Emerging roles of GLIS3 in neonatal diabetes, type 1 and type 2 diabetes

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Abstract

GLI-similar 3 (GLIS3), a member of the Krüppel-like zinc finger protein subfamily, is predominantly expressed in the pancreas, thyroid and kidney. Glis3 mRNA can be initially detected in mouse pancreas at embryonic day 11.5 and is largely restricted to β cells, pancreatic polypeptide-expressing cells, as well as ductal cells at later stage of pancreas development. Mutations in GLIS3 cause a neonatal diabetes syndrome, characterized by neonatal diabetes, congenital hypothyroidism and polycystic kidney. Importantly, genome-wide association studies showed that variations of GLIS3 are strongly associated with both type 1 diabetes (T1D) and type 2 diabetes (T2D) in multiple populations. GLIS3 cooperates with pancreatic and duodenal homeobox 1 (PDX1), v-maf musculoaponeurotic fibrosarcoma oncogene family, protein A (MAFA), as well as neurogenic differentiation 1 (NEUROD1) and potently controls insulin gene transcription. GLIS3 also plays a role in β cell survival and likely in insulin secretion. Any perturbation of these functions may underlie all three forms of diabetes. GLIS3, synergistically with hepatocyte nuclear factor 6 (HNF6) and forkhead box A2 (FOXA2), controls fetal islet differentiation via transactivating neurogenin 3 (NGN3) and impairment of this function leads to neonatal diabetes. In addition, GLIS3 is also required for the compensatory β cell proliferation and mass expansion in response to insulin resistance, which if disrupted may predispose to T2D. The increasing understanding of the mechanisms of GLIS3 in β cell development, survival and function maintenance will provide new insights into disease pathogenesis and potential therapeutic target identification to combat diabetes.

Key Words
- GLIS3
- neonatal diabetes
- type 1 diabetes
- type 2 diabetes
- insulin
- NGN3

Introduction

Type 1 (T1D) and type 2 diabetes (T2D) share some clinical and pathologic similarities, presenting with hyperglycemia resulting from islet β cell dysfunction and/or defect of insulin action. Hyperglycemia associated with both T1D and T2D may lead to similar chronic clinical complications. However, genome-wide association studies (GWAS) indicate that their susceptibility loci are mostly distinct. To date, more than 50 and 100 susceptibility loci are found to be associated with T1D and T2D, respectively (Todd 2010, Bonnefond & Froguel 2015, Yang & Chan 2016). Remarkably, only a limited number of them are associated with both T1D and T2D. These include: insulin, GLI-similar 3 (GLIS3), RAS guanyl nucleotide-releasing protein 1 (RASGRP1), cordon-bleu WH2 repeat protein (COBL), renalase and breast cancer anti-estrogen resistance 1 (BCAR1) (Basile et al. 2014, Yang & Chan 2016).
Within these shared susceptibility loci, insulin and GLIS3 are the only two known monogenic diabetes genes (Yang & Chan 2016).

GLIS3 is a member of the Krüppel-like zinc finger protein subfamily that was named due to its similarity to Drosophila regulatory protein Krüppel (Kim et al. 2003). Mutations of GLIS3 cause a neonatal diabetes syndrome characterized by neonatal diabetes, congenital hypothyroidism and polycystic kidney (Senee et al. 2006), which can be phenocopied in Glis3-deficient mice (Kang et al. 2009b, Watanabe et al. 2009, Yang et al. 2011). GWAS have also identified that variations of GLIS3 are associated with a number of other diseases. For example, GLIS3 rs1571583 is associated with elevated serum thyroid-stimulating hormone (Porcu et al. 2013). GLIS3 rs514716 is a risk variant for the levels of cerebrospinal fluid tau and ptau 181, biomarkers for Alzheimer’s disease (Cruchaga et al. 2013). GLIS3 rs736893 is associated with primary angle closure glaucoma (Khort et al. 2016). In addition, increased expression of GLIS3 has been observed in several types of tumors, such as ependymoma (Lukashova-v-Zangen et al. 2007), proneural glioblastoma (Cooper et al. 2010), chromophobe renal cell carcinoma (Yusenko & Kovacs 2009), breast cancer (Rami et al. 2016) and metastatic melanoma (Jayachandran et al. 2016).

