### Sodium-glucose co-transporter 1 (SGLT1) differentially regulates gluconeogenesis and GLP-1 receptor (GLP-1R) expression in different diabetic rats: a preliminary validation of the hypothesis of "SGLT1 bridge" as an indication for "surgical diabetes"

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**Background:** Sodium-glucose co-transporter 1 (SGLT1) may play a synergistic role in gluconeogenesis (GNG) and glucagon-like peptide-1 (GLP-1) expression. We proposed the hypothesis of a "SGLT1 bridge" as an indication for "surgical diabetes" that was preliminary validated in the present study.

**Methods:** We selected nonobese diabetic Goto-Kakizaki (GK) rats and Zuker diabetic fat (ZDF) rats to represent advanced and early diabetes, respectively. Based on glucose gavage with or without SGLT1 inhibitor phlorizin, the rats were divided into 4 groups: Gk-Glu, GK-P, ZDF-Glu, and ZDF-P. The expressions of SGLT1, GLP-1 receptor (GLP-1R), glucose-6 phosphatase (G6Pase), and phosphoenolpyruvate carboxykinase-1 (Pck1) were determined by immunohistochemistry (IHC) or quantitative reverse transcription polymerase chain reaction (RT-qPCR), and the effects of phlorizin were analyzed.

**Results:** Glucose tolerance was worse in GK rats and the homeostasis model assessment-insulin resistance (HOMA-IR) was higher in ZDF rats, indicating different pathophysiological conditions between the different diabetic rats. GK rats showed higher activity of duodenal SGLT1 (P=0.022) and jejunal SGLT1 mRNA expression (P=0.000) and lower SGLT1 mRNA expression in the liver (P=0.000) and pancreas (P=0.000). Phlorizin effectively inhibited the activity of duodenal SGLT1 in both GK rats (P=0.000) and ZDF rats (P=0.000). In ZDF rats, the expression of GLP-1R mRNA was downregulated in the jejunum (P=0.001) and upregulated in the pancreas (P=0.021) by phlorizin, but there were no regulatory effects on GLP-1R mRNA in the jejunum and pancreas of GK rats. As for the regulatory effects on GNG, phlorizin upregulated Pck1 mRNA in the duodenum (P=0.000) and Pck1 mRNA expression in GK rats (P=0.001), suggesting that SGLT1 inhibitor may have upregulated intestinal GNG in ZDF rats and downregulated hepatic GNG in both ZDF and GK rats.

**Conclusions:** SGLT1 showed synergistic regulatory effects on the entero-insular axis (EIA) and the gut-brain-liver axis (GBLA), preliminarily validating the hypothesis of a "SGLT1 bridge". The distinct

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expression of SGLT1 and its differentially regulatory effects on diabetic rats with different pathophysiological conditions may provide probable potential indications involved in the "Surgical Diabetes" that is supposed as the inclusion for diabetic surgery.

**Keywords:** Sodium-glucose co-transporter 1 (SGLT1); diabetes; glucagon-like peptide-1 (GLP-1); gluconeogenesis (GNG); metabolic surgery

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### Introduction

For decades, the entero-insular axis (EIA) hypothesis has been the most popular and acceptable theory for elucidating the mechanisms of diabetes remission after metabolic and bariatric surgery (MBS). The Roux-en-Y gastric bypass (RYGB) is superior to sleeve gastrectomy (SG) for achieving diabetes remission (1) because more EIA-related hormones, known as incretin, are changed by bypass surgery. Glucagon-like peptide-1 (GLP-1) is considered one of the most important factors in the EIA hypothesis (2) and GLP-1 analogues and its receptor (GLP-1R) agonist are used for antidiabetic therapy (3). However, some studies (4-11) have expressed doubt over the role of GLP-1 in the context of the EIA hypothesis. Firstly, GLP-1 as a clinical antidiabetic drug has far fewer therapeutic effects than MBS. Secondly, the amount of GLP-1 secretion is not correlated with diabetes remission (8), and both increased (12) and decreased (13) GLP-1 secretion have been found after surgery. Further, in GLP-1R knockout mice, RYGB still exhibited improved glucose homeostasis (9,14), and a GLP-1R antagonist did not deteriorate glucose homeostasis in patients who achieved diabetes remission following RYGB (5). Our previous study (15) involving ileal transposition performed on Goto-Kakizaki (GK) rats showed rapid improvement of glucose tolerance and a delayed improvement of insulin resistance, accompanied with a decreased insulin level instead of the increased insulin secretion subsequently induced by increased GLP-1 expression (16,17), suggesting that it might have been glucose tolerance improvement rather than increased GLP-1 expression that led to the improvement of insulin resistance. Taken together, the EIA hypothesis cannot fully explain diabetic improvement in MBS, and further studies are required to define the role of GLP-1 in glucose metabolism (18).

Since the phenomenon cannot be well explained by the

EIA hypothesis, the gut-brain-liver axis (GBLA) hypothesis has been raised as an alternative theory for elucidating the mechanisms of diabetes remission after MBS (10,19). Glucose in blood initiates a signal to the portal vein in fasting animals. The portal glucose signal (PGS) interferes with glucose homeostasis by regulating the production of glucose by the liver [hepatic gluconeogenesis (HGNG)] (20-22), transmitted by vagal afferents to the energy homeostasis center (the hypothalamus) and via the efferent nervous system to the liver. Ideally located just upstream of the PGS, intestinal gluconeogenesis (IGNG), which enhances the gluconeogenic effect by up to 20% during prolonged hunger (19), controls the intestinal glucose release into the portal vein to activate the PGS. In normal situations, during the postabsorptive period, the gluconeogenic function is expressed in the proximal intestine (23-25), whereas after gastric bypass, high expression of IGNG regulatory genes glucose-6 phosphatase (G6Pase) and phosphoenolpyruvate carboxykinase (PCK) occurs in the distal small intestine (10). The increased G6pase and PCK expression and activity can be seen in the duodenum and alimentary limb after RYGB (26,27). Thus, it has been suggested (10,28,29) that the induction of IGNG plays a major role in endogenous glucose production (EGP), and the intact GBLA axis is the mechanical link key to rapid glucose improvement after gastric bypass.

