT migrating into the decidua (Coan *et al.* 2006). *Ldoc1*, *HtrA1* and *Tfap2c* single knockout mutations lead to placentas with GlyT that have mislocalized to the Lz (Naruse *et al.* 2014, Hasan *et al.* 2015, Kaiser *et al.* 2015). The Jz naturally interdigitates with the Lz (Soares & Hunt 2014), the extent of which depends upon gestational stage and genetic background (Tunster *et al.* 2012). Therefore, it is important to be cautious when histologically characterizing the clusters of GlyT located in the Lz. Serial sections of placenta can be assessed to differentiate a GlyT cluster from a Jz finger protruding in to the Lz. Alternatively, failure of GlyT to migrate into the decidua, as in *Ptp4a2*^{-/-} or *Phlda2* overexpression mice (Tunster *et al.* 2010, Dong *et al.* 2012), might affect maternal-fetal interactions. Whether defective GlyT migration in these models results from altered cell-signalling pathways associated with adhesion and cytoskeleton or an inappropriate response to chemotactic signals remains to be determined. However, appropriate localization of GlyT appears to be important for normal fetal growth.

Increased placental glycogen storage is also associated with impaired fetal growth

Unexpectedly, FGR can also occur in the context of increased placental glycogen storage. For example, when the number of GlyT cells exceeded 35% of the Jz, as in interspecific mouse hybrids, fetal growth was inversely correlated with GlyT abundance (Kurz *et al.* 1999). Additionally, several genetic mouse lines exist that demonstrate increased placental glycogen storage associated with FGR (Table 3). One potential explanation for these counterintuitive findings is that the mutant placentas are able to store glycogen but cannot effectively mobilize and release the glycogen. Further work is necessary to elucidate the mechanism, with a specific focus on whether glycogenesis is increased, leading to enhanced glycogen storage, whether glycogenolysis is impaired, leading to failed glucose release, or whether transport mechanisms are defective. Alternatively, FGR in models associated with increased placental glycogen storage might be caused by a mechanism independent of the GlyT or placental glycogen. Of note, some models (e.g. *Ascl2*-Tg, *Pcdh12*^{-/-} and *Plac1*^{-/-}) with increased glycogen storage also display mislocalization of GlyT clusters within the Lz (Rampon *et al.* 2008, Jackman *et al.* 2012, Tunster *et al.* 2016). This result is consistent with a role for the

normal microenvironment of the Jz in modulating the mobilization of glycogen stores by the GlyT.

Enhanced fetal growth might be independent of a GlyT phenotype

It is possible for enhanced fetal growth to associate with aberrant placental glycogen storage, as occurs in *Cdkn1c*^{-/+} and *H19*^{-/-} mice (Esquiliano *et al.* 2009, Tunster *et al.* 2011) (Table 4). However, it is unlikely that these placental phenotypes directly cause fetal overgrowth, since these genes exert an intrinsic effect on fetal growth. For instance, conditional overexpression of *Cdkn1c* in a subset of fetal, but not placental, tissues restricts fetal growth (John *et al.* 2001, Andrews *et al.* 2007). In contrast, while *Cdkn1c* knockout mice exhibit fetal overgrowth and placentomegaly at E15.5 and E18.5, fetal weights are normalized at birth (Tunster *et al.* 2011). This failure to sustain fetal overgrowth may be attributable to the manifestation of severe defects in *Cdkn1c*^{-/+} placentas including substantially diminished glycogen stores (Tunster *et al.* 2011), although GlyT abundance is unaffected (Takahashi *et al.* 2000). Similarly, ablation of *H19* drives overexpression of the growth-promoting gene *Igf2*, resulting in neonates that are 30% heavier than their littermates (Leighton *et al.* 1995), and placentas with increased GlyT number and placental glycogen content (Esquiliano *et al.* 2009). However, since the *H19*-driven fetal overgrowth phenotype persists to adulthood, the cause is likely independent of increased placental glycogen stores.

GlyT phenotypes associated with early embryonic lethality

Several genetic mouse models display a GlyT phenotype and result in embryonic lethality at or around mid-gestation (Table 5). This outcome occurs before GlyT cells mature and begin accumulating glycogen stores in earnest. Early fetal demise prevents a meaningful assessment of the effect of placental glycogen stores on fetal growth in this context. It is clear that embryonic lethality is attributable to a placental defect in the case of *Ascl2* and *Peg10* knockouts, since lethality was rescued using a tetraploid aggregation approach (Guillemot *et al.* 1994, 1995, Ono *et al.* 2006). This method generates a chimeric conceptus in which a mutant fetus is supported by a placenta containing WT tetraploid cells (Tarkowski *et al.* 1977, Nagy *et al.* 1990). In this context, rescue of embryonic lethality indicates a placental cause. Embryonic lethality in the remaining models coincides with the appearance of congenital malformations (Table 5). A conditional knockout approach is required to elucidate the role of these genes in later stage placentas, including in GlyT development and function. A recent study demonstrated that defects in placental

development and/or function might contribute to the formation of congenital malformations in the fetus, particularly those affecting heart, brain and vascular development (Perez-Garcia *et al.* 2018). The extent to which GlyT and placental glycogen stores play a role in this phenomenon is yet to be determined.