GLIS3, interacting with its co-activator WW domain containing transcription regulator 1 (WWTR1), plays a critical role in maintaining proper renal functions (Kang et al. 2009a). A recent report showed that GLIS3 is also involved in the early postnatal spermatogenesis in mice (Kang et al. 2016a). In the present review, we will focus on GLIS3 and diabetes, summarizing its roles in monogenic neonatal diabetes (Table 1), T1D and T2D (Table 2), as well as the underlying mechanisms explored in animal models.

Molecular characteristics of GLIS3

GLI-similar subfamily contains three Krüppel-like zinc finger proteins, such as GLIS1–3. They share a highly homologous zinc finger domain (ZFD) consisting of five Cys3His1-type zinc finger motifs. The ZFD in mouse GLIS3 exhibits 93% and 59% identities with that in mouse GLIS1 and GLIS2, respectively (Kim et al. 2003). The full length of mouse Glis3 gene (NM_175459) contains 11 exons and encodes a protein of 935 amino acids with a calculated molecular weight 99.7kDa. Part of exon 4 encodes the five ZFDs, and all of them are required for the binding to target DNA (Fig. 1A). The ZFDs are well conserved between rodents and human. A potential bipartite nuclear localization signal (NLS) is located between Arg645 and Lys661, which overlaps with the fifth zinc finger. Interestingly, deletion and mutation analyses revealed that the nuclear localization of GLIS3 does not require the putative NLS, whereas the fourth zinc finger is completely required. C-terminal truncated GLIS3 can localize to the nucleus, but loses its transactivational activity, suggesting that the transactivation domain (TAD) of GLIS3 resides at its C-terminus (Fig. 1A) (Beak et al. 2008).

RNA blot hybridization detected two dominant transcripts of human GLIS3 gene, long (7.5 kb) and smaller (0.8–2.0 kb), in multiple tissues. The 7.5 kb transcript is highly expressed in the pancreas, kidney and thyroid; in contrast, the smaller transcript is strongly expressed in the heart, liver and skeletal muscle (Senee et al. 2006). A number of alternatively spliced variants of human GLIS3 gene that encode different protein isoforms have been reported. However, only two major variants that encode GLIS3 protein isoforms a and b have been determined. These two variants share the last 9 exons. Compared to the variant 1 (NM_001042413), the variant 2 (NM_152629) harbors a distinct 5′ untranslated region (UTR) and lacks an in-frame portion of the 5′ coding region, resulting in a shorter N-terminus in isoform b (Fig. 1B). These alternatively spliced variants of human GLIS3 gene may contribute to the heterogeneities of clinical presentations.

GLIS3 may function as a cell-type-dependent transactivator or repressor. Early study showed that GLIS3 may bind to the GLI consensus sequence GACCACCCAC, suggesting a cross-talk between the GLIS3 and GLI signaling pathways (Kim et al. 2003). To identify the specific binding site for GLIS3, Beak and coworkers combined PCR and electrophoretic mobility shift assay (EMSA) to screen a mixture of 60bp oligonucleotides that contain 22 random nucleotides. They reported that (G/C) TGGGGGTA(T/A)C is the optimal DNA-binding site for GLIS3 (Beak et al. 2008). Subsequently, an endogenous consensus GLIS3 response element (GLIS3RE), G(T/C) CCC(T/A)GCTGTGA(A/G), was identified in the promoter/enhancer regions of insulin (Yang et al. 2009), neurogenin 3 (Ngn3) (Yang et al. 2011) and cyclin d2 (Ccn2) (Yang et al. 2013) in islet progenitors or adult β cells.

The temporal and spatial expression of GLIS3 in mouse pancreas

The pancreas has both exocrine and endocrine functions. The exocrine pancreas, consisting of acinar and ductal cells, involves the secretion of digestive enzymes that aid
### Table 1  Clinical characteristics of neonatal diabetes syndrome in patients with GLIS3 mutation.