Sodium-glucose co-transporter 1 (SGLT1), mainly located in the intestine, predominantly mediates glucose across the intestinal brush-border membrane (BBM) (30-32). The expression of SGLT1 in diabetic humans is 2–3 folds higher than in nondiabetics (33). SGLT1 has been identified as the primary pathway for the transport of glucose across the BBM during glucose mass absorption, and SGLT1 is essential for the glucose-induced release of GLP-1 into the peripheral circulation (30,34-37). Downregulation of SGLT1 in the jejunal segment that

remains in the alimentary limb after duodenojejunal bypass (DJB) has been found in diabetic rats (38), whereas upregulated expression of SGLT1 (28,39) has been observed in nondiabetic Sprague-Dawley (SD) rats after DJB, with (28) or without (39) upregulated expression of G6Pase and PCK, which are well known as key ratelimiting enzymes of IGNG in the intestine. Therefore, we hypothesized that SGLT1 might play a synergic role in EIA and GBLA that accounts for the mechanisms of glucose remission in MBS. We present the following article in accordance with the ARRIVE reporting checklist (available at https://atm.amegroups.com/article/view/10.21037/atm-22-1769/rc).

### Methods

### Animals

A protocol was prepared before the study without registration. The study protocol was approved by the Animal Ethics and Welfare Committee of Shenzhen University (No. YSDW202009030), in compliance with Chinese national guidelines for the care and use of animals.

Four 7-week-old male GK rats [Cavens Biogle (Suzhou) Model Animal Research Co. Ltd., Jiangsu, China] and four 7-week-old male Zuker diabetic fatty (ZDF) rats (fa/fa; Charles River Laboratories, Wilmington, MA, USA) were housed individually in a sound-proof environment (to avoid the stressed hyperglycemia) with a specific pathogen-free (SPF) system and acclimatized at a temperature of 20–24 °C, relative humidity of 50–70%, and 12 hour/12 hour light/dark cycles with a daylight lamp of 40 watts (lights on at 7:00 AM). Standard chow (carbohydrates 58.0%, fat 13.5%, and protein 28.5%) and water were provided ad libitum to rats.

### Experimental set-up: tissue harvesting and blood assays

At 10 weeks, the GK rats and ZDF rats weighed 374.4±10.5 and 301.1±6.9 g, respectively, and were ready for specimen harvest. Based on the infusion regime, the GK rats and ZDF rats were assigned to the following groups: the GK-Glu group, ZDF-Glu group, GK-P group, and ZDF-P group (n=2 for each group). The rats in the GK-Glu group and ZDF-Glu group were intragastrically administered glucose solutions as the control groups to the GK-P group and ZDF-P group, in which the rats were infused with a glucose solution mixed with a SGLT1 inhibitor, phlorizin (MedChemExpress, Monmouth Junction, NJ, USA). The research team, with the exception of the principal investigator, was blinded to the assignment of rats to infusion regimes.

The rats were fasted for 18–20 hours before anesthetization. Inhalation anesthesia (2–3% isoflurane in oxygen) was applied. Based on the individual infusion regime, gavage was performed before tissue harvesting. Approximately 30 minutes after gastric infusion, a midline incision was performed. The cecum was displayed to identify the terminal ileum, and the ligament of Treitz was exposed to accurately locate the start of the jejunum.

Segments (2 cm long) from 3 intestinal locations (the horizontal part of duodenum, ~15 cm distal to the Treitz ligament, and ~15 cm proximal to the ileo-cecal) were acquired approximately 90 minutes after infusion. Each segment was divided into 2 1-cm-long loops. The intestinal tissues were harvested for mucosal scrapings and subsequent RNA extraction. The pancreatic tissue was harvested from the caudal junction of the pancreas, and the hepatic tissues were dissected from the middle lobe of the liver 2 hours after gavage was performed. The tissues were immediately snap frozen in liquid nitrogen and stored at ~80 °C for subsequent RNA extraction. After the tissue harvesting was completed, the rats were sacrificed and properly buried.

After 18 hours of fasting, blood samples were collected at 9:00-11:00 am to detect glycometabolic parameters fasting plasma glucose (FPG) and fasting insulin (F-ins). Blood glucose (BG) in oral glucose tolerance tests (OGTTs) was assessed by a glucometer (GM9, Analox, Stokesley, UK). Trapezoidal integration was used to calculate the area under the curve (AUC) of OGTT. The AUC was calculated according to the following formula: AUC  $(\text{mmol·min/L}) = \text{BG0h} \times 0.5 + \text{BG1h} \times 0.75 + \text{BG2h} \times$ 0.25, with BG0h, BG1h, and BG2h indicating BG levels at 0, 1 hour, and 2 hours, respectively. Plasma insulin was measured with insulin enzyme-linked immunosorbent assay (ELISA) kits (Nanjing Jiancheng Bioengineering Institute, China) according to the manufacturer's instructions. The homeostasis model assessment-insulin resistance (HOMA-IR) index was calculated according to the formula (40): HOMA-IR = FPG (mmol/L) × F-ins (pmol/L)/135.