Limitations

While the studies presented here broadly support a role for placental glycogen in regulating fetal growth, a major limitation to understanding the true cause-effect relationship is that the Lz structure is also disrupted in many of these models (Tables 2, 3, 4 and 5). The Lz facilitates the exchange of nutrients, gases and waste products between maternal and fetal circulations (Watson & Cross 2005). Reduced branching morphogenesis in the Lz decreases the surface area for nutrient transport, compromising placental function (Cross *et al.* 2006). Consequently, it is difficult to directly attribute the adverse fetal growth outcomes specifically to aberrant placental glycogen storage for most genes. One model in which fetal growth and placental glycogen content might show a direct link is the *Egfr* hypomorph mutation. These mutant mice have placentas with a GlyT-specific phenotype characterized by reduced PAS staining and diminished GlyT-marker expression but no other placental defect. Associated fetuses were growth restricted in a background-specific manner, with *Egfr* hypomorphs growth restricted on the 129Sv and BTBR/J backgrounds but not the C57BL/6J background (Dackor *et al.* 2009a). Crucially, while PAS staining of *Egfr* hypomorphic placentas was reduced on the 129Sv and BTBR/J backgrounds, abundant PAS staining was evident on the C57BL/6 genetic background (Dackor *et al.* 2009b). This emphasizes a potential relationship between glycogen storage and fetal growth.

The ability to ascertain the mechanism driving aberrant glycogen storage from existing studies is difficult given that GlyT abundance and total placental glycogen content are not always assessed together. Therefore, it is unclear whether an early defect in GlyT progenitor maintenance or differentiation leading to a reduction in mature GlyT cells is the main cause of glycogen storage defects. This appears to be the case for at least 11 mutant mouse lines where both parameters have been assessed (Table 1). The majority of studies have assessed only a single parameter: GlyT abundance or placental glycogen content. This will affect the conclusions drawn by each study and not necessarily reflect whether the mechanism is developmental or metabolic in origin. The only known model whereby placental glycogen stores are independent of GlyT differentiation and abundance is the *Cdkn1c* null line (Tunster *et al.* 2011, Takahashi *et al.* 2000). From this model, we might better understand how glycogen metabolism occurs in the placenta and how fetal growth responds.

Future directions

Considerable work is required to fully elucidate the normal physiological role of placental glycogen stores in humans given that we are only beginning to understand its role during pregnancy. To improve our understanding, a systematic analysis of the GlyT population is required in known mouse models with placenta phenotypes and as part of the routine assessment of new mouse placenta phenotypes. We have proposed four key parameters to assess the GlyT lineage to better understand their development and function: (1.) quantification of GlyT cell number as determined by nuclear counts on histological sections; (2.) assessment of GlyT-specific marker gene expression (e.g. *Pcdh12*, *Aldh1a3* and *Gjb3*) either by *in situ* hybridization on histological sections (Fig. 2) or by qPCR analysis at multiple stages of development. This should occur in concert with assessment of other trophoblast lineage marker expression; (3.) analysis of the localization of GlyT cells by undergoing *in situ* hybridization for the migratory (*Prl7b1*) and non-migratory (*Prl6a1*) markers. This will indicate the migratory capacity of these cells and whether placental structure is affected and (4.) exploring placental glycogen content by performing PAS staining of histological sections (Fig. 2) alongside quantification of total placental glycogen content using a biochemical assay (Lo *et al.* 1970). Altogether, these criteria will help to direct subsequent phenotype evaluation and ultimately identify further molecules and pathways important for GlyT formation and function and for the regulation of placental glycogen stores.

Given the highly dynamic nature of the GlyT cells over the course of pregnancy, it is important to assess placental glycogen-related phenotypes (and arguably other placental phenotypes) at multiple gestational stages. Characterization of a single developmental stage might misrepresent the full extent of the phenotype. One model that exemplifies this issue is the *Pthlh* knockout mouse (Duval *et al.* 2017), whereby placental glycogen content was reduced at E12.5 and E14.5. By E16.5, glycogen had normalized to control levels. However, glycogen content was elevated at E18.5 relative to controls, failing to exhibit the anticipated decline toward term that is normally attributed to the mobilisation of glycogen stores in late gestation. Coinciding with the glycogen phenotype, fetal growth was restricted from E16.5 (Duval *et al.* 2017). Although *Pthlh*-null mice exhibit severe skeletal abnormalities and die soon after birth (Karaplis *et al.* 1994, Bond *et al.* 2008), the late-onset FGR observed in this model implicates a causal role for placental dysfunction. However, it is unclear whether FGR can be attributed to impaired glycogen storage during mid-gestation or the apparent failure to mobilize placental glycogen stores at term. Assessing phenotypes at multiple stages of development will

potentially allow for better separation of developmental defects from functional defects.