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Ethnicity</th>
<th>Family/patient</th>
<th>NDM</th>
<th>CH</th>
<th>PKD</th>
<th>Other features</th>
<th>Alive/dead</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>p.625fs703Stop&lt;sup&gt;a&lt;/sup&gt;</td>
<td>Arabia</td>
<td>1/3</td>
<td>Y</td>
<td>Y</td>
<td>Y&lt;sup&gt;b&lt;/sup&gt;</td>
<td>Liver fibrosis, IUGR, facial dysmorphism, congenital glaucoma</td>
<td>Died at 10 d, 6 and 16 months</td>
<td>Senee et al. (2006)</td>
</tr>
<tr>
<td>p.Cys536Trp</td>
<td>Arabia</td>
<td>1/1</td>
<td>Y</td>
<td>N</td>
<td>N</td>
<td>IUGR, hyperactivity</td>
<td>Alive (6.8 years)</td>
<td>Dimitri et al. (2015)</td>
</tr>
<tr>
<td>p.Gly311Alafs</td>
<td>Pakistani</td>
<td>1/1</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>Right sensorineural deafness, skeletal disease</td>
<td>Alive (2.5 years)</td>
<td>Dimitri et al. (2015)</td>
</tr>
<tr>
<td>p.His561Tyr</td>
<td>Kurds</td>
<td>1/1</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>Liver fibrosis, facial dysmorphism, congenital glaucoma, patent ductus arteriosus</td>
<td>Alive (4.5 years)</td>
<td>Dimitri et al. (2015)</td>
</tr>
<tr>
<td>p.Arg589Trp/exons 1–11 del&lt;sup&gt;c&lt;/sup&gt;</td>
<td>Caucasian</td>
<td>1/1</td>
<td>Y</td>
<td>N</td>
<td>N</td>
<td>IUGR, choanal atresia, hiatus hernia</td>
<td>Alive (36 years)</td>
<td>Dimitri et al. (2015)</td>
</tr>
<tr>
<td>426 kb deletion Chr9:4176077–4601776</td>
<td>Arabia</td>
<td>1/1</td>
<td>Y</td>
<td>Y</td>
<td>N</td>
<td>IUGR, congenital glaucoma</td>
<td>Alive (2 years)</td>
<td>Senee et al. (2006)</td>
</tr>
<tr>
<td>149 kb deletion Chr9:4249915–4398572</td>
<td>French</td>
<td>1/2</td>
<td>Y</td>
<td>Y</td>
<td>N</td>
<td>IUGR</td>
<td>Alive (14 and 22 years)</td>
<td>Senee et al. (2006)</td>
</tr>
<tr>
<td>Exons 1–2 deletion</td>
<td>Arabia</td>
<td>2/2</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>Insulin resistance or high insulin sensitivity, ostium secundum atrial, septal defect, facial dysmorphism, congenital glaucoma</td>
<td>Alive (6 years and 7 months)</td>
<td>Dimitri et al. (2015)</td>
</tr>
<tr>
<td>Exons 1–4 deletion</td>
<td>Caucasian</td>
<td>1/2</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>Exocrine insufficiency, liver fibrosis, IUGR, bilateral sensorineural deafness, facial dysmorphism, pancreatic cyst</td>
<td>Alive (6 years and 20 months)</td>
<td>Dimitri et al. (2011, 2015)</td>
</tr>
<tr>
<td>Exons 3–4 deletion</td>
<td>Turkish</td>
<td>1/1</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>IUGR, liver fibrosis, facial dysmorphism</td>
<td>Died at 6 months</td>
<td>Dimitri et al. (2015)</td>
</tr>
<tr>
<td>Exons 5–9 deletion</td>
<td>Arabia</td>
<td>1/1</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>IUGR, liver fibrosis, facial dysmorphism</td>
<td>Alive (4.7 years)</td>
<td>Dimitri et al. (2015)</td>
</tr>
<tr>
<td>Exons 9–11 deletion</td>
<td>African–American</td>
<td>1/1</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>IUGR, liver fibrosis, facial dysmorphism, skeletal disease, congenital glaucoma</td>
<td>Died at 6 years</td>
<td>Dimitri et al. (2015)</td>
</tr>
<tr>
<td>Exons 10–11 deletion</td>
<td>Yemeni</td>
<td>1/1</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>IUGR, liver fibrosis, exocrine insufficiency, facial dysmorphism, congenital glaucoma</td>
<td>Alive (3 years)</td>
<td>Dimitri et al. (2015)</td>
</tr>
<tr>
<td>p.Phe857Tyr&lt;sup&gt;c,d&lt;/sup&gt;</td>
<td>Chinese</td>
<td>1/1</td>
<td>Y</td>
<td>N</td>
<td>N/A</td>
<td>Liver and kidney failure</td>
<td>Died at 1.5 years</td>
<td>Cao et al. (2016)</td>
</tr>
</tbody>
</table>

<sup>a</sup>Equal to p.779fs858Stop in the updated version of human GLIS3 gene (NM_001042413); <sup>b</sup>the patient who died at 10 day of age did not present PKD; <sup>c</sup>indicates heterozygous mutation. All others are homozygous mutations in GLIS3; <sup>d</sup>it is unclear if this mutation was causative; whether this patient developed PKD was not documented, although we note that the patient died of liver and kidney failure.