### Histological determination

Immunohistochemistry (IHC) was performed to determinate the activity of intestinal SGLT1 expression, while quantitative reverse transcription polymerase chain



**Figure 1** The processing steps of IMAGE J software for IHC image (Envision methods). (A) Import the original image into Image J (Version 1.53E). (B) Remove the background with "Subtract Background" tools, and (C) extract IHC staining signal with "IHC Toolbox" plug-in. (D) Read the gray value, and finally identify the true positive peak signal, and take the peak signal as the staining intensity of the site. Six sites were randomly selected from each image and three sites for analyzing by each pathologist. The expression activity was represented by gray value from 0 to 255, and the smaller the gray value was, the higher the expression activity. The magnification is 200× in *Figure 1A-1C*. IHC, immunohistochemistry.

reaction (RT-qPCR) was applied to detect the following expression levels: SGLT1 mRNA in the duodenum, jejunum ileum, liver, and pancreas; GLP-1R in the jejunum, ileum, and pancreas; and G6Pase and phosphoenolpyruvate carboxykinase-1 (Pck1) in the duodenum, jejunum ileum, and liver.

### IHC

The tissues were harvested and 4-µm thick sections of fixed intestinal tissue were cut and dewaxed. Following rehydration, antigen retrieval was performed in citrate buffer (pH 6.0) and incubated in phosphate-buffered saline (PBS) solution. The sections were blocked by incubation with 3% hydrogen peroxide and incubated in PBS overnight in a refrigerator with affinity-purified rSGLT1-Ab (1:500, Abcam, Cambridge, MA, USA). The sections were rinsed and incubated in PBS for 30 minutes at room temperature, and then dropwise added with secondary antibody horseradish peroxidase (HRP; DAKO, Glostrup, Denmark). Following incubating at 37 °C for 60 min, the sections were stained in diaminobenzidine (DAB) for 5-10 min and stained with hematoxylin for 2 min. The stained slides were photographed with a fluorescent Microscope (Eclipse TI-SR, Nikon Corp., Japan). Semiquantification was performed using the Image J 1.53e software program (Bethesda, MD, USA), via measuring the gray values (*Figure 1*) that were negatively correlated with the activity of SGLT1 expression, Every single image was analyzed by 2 pathologists who were blinded to the relationships between images and related rats.

### RNA extraction and RT-qPCR

RNA was extracted from frozen tissue samples with an Ambion mirVana mRNA Isolation Kit and the BioPhotometer plus (Eppendorf, Germany) and quantified with a microplate reader (Invitrogen, Carlsbad, CA, USA).

Gene	bp	Primer sequence-forward	Primer sequence-reverse
SGTL1	170	CATGCCTAACGGACTTCGA	TGAACAACCTTCCTGCAATC
GLP-1R	150	ACTCGCGAAGTCCACTCTGA	ACCATAAAGCCCTGGAAGGA
G6Pase	100	GCAAGAGCTGCAAAGGAGAA	GGCTTCAGCGAGTCAAAGAG
Pck1	130	GATCCTGGGCATAACTAACC	ACCCACACATTCAACTTTCC
$\beta$ -actin	150	AGGGAAATCGTGCGTGACAT	GAACCGCTCATTGCCGATAG

Table 1 Primers of RT-qPCR for rat genes

RT-qPCR, quantitative reverse transcription polymerase chain reaction; SGTL1, sodium glucose cotransporter 1; GLP-1R, glucagon-like peptide-1 receptor; G6Pase, glucose-6 phosphatase; Pck1, phosphoenolpyruvate carboxykinase-1; β-actin, housekeeping gene.

Reverse transcription was performed simultaneously on 1.0 µg of RNA from each rat with EasyScript First-Strand cDNA Synthesis SuperMix and oligo-dT (Invitrogen). To facilitate inter- and intragroup comparisons of gene expression, quantitative PCR (qPCR) of all complementary DNA (cDNA) samples were run on a single 96-well plate. The cDNA product was diluted and added to forward and reverse primers [SGTL1, GLP-1R, G6Pase, Pck1, and  $\beta$ -actin (housekeeping gene); Invitrogen; *Table 1*], together with SYBR Green SuperMix (Applied Biosystems, Waltham, MA, USA). The qPCR was performed in triplicate with diluted cDNA primers and SYBR Green SuperMix using an ABI PRISM<sup>®</sup> 7500 Sequence Detection System.

The thermal cycler conditions used were 5 minutes at 95 °C, 15 seconds at 95 °C, and 32 seconds at 60 °C for 40 cycles. Dissociation curves were obtained to ensure a single amplicon at 60-95 °C.

### Statistical analysis

Statistical analyses were performed using the Statistical Package for the Social Sciences (SPSS) 21.0 (IBM Corp., Armonk, NJ, USA) and GraphPad Prism 9.0 for Windows (GraphPad Software, San Diego, CA, USA). Data are presented as means  $\pm$  standard error of mean (SEM) and analyzed using Student's *t*-test or 1-way analysis of variance (ANOVA) and post hoc analysis with the least significant difference (LSD) comparison test. Differences were considered statistically significant at P<0.05.

### Results

### Glucose metabolism

All the animals were tested for comparable weight, FPG, F-ins, and OGTT before harvesting.

### No differences in glycometabolic parameters before intragastric infusion (Figure 2)

No significant differences in terms of weight, FPG, F-ins, and HOMA-IR were observed between the GK-P group and GK-Glu group (each P>0.05) or between the ZDF-P group and ZDF-Glu group (P>0.05), providing comparability of glucose metabolism between groups after intragastric infusion.

