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Glucose transporters in diabetic nephropathy

Received: 22 July 2004 / Accepted: 5 October 2004 / Published online: 17 February 2005
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Abstract Changes in glucose transporter expression in glomerular cells occur early in diabetes. These changes, especially the GLUT1 increase in mesangial cells, appear to play a pathogenic role in the development of ECM expansion and perhaps other features of diabetic nephropathy. In addition, it appears that at least some diabetic patients may be predisposed to nephropathy because of polymorphisms in their GLUT1 genes. GLUT1 overexpression leads to increased glucose metabolic flux which in turn triggers the polyol pathway and activation of PKC α and B1. Activation of these PKC isoforms can lead directly to AP-1 induced increases in fibronectin expression and ECM accumulation. Other, more novel effects of GLUT1 on cellular hypertrophy and injury could also promote changes of diabetic nephropathy. Strategies to prevent GLUT1 overexpression could ameliorate or prevent the progression of diabetic nephropathy.

Keywords Podocyte · Diabetic nephropathy · Type 1 diabetes mellitus · Reactive oxygen species · Mouse · Rat

Introduction

Since the publication of the Diabetes Control and Complications Trial (DCCT) over a decade ago [1], the link between hyperglycemia and the development of microvascular diabetic complications has been incontrovertible. This landmark trial and a number of other clinical studies

have strongly supported the hypothesis that enhanced cellular glucose uptake and metabolism in susceptible cells contribute to the progressive tissue damage and functional decline that characterize diabetic microvascular complications. However, the implied corollary of these studies, that glucose uptake by cells is directly proportional to extracellular glucose levels, is not true for many cells and tissues that in fact show a reduction in glucose uptake in the face of hyperglycemia [2, 3, 4]. Indeed, the failure of skeletal muscle and other insulin responsive tissues to augment glucose uptake in the face of elevated glucose levels contributes to hyperglycemia in both type 1 and type 2 diabetes mellitus. It is therefore not surprising that these tissues are generally protected from diabetic microvascular complications.

Nonetheless, at least some cells in the body do show enhanced glucose uptake in diabetes and therefore are candidates for diabetic injury. It has been our fundamental hypothesis for the past decade that susceptibility of renal cells to glucose-induced injury is mediated by increased expression or activity of facilitative glucose transporters, which are integral plasma membrane proteins that conduct glucose into cells. Since the initial pathologic hallmarks of diabetic nephropathy are confined to the glomerulus and include glomerular basement thickening and mesangial expansion [5], as well as a loss of glomerular podocytes [6, 7], we and others have focused attention on glomerular glucose transporters.

Glomerular facilitative glucose transporters in diabetes

The facilitative glucose transporters comprise a family of at least 13 members, most of which function to allow glucose to diffuse down its concentration gradient across the plasma membrane [2]. Initial studies of renal facilitative glucose transporters revealed significant expression of GLUT1 and GLUT4 in glomerular cells [8, 9], though the intensity of GLUT1 and GLUT4 immunostaining in glomeruli was much lower than in many renal tubular

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segments, possibly due to the relatively low rate of metabolism compared to that of renal tubules [10]. Both GLUT1 and GLUT4 are expressed in mesangial cells and podocytes [8, 9, 11]. In cultured mesangial cells, GLUT1 appears to be the predominant transporter, but because GLUT4 is often downregulated in culture it is not absolutely certain that GLUT1 predominates in mesangial cells *in vivo*. GLUT3 was also detected at low levels in glomeruli [9], though the exact cellular localization has not been determined. In addition, a recent preliminary report found that GLUT8, another insulin-responsive transporter identified in the last several years, is expressed in podocytes as well as in tubular cells [12]. It is not yet known whether any of the other, more novel glucose transporters, including GLUT11, are expressed in glomerular cells. Finally, one group has identified sodium-glucose cotransporter (SGLT) activity in cultured mesangial cells [13]. However, there have been no additional studies reported to suggest that sodium-coupled glucose transport plays a major role in glucose uptake and metabolism in mesangial cells in culture or *in vivo*.

Hyperglycemia and diabetes mellitus often result in a reduction of glucose transporter expression in tissues, and GLUT4 expression is reduced in glomeruli from streptozotocin rats [14]. This implies that glucose uptake via GLUT4 is reduced in diabetes in both mesangial cells and podocytes [14]. However, Saleem and colleagues have shown that GLUT4 redistributes to the basal surface of podocyte foot processes during type 2 diabetes in humans [11], suggesting that functional (i.e., plasmalemmal) GLUT4 transporters may not be reduced in diabetic podocytes. More definitive studies will be required to determine the effects of GLUT4 in these cells.