CH, congenital hypothyroidism; IUGR, intrauterine growth restriction; NDM, neonatal diabetes mellitus; N, no; PKD, polycystic kidney disease; Y, yes.

nutrient digestion. The endocrine pancreas (also called islet), containing five types of hormone-expressing cells such as α, β, δ, ε and pancreatic polypeptide (PP), that is responsible for the regulation of glucose homeostasis. Both pancreatic exocrine and endocrine cells arise from a common origin of progenitor cells in the gut endoderm. Pancreas specification becomes morphologically evident around embryonic day (E) 8.5–9.0 with the expression of pancreatic and duodenal homeobox 1 (PDX1). Pancreatic progenitors adopt either tip identity that develops to an acinar phenotype or trunk identity that is bipotential for the ductal and endocrine cell fate (Shih et al. 2013). Mouse pancreas development contains a primary transition from E9.5 to E12.5 and a secondary transition from E12.5 to birth. During the primary transition, a subset of progenitor cells initiate the expression of NGN3, which marks the onset of endocrine cell differentiation, whereas the subset of trunk epithelial cells that do not express NGN3 develop into ductal cells. During the secondary transition, endocrine hormone-expressing cells are rapidly expanded in the developing pancreas starting from E13.5 (Oliver-Krasinski & Stoffers 2008, Shih et al. 2013).

GLIS3 is predominantly expressed in the pancreas, thyroid and kidney, with modest expression in the heart,
### Variations of GLIS3 and T1D