# Differences in glucose metabolism between GK rats and ZDF rats were observed (Figure 3)

(I) Insulin resistance in ZDF rats was significantly higher than that in GK rats: HOMA-IR in ZDF rats was significantly higher than that in GK rats (P=0.021). (II) The impaired glucose tolerance of GK rats was worse than that of ZDF rats: the AUC area of OGTT in GK rats was larger than that in ZDF rats (P=0.009), whereas the insulin level of GK rats was lower than that of ZDF rats.

### Histological analysis

### SGLT1 expression

## Discrepant expressions of SGLT1 were found in different rat groups

(I) The activity of duodenal SGLT1 in GK rats was higher than that of ZDF rats (P=0.022; *Figures 4,5*). (II) The expression of SGLT1 mRNA in the jejunum in the GK-Glu group was significantly higher than that in the ZDF-Glu group ( $1.10\pm0.05 vs. 0.58\pm0.05$ , P=0.000; *Figure 6*). (III) The expression of SGLT1 mRNA in the pancreas and liver of ZDF rats was significantly higher than that of GK rats: ZDF-Glu group vs. GK-Glu group:  $6.91\pm0.40 vs. 2.50\pm0.53$  (P=0.000) in the pancreas and  $1.66\pm0.07 vs. 1.12\pm0.06$  (P=0.000) in the liver (*Figure 7*).

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**Figure 2** Weight and glycometabolic parameters before harvesting. FPG, fasting plasma glucose; GK, Goto-Kakizaki; ZDF, Zuker diabetic fat; F-ins, fasting insulin; HOMA-IR, homeostasis model assessment-insulin resistance.



**Figure 3** Differences in glucose metabolism between GK and ZDF rats. (A) No differences showed in FPG between GK rats and ZDF rats (P>0.05) before harvest. (B) F-ins in GK rats was lower than that in ZDF rats before harvest (GK rats group *vs.* ZDF rats group:  $62.9\pm2.0 vs.$  71.1 $\pm$ 1.7, P=0.021). (C) HOMA-IR of GK rats was lower than that of ZDF rats one week before harvest (GK group *vs.* ZDF group:  $3.17\pm0.13 vs.$   $3.63\pm0.06$ , P=0.021). (D) The AUC of OGTT in GK rats was higher than that in ZDF rats (GK group *vs.* ZDF group:  $29.3\pm1.1 vs.$  23.5 $\pm1.1$ , P=0.009) before harvest. Data were analyzed using *t*-test. \*P<0.05, \*\*P<0.01. FPG, fasting plasma glucose; F-ins, fasting insulin; GK, Goto-Kakizaki; ZDF, Zuker diabetic fat; HOMA-IR, homeostasis model assessment-insulin resistance; AUC, area under the curve; OGTT, oral glucose tolerance test.



**Figure 4** The activity of SGLT1 expression in the intestine (in gray value). The gray value of duodenal SGLT1 in ZDF-Glu group was higher than that in GK-Glu group (160.9±6.5 vs. 152.6±5.5, P=0.022). No statistical differences in gray value of SGLT1 in the jejunum (P>0.05) between ZDF-Glu and GK-Glu group were observed, as well as that in the ileum (P>0.05) between ZDF-Glu and GK-Glu group (181.7±5.0 vs. 152.6±5.5, P=0.000). The gray value of duodenal SGLT1 in GK-P group was significantly higher than that of GK-Glu group (181.7±5.0 vs. 152.6±5.5, P=0.000). The gray value of duodenal SGLT1 in ZDF-P group was significantly higher than that of ZDF-Glu group (185.7±1.9 vs. 160.9±6.5, P=0.000). In the jejunum and ileum, no statistical differences between GK-P group and GK-Glu group (jejunum: P=0.743; ileum: P=0.189), or between GK-P group and GK-Glu group (jejunum, P=0.748; ileum, P=0.835) were observed. Data were analyzed using one-way ANOVA with post hoc analysis with LSD's comparison test. \*P<0.05, \*\*P<0.01, \*\*\*P<0.01. SGLT1, sodium-glucose co-transporter 1; GK, Goto-Kakizaki; ZDF, Zuker diabetic fat; ANOVA, analysis of variance; LSD, least significant difference.



Duodenal SGLT1 in ZDF-Glu rats (400×)

Duodenal SGLT1 in ZDF-P rats (400×)

**Figure 5** SGLT1 activity expression in the duodenum (immunohistochemistry: envision methods). The activity of duodenal SGLT1 in GK rats was higher than that ZDF rats (A>C, P=0.022). As to the effects of the SGLT1 inhibitor, the activity of SGLT1 expressed in duodenum of both GK rats (B<A, P=0.000) and ZDF rats (D<C, P=0.000) was effectively inhibited by phlorizin. SGLT1, sodium-glucose co-transporter 1; GK, Goto-Kakizaki; ZDF, Zuker diabetic fat.



**Figure 6** SGLT1 mRNA expression in the intestine. No significant differences in duodenal SGLT1 mRNA expression were observed between the GK-Glu and ZDF-Glu groups (P=0.546), or between GK-Glu and GK-P groups (P=0.829), or between ZDF-Glu and ZDF-P groups (P=0.914). The jejunal SGLT1 mRNA expression in ZDF-Glu group was significantly lower than that in GK-Glu group (0.58±0.05 vs. 1.10±0.05, P=0.000), and lower than that in ZDF-P group (0.58±0.05 vs. 0.85±0.04, P=0.000), but no significant differences were investigated between GK-Glu and GK-P groups (P=0.856). The ileal SGLT1 mRNA expression in ZDF-P group was significant differences were found between GK-Glu and GK-P groups (0.73±0.11 vs. 0.99±0.04, P=0.008), but no significant differences were found between GK-Glu and GK-P groups (P=0.811). Data were analyzed using one-way ANOVA with post hoc analysis with LSD's comparison test. \*P<0.05, \*\*P<0.01, \*\*\*P<0.001. SGLT1, sodium-glucose co-transporter 1; GK, Goto-Kakizaki; ZDF, Zuker diabetic fat; ANOVA, analysis of variance; LSD, least significant difference.