In contrast to the decline in GLUT4 expression, exposure of mesangial cells to elevated extracellular glucose concentrations (an increase from 8 to 20 mM glucose) for 3 days enhances GLUT1 levels in cultured mesangial cells [15]. Similar changes occur in diabetic glomeruli. For example, diabetes induces GLUT1 in the cortex from type 1 streptozotocin diabetic rats [16] and in glomeruli from streptozotocin diabetic mice as well as in type 2 db/db diabetic mice [17]. These increases in GLUT1 occur relatively rapidly after the onset of diabetes, at least within 5–6 weeks in the db/db model and probably earlier. In addition, high glucose levels stimulate IGF-1 mediated glucose uptake in cultured mesangial cells [15], suggesting that glucose may stimulate the translocation or the activity of individual glucose transporters as well as GLUT1 gene expression in these cells. Together these data strongly suggest that mesangial cells manifest enhanced glucose uptake via GLUT1 during diabetes. As noted above, since GLUT1 appears to be the predominant glucose transporter in mesangial cells, it is likely, although not absolutely proven, that mesangial cell glucose uptake increases in diabetes despite the concomitant reduction in GLUT4 levels.

The association between GLUT1 and diabetes is less certain in podocytes. However, we have preliminary data suggesting that high glucose induces expression of

GLUT1 in cultured podocytes within 4–12 h (F.C. Brosius et al., unpublished observations). Thus, it may be the case that hyperglycemia affects both mesangial cells and podocytes similarly by enhancing GLUT1 expression and glucose uptake. However, whether this occurs in podocytes remains to be demonstrated *in vivo*. Finally, podocyte GLUT8 levels are increased in type 2 db/db mice [12]. This could further enhance glucose metabolic flux in diabetic podocytes. On balance, it seems likely that glucose uptake and glucose metabolic flux are enhanced in diabetic glomerular podocytes.

Effects of increased GLUT1 and glucose metabolic flux on glomerular cells

Previous studies indicate that GLUT1 is rate-limiting, or nearly so, for glucose metabolism in cultured mesangial cells and that increased GLUT1 expression in glomerular cells drives many of the changes that are characteristic of diabetic nephropathy such as ECM production and accumulation [18, 19]. Overexpression of GLUT1 in cultured mesangial cells without any other changes leads to excessive ECM production and release [18], while suppression of mesangial cell GLUT1 leads to reduced ECM production [19]. Similar findings appear to take place *in vivo*. Preliminary data indicate that transgenic overexpression of GLUT1 in db/m mice leads to enhanced glomerular ECM accumulation (Heilig et al., unpublished observations). In these transgenic mice, a modified β -actin promoter drives expression of the GLUT1 transgene. This promoter was chosen specifically to enhance GLUT1 expression in glomerular mesangial cells where it is robustly active [20, 21], although it is active in a number of other tissues as well. At 6 months of age, the nondiabetic mice that overexpress GLUT1 show normal blood sugars, but demonstrated a 67–200% increase in albuminuria by 4.5 and 6.5 months of age with substantial increases in ECM expansion when compared to nontransgenic mice [22]. At present, diabetic mice overexpressing GLUT1 in mesangial cells are being evaluated to determine whether augmented GLUT1 expression, beyond that which normally occurs in diabetes, accentuates diabetic injury. The effect of specific GLUT1 overexpression in diabetic podocytes is also being evaluated in another transgenic mouse model in a db/m background.

While the studies of glomerular GLUT1 overexpression in diabetes are still being assessed, the effects of preventing GLUT1 overexpression are clear. Transduction of cultured mesangial cells with a GLUT1 antisense construct resulted in a >50% reduction in GLUT1 expression and glucose uptake [19]. In addition, when these cells were exposed to elevated extracellular glucose concentrations, the expected increases in GLUT1 levels and glucose uptake were prevented [19]. Most importantly, GLUT1 antisense expression also prevented the increase in ECM expression, the *in vitro* corollary of diabetic nephropathy. Such prevention of diabetic nephropathy has recently been confirmed in an *in vivo* model.