<table>
<thead>
<tr>
<th>Study type</th>
<th>Sample size</th>
<th>Ethnicity</th>
<th>Major findings</th>
<th>Effect size*</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>GWAS/meta-analysis</strong></td>
<td>7514 cases/9045 controls</td>
<td>European</td>
<td>GLIS3 rs7020673 associated with T1D</td>
<td>0.88, 0.97</td>
<td>Barrett et al. (2009)</td>
</tr>
<tr>
<td><strong>GWAS</strong></td>
<td>858 general population children/851 first-degree relatives of T1D patients</td>
<td>Non-Hispanic White</td>
<td>GLIS3 rs7020673 associated with the development of islet autoimmunity</td>
<td>N/A</td>
<td>Steck et al. (2014)</td>
</tr>
<tr>
<td><strong>GWAS</strong></td>
<td>4574 cases/1207 controls, validated in 765 cases/423 controls</td>
<td>T1D genetics consortium, Germans</td>
<td>GLIS3 rs7020673 contributes to the prediction of T1D</td>
<td>N/A</td>
<td>Winkler et al. (2014)</td>
</tr>
<tr>
<td><strong>GWAS replication analysis</strong></td>
<td>23 cases/39 controls (related individuals); 68 cases/61 controls (unrelated individuals)</td>
<td>Pakistani</td>
<td>GLIS3 rs7020673 associated with T1D</td>
<td>N/A</td>
<td>Kiani et al. (2015)</td>
</tr>
<tr>
<td><strong>GWAS</strong></td>
<td>706 cases/863 controls</td>
<td>Japanese</td>
<td>GLIS3 A908V associated with resistance to T1D</td>
<td>0.046</td>
<td>Awata et al. (2013)</td>
</tr>
<tr>
<td><strong>GWAS meta-analysis</strong></td>
<td>46,186 non-diabetic participants and follow-up in 76,558 additional subjects</td>
<td>European</td>
<td>GLIS3 rs7034200 associated with fasting glucose and impaired β cell function</td>
<td>0.018</td>
<td>Dupuis et al. (2010)</td>
</tr>
<tr>
<td><strong>GWAS</strong></td>
<td>6784 middle-aged participants</td>
<td>Danish</td>
<td>GLIS3 rs7034200 associated with reduced glucose-stimulated β cell function</td>
<td>-0.02</td>
<td>Boesgaard et al. (2010)</td>
</tr>
<tr>
<td><strong>GWAS replication analysis</strong></td>
<td>3410 T2D patients and 3412 controls</td>
<td>Chinese</td>
<td>GLIS3 rs7034200 associated with T2D</td>
<td>1.103</td>
<td>Hu et al. (2010)</td>
</tr>
<tr>
<td><strong>GWAS meta-analysis</strong></td>
<td>Over 6000 healthy children and adolescents</td>
<td>European and Australians</td>
<td>GLIS3 rs7034200 associated with impaired β cell function and altered fasting glucose</td>
<td>-0.023</td>
<td>Barker et al. (2011)</td>
</tr>
<tr>
<td><strong>GWAS</strong></td>
<td>1678 cases/1584 controls</td>
<td>South Asians</td>
<td>GLIS3 rs7034200 associated with T2D</td>
<td>1.03</td>
<td>Rees et al. (2011)</td>
</tr>
<tr>
<td><strong>GWAS</strong></td>
<td>3210 unrelated individuals</td>
<td>Chinese Han</td>
<td>GLIS3 rs7034200 associated with fasting glucose, β cell function and T2D</td>
<td>1.27</td>
<td>Liu et al. (2011)</td>
</tr>
<tr>
<td><strong>GWAS meta-analysis, replication analysis</strong></td>
<td>Meta-analysis: 6952 cases/11,865 controls; in silico replication: 5843 cases/4,574 controls; de novo replication: 12,284 cases/13,172 controls</td>
<td>East Asians</td>
<td>GLIS3 rs7041847 associated with T2D</td>
<td>1.1</td>
<td>Cho et al. (2012)</td>
</tr>
<tr>
<td><strong>GWAS</strong></td>
<td>2632 cases/2050 controls</td>
<td>Japanese</td>
<td>GLIS3 rs7034200 borderline associated with T2D</td>
<td>1.09</td>
<td>Fujita et al. (2012)</td>
</tr>
<tr>
<td><strong>GWAS replication analysis</strong></td>
<td>3548 DPP participants</td>
<td>Multiple ethnics</td>
<td>No impact of GLIS3 rs7034200 on diabetes incidence or interaction with preventive interventions</td>
<td>N/A</td>
<td>Florez et al. (2012)</td>
</tr>
<tr>
<td><strong>GWAS meta-analysis</strong></td>
<td>1329 participants in 329 families</td>
<td>Hispanic-American</td>
<td>GLIS3 rs2380949 associated with insulin dearance</td>
<td>N/A</td>
<td>Goodarzi et al. (2013)</td>
</tr>
<tr>
<td><strong>GWAS replication analysis</strong></td>
<td>5315 cases/2064 controls</td>
<td>Japanese</td>
<td>GLIS3 rs7041847 confers susceptibility to T2D</td>
<td>1.03</td>
<td>Sakai et al. (2013)</td>
</tr>
<tr>
<td><strong>GWAS</strong></td>
<td>8569 cases/8923 controls</td>
<td>Chinese Han, East Asians</td>
<td>GLIS3 rs10814916 associated with the risk of T2D</td>
<td>1.11</td>
<td>Li et al. (2013)</td>
</tr>
<tr>
<td><strong>GWAS meta-analysis</strong></td>
<td>5974 non-diabetic subjects</td>
<td>Koreans</td>
<td>GLIS3 rs7034200 associated with impaired β cell function</td>
<td>-0.02</td>
<td>Hong et al. (2014)</td>
</tr>
<tr>
<td><strong>Matched case-control</strong></td>
<td>160 T2D/160 controls, 195 impaired glucose regulation/195 controls</td>
<td>Chinese Han</td>
<td>GLIS3 rs7034200 associated with the risk of T2D</td>
<td>1.625</td>
<td>Dou et al. (2016)</td>
</tr>
</tbody>
</table>

*Effect size is presented as odds ratio unless specified; hazard ratio; Haldane’s odds ratio; per-allele effect; β-coefficient. N/A, not available.
Figure 1
Schematic diagrams of mouse and human GLIS3 gene and protein structures. (A) Mouse Glis3 gene and protein structures. The full-length mouse Glis3 gene contains 11 exons and encodes a protein of 935 aa. The ZFD is encoded by part of exon 4 and is responsible for the binding to the consensus GLIS3RE of its target genes such as insulin, Ngn3 and Ccnd2. TAD is localized at its C-terminus. CUL3 and ITCH promote GLIS3 polyubiquitination and degradation via the proteasomal pathway. SUFU, interacting with GLIS3 through the conserved VYGHF motif at N-terminus of GLIS3, was shown to inhibit the association of CUL3 with GLIS3, thereby protecting GLIS3 protein from proteolytic degradation. (B) Human GLIS3 gene and protein structures. Human GLIS3 gene have two major variants that encode GLIS3 protein isoforms a and b that share the last 9 exons. The variant 1 encodes the longest isoform a with 930 aa. The variant 2 harbors a distinct 5′ UTR and lacks an in-frame portion of the 5′ coding region, resulting in a shorter N-terminus in isoform b with 775 aa, compared to variant 1.