**Figure 7** SGLT1 mRNA expressions in the liver and the pancreas. (A) The hepatic SGLT1 mRNA expression was significantly higher in ZDF-Glu group than that in GK-Glu group (1.66±0.07 vs. 1.12±0.06, P=0.000), but no significant differences in hepatic SGLT1 mRNA expression were found between ZDF-Glu and ZDF-P (P=0.550), or between GK-Glu and GK-P groups (P=0.303). (B) The pancreatic SGLT1 mRNA expression in ZDF-Glu group was significantly higher than that in GK-Glu group (6.91±0.40 vs. 2.50±0.53, P=0.000), and higher than that in ZDF-P group (6.91±0.40 vs. 4.47±0.32, P=0.000), but no significant differences were found between GK-Glu and GK-P groups (P=0.244). Data were analyzed using one-way ANOVA with post hoc analysis with LSD's comparison test. \*P<0.05, \*\*P<0.01, \*\*\*P<0.001. SGLT1, sodium-glucose co-transporter 1; GK, Goto-Kakizaki; ZDF, Zuker diabetic fat; ANOVA, analysis of variance; LSD, least significant difference.

### The effects of SGLT1 inhibitor

### The effects of SGLT1 inhibitor in regulating the expression of SGLT1 in the intestine

(I) The expression of duodenal SGLT1 was effectively inhibited by SGLT1 inhibitors (*Figures 4*, 5) in both GK rats

(P=0.000) and ZDF rats (P=0.000). (II) The expression of jejunal SGLT1 mRNA of ZDF rats was effectively inhibited by SGLT1 inhibitors (*Figure 6*). The jejunal SGLT1 mRNA expression in the ZDF-Glu group was significantly lower than that in the ZDF-P group (P=0.000), but no significant



**Figure 8** GLP-1R mRNA expression in the intestine and the pancreas. The jejunal GLP-1R mRNA expression in ZDF-P group was significantly lower than that in the ZDF-Glu group (0.55±0.08 vs. 0.95±0.07, P=0.001), but no significant differences were found between GK-Glu and GK-P groups (P=0.652), or between GK-Glu and ZDF-Glu groups (P=0.250). No significant differences were found in ileal GLP-1R mRNA expression between the GK-Glu and ZDF-Glu groups (P=0.920), or between GK-Glu and GK-P groups (P=0.936), or between ZDF-Glu and ZDF-P groups (P=0.099). The pancreatic GLP-1R mRNA expression in ZDF-P group was significantly higher than that in the ZDF-Glu group (1.37±0.24 vs. 0.80±0.07, P=0.021), but no significant differences were found between GK-Glu and GK-P groups (P=0.097), or between GK-Glu and ZDF-Glu groups (P=0.556). Data were analyzed using one-way ANOVA with post hoc analysis with LSD's comparison test. \*P<0.05, \*\*P<0.01, \*\*\*P<0.001. GLP-1R, glucagon-like peptide-1 receptor; GK, Goto-Kakizaki; ZDF, Zuker diabetic fat; ANOVA, analysis of variance; LSD, least significant difference.

differences were found between the GK-Glu and GK-P groups (P=0.856).

### The effects of SGLT1 inhibitor in regulating the expression of SGLT1 mRNA in the liver and pancreas

(I) No significant differences in hepatic SGLT1 mRNA expression were observed between the ZDF-Glu and ZDF-P groups (P=0.550) or between the GK-Glu and GK-P groups (P=0.303; *Figure 7A*). (II) The SGLT1 inhibitor downregulated the expression of pancreatic SGLT1 mRNA in ZDF rats (ZDF-P group *vs.* ZDF-Glu group: 4.47±0.32 *vs.* 6.91±0.40, P=0.000), but there was no regulatory effect on SGLT1 mRNA in GK rats (P=0.244; *Figure 7B*).

# Different effects of SGLT1 inhibitors in inducing the mRNA expression of G6Pase and Pck1 as well as GLP-1R were found

(I) the SGLT1 inhibitor downregulated the expression of GLP-1R mRNA in the jejunum of ZDF rats (the ZDF-P group vs. ZDF-Glu group:  $0.55\pm0.08$  vs.  $0.95\pm0.07$ , P=0.001), but there was no regulatory effect on GLP-1R mRNA in the jejunum of GK rats (P>0.05; *Figure 8*). (II) No significant differences in intestinal G6Pase mRNA expression were found in the duodenum, jejunum, and ileum between the GK-Glu and GK-P groups (P=0.789, 0.657, and 0.445, respectively) or between the ZDF-Glu and ZDF-P groups (P=0.363, 0.129, and 0.115, respectively; *Figure 9*). The SGLT1 inhibitor upregulated Pck1 mRNA in the duodenum (ZDF-P group vs. ZDF-

Glu group: 1.13±0.09 vs. 0.24±0.03, P=0.000) and the jejunum (ZDF-P group vs. ZDF-Glu group: 1.47±0.07 vs. 1.18±0.11, P=0.038) of ZDF rats, but no significant differences in intestinal Pck1 mRNA were found between the GK-P group and GK-Glu group (Figure 10). (III) The SGLT1 inhibitor downregulated G6Pase mRNA in the liver of ZDF rats (ZDF-P group vs. ZDF-Glu group: 3.05±0.53 vs. 4.27±0.23, P=0.005; Figure 11A) and Pck1 mRNA expression in GK rats (GK-P group vs. GK-Glu group: 0.74±0.05 vs. 1.00±0.05, P=0.001; Figure 11B). (IV) The SGLT1 inhibitor upregulated GLP-1R mRNA in the pancreas of ZDF rats (Figure 8). Pancreatic GLP-1R mRNA expression in the ZDF-P group was significantly higher than that in the ZDF-Glu group (1.37±0.24 vs. 0.80±0.07, P=0.021), but no significant differences were found between the GK-Glu and GK-P groups (P=0.097).