Diabetic db/db mice carrying an antisense-GLUT1 transgene have been found to have GLUT1 levels and glomerular glucose uptake reduced to approximately 50% of levels in wild-type diabetic mice, levels that are not significantly different from levels in nondiabetic wild-type mice. In these GLUT1 antisense diabetic mice the mesangial cell glucose uptake rate is also reduced by 50%. Such mice with diabetes demonstrate protection against the development of glomerulosclerosis [17]. Therefore, both in cultured mesangial cells and in glomeruli in vivo, the GLUT1 transporter appears to be an important regulator of ECM production.

Possible role of GLUT1 polymorphisms in the genetic predisposition to diabetic nephropathy

Because of the likely role of enhanced glomerular GLUT1 expression in predisposing to diabetic nephropathy in animals, GLUT1 has been considered a potential disease gene in humans. Several case-control studies have implicated GLUT1 polymorphisms in the risk of developing nephropathy in different type 1 and type 2 diabetic populations. One study in British type 1 patients found that an *Xba* I (-) restriction fragment length polymorphism was associated with an increased risk for diabetic nephropathy [23]. A more recent study found that Caucasian type 1 diabetic patients who were homozygous for the A allele of a single-nucleotide polymorphism (SNP) in the enhancer-2 region in the second intron of the GLUT1 gene had a 2.4-fold increased risk for diabetic nephropathy compared to patients who did not have this genotype [24]. This SNP is very tightly linked to the *Xba* I polymorphism site identified in the previous study [23, 24]. The enhancer-2 SNP of GLUT1 is inside a predicted binding site for USF transcription factors which regulate gene expression in response to high glucose [24, 25] and therefore could be functionally significant in regulating GLUT1 expression in diabetes. In another study, recent preliminary data indicate that Caucasian type 2 diabetics and nondiabetics who were homozygous for the A allele of the GLUT1 enhancer-2 SNP were also at increased risk for renal disease manifested by albuminuria [26]. Invest-

igations are currently underway to determine whether this SNP may affect GLUT1 expression.

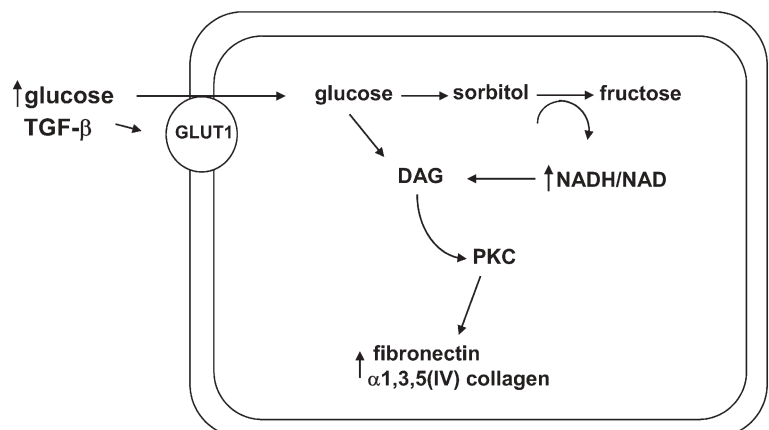
Whether such an association between the GLUT1 polymorphisms and diabetic nephropathy occurs in all populations is uncertain. One study in Chinese type 2 patients has found that the *Xba* I (-) genotype is associated with a higher incidence of diabetic nephropathy [27], while another study found that the *Xba* I (+) allele was associated with increased risk in Caucasian type 2 patients in Poland [28]. Finally, another study has found no association between the GLUT1 polymorphism and diabetic nephropathy [29].

Effects of increased GLUT1 expression on signaling in glomerular mesangial cells

Since expression of the GLUT1 gene leads to morphologic features of diabetic nephropathy and since the GLUT1 gene appears to be linked to the development of diabetic nephropathy in some populations, it is important to understand the mechanisms by which GLUT1 expression can lead to such outcomes. Several studies over the past decade have helped to reveal at least some of the pathways involved, especially in cultured mesangial cells. Chronic overexpression of GLUT1 leads to activation of the polyol pathway [30], as well as PKC α and β 1 activation [30, 31]. Enhanced glucose metabolism through the polyol pathway can lead to synthesis of diacylglycerol and phosphatidic acid, which may account for increased mesangial cell PKC isoform activation as well as increased PKC levels [32]. In turn, PKC α and β 1 activation by GLUT1 leads to increased AP-1 levels which enhance transcription of several genes, such as those of fibronectin and other ECM proteins [31]. Thus, increased GLUT1 expression, independent of elevated extracellular glucose levels, can directly enhance ECM production through a PKC and AP-1 dependent pathway (see Fig. 1).