The regulation of glycogenesis and glycogenolysis pathway activity by GlyT will provide further insight into placental glycogen metabolism. Central to glucose release from a cell is the enzyme glucose 6-phosphatase, which is responsible for generating free glucose by hydrolyzing the polar phosphate group from glucose 6-phosphate and allowing its transport out of the cell (van Schaftingen & Gerin 2002). The absence of glucose 6-phosphatase activity in GlyT cells would prevent the release of glucose for consumption by the fetus, mother or trophoblast cells. While expression of glucose 6-phosphatase has not been investigated in the mouse placenta to date, its activity in the human placenta is attributed to the *G6PC3* isoform (Guionie *et al.* 2003). This isoform is distinct from the liver-specific *G6PC1* isoform and is expressed in the placenta from at least week 28 of human pregnancy (Matsubara *et al.* 1999) and may be associated with the production of glucose in the placenta at term (Prendergast *et al.* 1999). However, the ultimate destination of glucose derived from placental glycogen stores remains unclear. It is possible that it is directed for fetal use and/or placental consumption. Signals from the fetus that release placental glycogen stores have not been identified.

It is also possible that placental glycogen stores support maternal physiology. The localization of non-migratory GlyT around channels that drain maternal blood from the placenta suggests that some of the glucose released from placental glycogen stores may first be available for uptake by the mother. GlyT express several *Prl* genes and the localization of non-migratory GlyT suggest the encoded hormones may be released into maternal blood. While placental hormones are known to adapt maternal physiology to pregnancy, there is currently no evidence that the glucose metabolized from placental glycogen stores acts to the benefit of maternal physiology. Future studies should assess the effects of aberrant placental glycogen storage on maternal physiology. Indeed, genetic perturbations of several genes that regulate the GlyT lineage also have effects on maternal behavior, including *Peg3* (Li *et al.* 1999, McNamara *et al.* 2018) and *Phlda2* (Creeth *et al.* 2018). Little is known about changes to maternal physiology in these models. *Dlk1*^{+/-} mice are the only model in which maternal physiology was characterized in association with a placental GlyT phenotype (Appelbe *et al.* 2013, Cleaton *et al.* 2016). However, the effects on maternal physiology are more likely attributable to the loss of circulating DLK1 (also known as fetal antigen-1; FA1), rather than a consequence of altered placental glycogen metabolism.

Conversely, there is evidence that maternal physiology can regulate placental glycogen stores. A

loss-of-function allele of *Pik3ca*, which encodes for the catalytic subunit of phosphatidylinositol 3-kinase (PI3K), showed a maternal zygotic effect resulting in diminished glycogen stores (Sferruzzi-Perri *et al.* 2016), although the underlying mechanism is not well understood. While manipulation of maternal diet modulates fetal growth in mouse models (Zhang *et al.* 2005, 2009, Jones *et al.* 2009), only a few studies have investigated the effect of maternal diet upon placental glycogen storage. Both calorie and protein restriction in dams impair placental glycogen storage (Coan *et al.* 2010, Sferruzzi-Perri *et al.* 2011, Gonzalez *et al.* 2016), presumably as a consequence of diminished nutrient availability. A high sugar, high fat (HSHF) maternal diet results in FGR at E15.5, a phenotype that is normalized by E18.5 (Sferruzzi-Perri *et al.* 2013), potentially due to increased utilization of glycogen to support accelerated fetal growth during late gestation. Further work is necessary to explore the relationship between maternal diet, placental glycogen metabolism and fetal growth.

Attempts to infer the function of placental glycogen in models where the GlyT lineage is ablated or diminished might be confounded by additional functions of GlyT cells, which perform at least two additional functions to glycogen storage. First, GlyT cells contribute to placental endocrine function as evidenced by their expression of a subset of the *Prl* gene cluster (Simmons *et al.* 2008b). Secondly, GlyT expression of *ALDH1A3*, an enzyme that oxidises retinal to retinoic acid, implies that GlyT might be a source of retinoic acid, which is an important regulator of trophoblast differentiation (Outhwaite *et al.* 2015). Therefore, alterations in the GlyT population might have profound effects on placental structure and function independent of glycogen storage.

Overall, better characterization of GlyT phenotypes in mice will allow us to evaluate the glycogenesis and glycogenolysis pathways involved in storing and metabolizing glycogen in normal pregnancies and pathological contexts. More sophisticated approaches to constitutive gene knockout models will be necessary to elucidate the specific physiological role(s) of placental glycogen. These analyses should include single-cell sequencing approaches to better understand genetic and metabolic pathways within GlyT cells together with a more holistic approach that relates placental structure and glycogen metabolism to fetal growth and development and to maternal physiology. Only then will the normal function and relevance of aberrant placental glycogen stores to human pregnancy complications, such as PE and GDM, be clarified.

Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of this review.

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Author contribution statement

S J T conceived the study. S J T, E D W, A L F and G J B wrote and edited the manuscript. All authors have read and approved the final version of this manuscript.

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