### Discussion

The incidence of diabetes is increasing and finding effective treatment has become an urgent and important issue. MBS, represented by RYGB, has achieved encouraging results in the treatment of diabetes, with a postoperative remission rate as high as 83.7–98.9% (41). MBS is being performed in nonobese diabetes more and more (41,42). In 2008, the American Society for Bariatric Surgery (ASBS) was renamed as the American Society for Metabolic & Bariatric Surgery (ASMBS), reflecting the widespread acceptance of the



**Figure 9** G6Pase mRNA expression in the intestine. The higher expression of G6Pase mNRA in ZDF-Glu group than that in GK-Glu group, were observed in both duodenum (1.20±0.07 vs. 0.62±0.04, P=0.000) and jejunum (1.30±0.09 vs. 1.03±0.04, P=0.003), but dramatically changes were observed that the lower expression of G6Pase mNRA in ZDF-Glu group than that in GK-Glu group (0.27±0.04 vs. 0.87±0.03, P=0.000) occurred in the ileum. No significant differences were found in duodenum, jejunum and ileum between GK-Glu and GK-P groups (P=0.789, 0.657, 0.445, respectively), and between ZDF-Glu and ZDF-P groups (P=0.363, 0.129, 0.115, respectively). Data were analyzed using one-way ANOVA with post hoc analysis with LSD's comparison test. \*P<0.05, \*\*P<0.01, \*\*\*P<0.001. G6Pase, glucose-6 phosphatase; GK, Goto-Kakizaki; ZDF, Zuker diabetic fat; ANOVA, analysis of variance; LSD, least significant difference.



**Figure 10** Pck1 mRNA expression in the intestine. The lower expression in ZDF-Glu than that of in GK-Glu group (0.69±0.13 vs. 1.02±0.11, P=0.039) in ileum were found, but no significant differences were found in duodenum and jejunum between ZDF-Glu and GK-Glu groups (P=0.301, 0.178, respectively). The Pck1 mRNA expression in the ZDF-P group was significantly higher than ZDF-Glu group both in the duodenum (1.13±0.09 vs. 0.24±0.03, P=0.000) and in the jejunum (1.47±0.07 vs. 1.18±0.11, P=0.038), but no significant differences were found between GK-P group and GK-Glu group, in duodenum (P=0.483), jejunum (P=0.059) and ileum (P=0.056). Data were analyzed using one-way ANOVA with post hoc analysis with LSD's comparison test. \*P<0.05, \*\*\*P<0.001. Pck1, phosphoenolpyruvate carboxykinase-1; GK, Goto-Kakizaki; ZDF, Zuker diabetic fat; ANOVA, analysis of variance; LSD, least significant difference.

surgical treatment for diabetes by specialists (43). However, the mechanism of MBS in the treatment of diabetes is not fully understood, and the indications of diabetic patients for MBS (i.e., the definition of "surgical diabetes") are not well defined (44).

# The "SGLT1 bridge" bypothesis originally proposed and our interpretation of inconsistencies

The therapeutic mechanism of surgery cannot be convincingly explained by the classic theory of EIA based

on GLP-1 and GBLA initiated by IGNG. Postoperative glucose improvement is observed in RYGB with reserved or disconnected vagus nerve (44), raising questions about the ability of the GBLA hypothesis to explain the mechanism of the surgical treatment effect. As for the EIA hypothesis, numerous studies (4-11,13-15) have raised doubts on the importance of GLP-1 to diabetic remission in MBS, which is consistent with the findings of our previous research (15), which suggested that increased GLP-1 may be an "intermediate step" in glucose improvement after MBS. As for identifying an "upstream factor", the molecular



**Figure 11** G6Pase & Pck1 mRNA expression in the liver. (A) The hepatic G6Pase mRNA expression in ZDF-Glu group was significantly higher than that in GK-Glu group (4.27±0.23 vs. 0.97±0.04, P=0.000), and higher than that in ZDF-P group (4.27±0.23 vs. 3.05±0.53, P=0.005), but no significant differences were found between GK-Glu and GK-P groups (P=0.923). (B) The hepatic Pck1 mRNA expression in GK-Glu group was significantly higher than that in ZDF-Glu group (1.00±0.05 vs. 0.62±0.05, P=0.000), and higher than that in GK-P group (1.00±0.05 vs. 0.74±0.05, P=0.001), but significant differences were hardly found between GK-Glu group and ZDF-Glu group (P=0.052). Data were analyzed using one-way ANOVA with post hoc analysis with LSD's comparison test. \*\*P<0.01, \*\*\*P<0.001. G6Pase, glucose-6 phosphatase; GK, Goto-Kakizaki; ZDF, Zuker diabetic fat; Pck1, phosphoenolpyruvate carboxykinase-1; ANOVA, analysis of variance; LSD, least significant difference.

mechanisms of small intestinal nutrient sensing in metabolic homeostasis have physiological and pathological impact as well as therapeutic potential in diabetes (45). Our team believes that it is likely to be SGLT1 that induces the improvement of glycometabolism synergically via both the EIA and GBLA pathways (44). For the sake of description, we summarize it as the "SGLT1 bridge" hypothesis, which implies that SGLT1 acts as a bridge-like mechanistic link between EIA and GBLA and plays a synergistic role in these 2 axes.