Interestingly, chronic GLUT1 overexpression alone does not lead to activation of MAP kinase (ERK and p38) pathways, to induction of TGF- β , or to enhanced production of reactive oxygen species (ROS) [31]. Activation of MAP kinase and TGF- β pathways and enhanced ROS

Fig. 1 GLUT1 signaling in mesangial cells. Increased GLUT1 expression leads to enhanced polyol pathway and production of PKC. In turn, this enhances the synthesis of fibronectin and other ECM proteins. Increased extracellular glucose and TGF- β augment GLUT1 expression and enhance this signaling cascade



production have all been strongly implicated in the progression of diabetic nephropathy. This curious lack of GLUT1 effect on these pathways has several implications. First, it suggests strongly that increased GLUT1 expression can lead to enhanced ECM accumulation independent of these pathways. Second, increased glucose uptake and metabolic flux alone are clearly not sufficient to trigger MAP kinase and TGF- β signaling, at least in cultured cell systems. Perhaps, as Weigert et al. speculated, stimulation of these pathways may require ROS production. Since GLUT1 is chronically overexpressed in these experimental systems, it is possible that the cells have adapted to the enhanced metabolic flux and have increased mechanisms for dealing with oxidative stress. Additionally it appears that most of the excess glucose metabolic flux is glycolytic, not oxidative, and therefore mitochondrial oxidative stress is not enhanced [31]. Whether GLUT1 overexpression in diabetic tissues in vivo fails to enhance ROS production, and signaling via MAP kinase and TGF- β pathways, is uncertain. Perhaps the oscillatory nature of hyperglycemia, and hence GLUT1 expression, in diabetic patients would stimulate a more acute response in complications-prone tissues activating mitochondrial generation of ROS as well as TGF- β and MAP kinase pathways. Although GLUT1 does not stimulate TGF- β or MAP kinase pathways in cultured mesangial cells, there is evidence that TGF- β [33] and possibly ERK [34] can stimulate mesangial cell GLUT1 expression. Thus, these important pathways in diabetic nephropathy are still ultimately linked to GLUT1.

Newer areas of investigation examining the effect of GLUT1 overexpression on cellular signaling have been performed in nonrenal tissues that have clear implications for diabetic nephropathy. One recent report confirmed that GLUT1 was necessary for cardiac myocyte hypertrophy [35], which had previously been suggested in transgenic mouse studies. This recent study found that preventing the expected increases in GLUT1 expression with an adenoviral GLUT1 antisense approach before exposure to hypertrophic stimuli blocked induction of hypertrophy in cardiac myocytes. Surprisingly, this study found that all of the effects of GLUT1 overexpression occurred equally in the absence and presence of extracellular glucose and confirmed that the effects were independent of glucose transport. One possible explanation for these findings is that GLUT1 can influence cellular adaptation and signaling via direct protein-protein interactions that may be independent of the molecule's glucose transport function. A number of investigators have already demonstrated the direct interaction of GLUT1 and other proteins [36, 37, 38, 39] and have shown that GLUT1 can thereby affect signaling [37]. Morissette et al. [35] suggest that GLUT1 may interact with signaling molecules that result in Akt phosphorylation. While this latter mechanism remains to be demonstrated, such a finding would nicely complement pathways by which glucose uptake and metabolism also enhance Akt activation [40, 41]. The observation that GLUT1 is associated with lipid rafts in several cell types [39, 42] strengthens

this hypothesis since many plasma membrane signaling processes are localized adjacent to these detergent-insoluble domains in many cell types. Should similar, non-metabolic effects of GLUT1 be demonstrated in diabetic glomerular mesangial cells and/or podocytes, novel mechanisms for diabetic cellular hypertrophy and possible ECM expansion could be elucidated.

Acknowledgements These studies were supported by a grant from the Juvenile Diabetes Research Foundation Center for Excellence at the University of Michigan (Award N001280, Project 7), a Juvenile Diabetes Research Foundation Innovative Grant (5-2000-892), and the Animal Models of Diabetic Complications Consortium (National Institutes of Health, UO1 DK60994).

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