Controversially, in some studies of rats after MBS, i.e., DJB surgery, the expression of SGTL1 in the alimentary limb showed either upregulation (28,39) (in nondiabetic rats) or downregulation (in diabetic rats) (38). Consideration that SGLT1 expression may be related to the pathophysiological conditions of the diabetic rats has not received enough attention in previous metabolic studies. We hypothesized that the expression of SGLT1 is discrepant in different diabetic profiles. Consistent with our hypothesis, Chichger *et al.* (46) found that compared with Wistar rats with normal BG, enhanced expression of multiple sodiumglucose transporters (including SGLT1) was evident in the renal proximal tubule of diabetic GK rats, whereas only the expression of SGLT1 was enhanced in the proximal tubule of streptozotocin-induced diabetic rats. However, Chichger's study only examined SGLT1 expression in the kidney. Herein, we investigated the expression of SGLT1 in different diabetic rats in multiple digestive system organs, including the intestine, the liver, and the pancreas.

# Diabetic rats in distinct pathophysiological conditions present discrepant glycometabolic profiles

Several rat models have been applied to research on metabolic mechanisms and SGLT1 (28,46-55). ZDF rats are widely used to study physiology and pathology in obese diabetes (56-64), representing early-stage type 2 diabetes well. GK rats, a spontaneously nonobese diabetic rat model that exhibits stable hyperglycemia, marked glucose intolerance, insulin resistance, and impaired glucoseinduced insulin secretion (65), are considered an ideal model for the advanced stage of diabetes (46,66,67). Therefore, we chose ZDF rats and GK rats to investigate the differences that might result from the distinct pathophysiological conditions of diabetes.

The different glycometabolic profiles in rats representing different stages of diabetes were verified as follows: (I) the insulin resistance of ZDF rats was significantly higher than that of GK rats (*Figure 3C*), which may have been attributed to the obesity of ZDF rats that the nonobese GK

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rats did not possess; and (II) the impaired glucose tolerance in OGTT was more severe in GK rats than ZDF rats (*Figure 3D*), and the fasting insulin level was lower in GK rats than in ZDF rats (*Figure 3B*), consistent with progression in type 2 diabetes. In humans with a long duration of type 2 diabetes, further impaired glucose tolerance and a deficiency of insulin secretion may occur. Therefore, the ZDF rats and GK rats selected for the present study simulated the models of early and advanced stages of diabetes well, which contributed to the credibility of the conclusion.

### Distinct pathophysiological conditions might account for the discrepant expression of SGLT1 in diabetic rats

The notion that MBS has no effect on BG (41,42,44) is still hard to explain in clinical practice, and the indications of diabetic patients for surgery treatment have not yet been well defined. A high body mass index (BMI) is the most frequently considered indication, and the duration of diabetes is another important index that has been proposed as a significant predictor of prognosis (42), with the longer the duration of diabetes, the worse the efficacy of MBS. Nevertheless, there is no clear and reasonable explanation for the poor efficacy of surgery in patients with long duration of diabetes. It is generally believed that advanced type 2 diabetes is prone to secretion deficiency of insulin that is similar to type 1 diabetes. The "ABCD score system" (68,69) [comprising age (A), BMI (B), C peptide (C), and duration (D)] is applied to diabetic patients who are candidates for surgery and has improved the overall efficacy of surgery in the treatment of diabetes. However, invalid improvement and remission after MBS continue to occur (41). We hypothesized that the expression of SGLT1 might be different in diabetic rats with distinct pathophysiology, which might account for the remission of diabetes postoperatively.

SGLT1 is expressed mainly in the small intestine, with peak activity in the duodenum and less expression in the distal small intestine (70), which was inconsistent with the diabetic rats in the present study, indicating that the expression of SGLT1 in diabetic rats may possess inherent pathophysiological conditions. Higher expression of SGLT1 in diabetes has been reported (30,71-76). We compared rats in 2 distinct pathophysiological conditions, representing early and advanced stages of diabetes, and found that the activity of SGLT1 expressed in the duodenum of GK rats was higher than that in ZDF rats after glucose gavage

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(*Figure 4*). Further, the mRNA expression of SGLT1 in the jejunum of GK rats was higher than in ZDF rats (*Figure 6*), indicating the probability that the longer the duration of diabetes, the higher the expression of SGLT1 in the "foregut". Differences in SGLT1 expression levels should be regarded as distinct pathophysiological states of diabetes (75-77) and is worthy of further study involving humans with different duration of diabetes.

# SGLT1 may synergically regulate GLP-1 expression and gluconeogenesis (GNG)

The expression of SGLT1 has an obvious circadian rhythm (52,71); its peak expression at 9-10 am is 2-3 times higher (protein level) or 5 times higher (mRNA) than the lowest point, and its half-life is about 2 hours (58). Based on these inherent properties of SGLT1, the tissues of the small intestine were harvested at 10:30 am, and the tissues of the liver and pancreas were harvested at 11:00 am. It has been reported (52,78) that intestinal SGLT1 expression is independent of local luminal factors, not affected by paracrine of the pancreas, and seems to be regulated only by circadian rhythms. Taken together, it is reasonable to speculate that, as the "first gateway" for food contact in the intestine, SGLT1 could be considered "upstream" of IGNG and intestinal hormones. Phlorizin, a classic SGLT1 inhibitor we chose to verify the regulatory effect of SGLT1 in vivo, can effectively inhibit the expression of SGLT1 in the intestine.

SGLT1 plays an important role in mediating glucosedependent GLP-1 expression (34,35,79), both in the intestine and pancreas (15). Gorboulev et al. (30) found reduced GLP-1 expression in SGLT1-gene knockout mice compared with normal mice, indicating that SGLT1 is pivotal for intestinal glucose absorption and glucosedependent GLP-1 secretion. GSK-1614235, a highly selective SGLT1 inhibitor, can reduce glucose-dependent GLP-1 level in volunteers with normal BG (80). Multiple regulatory effects of SGLT1 inhibitor on GLP-1R were shown in our study (Figure  $\delta$ ): (I) the decreased expression of GLP-1R in the jejunum of ZDF rats after the use of SGLT1 inhibitor; and (II) upregulated GLP-1R expression in the pancreas of ZDF rats. SGLT1 regulation of GLP-1R expression in the intestine and the pancreas of ZDF rats was confirmed, whereas the regulatory effect of SGLT1 on the expression of intestinal and pancreatic GLP-1R mRNA was not shown in GK rats (Figure 8). Such differences might have resulted from the failure of an inhibiting effect

by phlorizin in the jejunum and the ileum of GK rats (Figure 6), while the expression of SGLT1 mRNA in the jejunum and ileum of ZDF rats was effectively regulated by the SGLT1 inhibitor (Figure 6). Combined with the finding mentioned above that the activity of SGLT1 expression in the duodenum of GK rats was stronger than that in ZDF rats (*Figures 4*, 5), we speculated that unlike ZDF rats in early diabetes, the regulation pathway of SGLT1- GLP-1R in GK rats with advanced diabetes may have been blocked. The differences seen in diabetic rats with varying durations may have been due to complex pathophysiological conditions, which may account for the lower remission rate or higher recurrence rate after surgery in diabetic patients with longer durations (42,77). Therefore, an intact SGLT1-GLP-1R regulation pathway might be an important indication for the "surgical diabetes" (44) that we have proposed.

G6Pase and Pck1 are the key rate-limiting enzymes of GNG, and expression will be enhanced when hungry (81), which plays a crucial role in EGP and the maintenance of BG homeostasis. Troy *et al.* (26) showed that IGNG was a key factor for early metabolic changes after gastric bypass in mice, which is consistent with other studies involving rats (10,28,29,39). This means that the GBLA pathway originating from IGNG and terminating at HGNG has been preliminarily validated in animal models of metabolic bariatric surgery.

However, inconsistencies remain regarding whether SGLT1 is located "upstream" of IGNG. After DJB surgery, the alimentary limb of rats with normal BG presented high expressions of SGLT1 with upregulation of IGNG (28,39) and downregulation of HGNG (28), whereas downregulated expression of intestinal SGLT1 and approximately a half-reduced function of glucose absorption were found in streptozotocin-induced diabetic rats (38). We believe that the inconsistencies may be caused by the glucose metabolism status of the rat models. Therefore, the ideal rat models representing early and advanced diabetes were adopted in the present study to explore the effect of SGLT1 on GBLA. The SGLT1 inhibitors downregulated activity of duodenal SGLT1 in both ZDF rats and GK rats (Figures 4,5), which resulted in upregulated expressions of Pck1 mRNA in the duodenum and jejunum of ZDF rats (Figure 10), whereas no regulatory effect of SGLT1 inhibitor on key enzymes of IGNG was found in GK rats (Figures 9,10). Additionally, the expression of G6Pase (Figure 11A) and Pck1 mRNA (Figure 11B) in the liver of ZDF rats was downregulated without any effect on

the expression of SGLT1 mRNA in the liver of ZDF rats (Figure 7A), suggesting that the effect of SGLT1 inhibitor on HGNG of ZDF rats was a "remote" induction rather than a local regulation, likely resulting from the IGNG-GBLA-HGNG pathway. These results indicated that SGLT1 might have had a negative regulatory effect on IGNG, and a positive regulatory effect on HGNG in ZDF rats. However, such regulatory effects on GNG were not found in GK rats, and combined with the aforementioned finding that GK rats had more severely impaired glucose tolerance than ZDF rats (Figure 3D), the results suggested that the IGNG-GBLA-HGNG pathway in GK rats with advanced diabetes may have been blunted or even blocked. Therefore, we speculated that the unsatisfactory improvement of glucose metabolism or easy relapse of diabetes after surgery may be caused by the failure of induction on the GBLA pathway due to certain pathophysiological changes in advanced diabetes. A wellretained SGLT1-IGNG-GBLA-HGNG pathway might be important and should be taken as one of the indications for "surgical diabetes".

Taken together, our results suggested that SGLT1 may synergistically induce both the EIA and GBLA pathways to improve glucose metabolism in a type of diabetes referred to as "surgical diabetes" and preliminarily validated the "SGLT1 bridge" hypothesis we have proposed. However, the exact mechanism of the "SGLT1 bridge" as an indication for "surgical diabetes" remains to be elaborated. The role of SGLT1 in "surgical diabetes" is worthy of further study.

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### Footnote

*Reporting Checklist:* The authors have completed the ARRIVE reporting checklist. Available at https://atm. amegroups.com/article/view/10.21037/atm-22-1769/rc

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ICMJE uniform disclosure form (available at https://atm. amegroups.com/article/view/10.21037/atm-22-1769/coif). The authors have no conflicts of interest to declare.

*Ethical Statement:* The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. The study protocol was approved by the Animal Ethics and Welfare Committee of Shenzhen University (No. YSDW202009030), in compliance with Chinese national guidelines for the care and use of animals.

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