lung, brain, liver, skeletal muscle and testis (Kim et al. 2003, Senee et al. 2006, Yang et al. 2009). RT-PCR and in situ hybridization showed that Glis3 mRNA can be initially detected at E11.5 and significantly increases at E12.5 in mouse pancreata (Kang et al. 2009b). Recently, Jetten and coworkers generated a GLIS3-enhanced green fluorescent protein (EGFP) knock-in mouse model and reported that GLIS3 protein was undetectable during the primary transition (E10.5–12.5), instead it was first detected at E13.5 in the nucleus of bipotent progenitors of the pancreas development (Kang et al. 2016b). Several possibilities might explain this discrepancy in the expression of GLIS3 mRNA and protein. These include delayed protein synthesis and accumulation due to post-transcriptional regulation and GLIS3 protein may be unstable in the pancreata between E11.5 and E12.5. However, distinct sensitivity of the approaches used in these experiments could more likely lead to this apparent difference. In Glis3-deficient mouse pancreas, the expression of NGN3, a direct downstream target of GLIS3, was drastically reduced at both mRNA and protein levels at E12.5, which reveals that Glis3 gene is functionally important in mouse endocrine pancreas development at early as E12.5, immediately before the secondary transition begins (Yang et al. 2011).

In the GLIS3-EGFP knock-in mice, GLIS3-EGFP mainly co-expresses with PDX1 and sex-determining region Y-box 9 (SOX9) in the trunk domains, but not in the tip domains at E13.5. This is consistent with the observation that GLIS3 is predominantly expressed in endocrine and preductal progenitors (Kang et al. 2016b). At later stages, GLIS3 is largely restricted to β cells and PP-expressing cells, as well as ductal cells. GLIS3 protein is also detected in a few δ cells, but neither in α and ε cells nor in acinar cells (Kang et al. 2016b), which is in agreement with the reports that exocrine pancreas was unaffected in Glis3-deficient mice (Kang et al. 2009b, Watanabe et al. 2009, Yang et al. 2011). We, however, note that some patients with GLIS3 mutations present exocrine pancreas insufficiency (Table 1). The reason

Figure 1
Schematic diagrams of mouse and human GLIS3 gene and protein structures. (A) Mouse Glis3 gene and protein structures. The full-length mouse Glis3 gene contains 11 exons and encodes a protein of 935 aa. The ZFD is encoded by part of exon 4 and is responsible for the binding to the consensus GLIS3RE of its target genes such as insulin, Ngn3 and Ccnd2. TAD is localized at its C-terminus. CUL3 and ITCH promote GLIS3 polyubiquitination and degradation via the proteasomal pathway. SUFU, interacting with GLIS3 through the conserved VYGHF motif at N-terminus of GLIS3, was shown to inhibit the association of CUL3 with GLIS3, thereby protecting GLIS3 protein from proteolytic degradation. (B) Human GLIS3 gene and protein structures. Human GLIS3 gene have two major variants that encode GLIS3 protein isoforms a and b that share the last 9 exons. The variant 1 encodes the longest isoform a with 930 aa. The variant 2 harbors a distinct 5′ UTR and lacks an in-frame portion of the 5′ coding region, resulting in a shorter N-terminus in isoform b with 775 aa, compared to variant 1.
Interacting partners of GLIS3

A previous high-throughput yeast two-hybrid screening suggested that GLIS3 may interact with suppressor of fused homolog (SUFU), a tumor suppressor and a negative regulator of hedgehog signaling (Rual et al. 2005). Subsequently, co-immunoprecipitation assay confirmed that the SUFU was able to interact with GLIS3 through the conserved VYGHF motif at N-terminus of GLIS3. Functional study showed that the SUFU repressed the activation of the insulin promoter mediated by GLIS3 (ZeRuth et al. 2011). In addition, the E3 ubiquitin ligase scaffolding protein Cullin 3 (CUL3) promotes GLIS3 polyubiquitination and degradation via the 26S proteasomal pathway. SUFU was shown to inhibit the association of CUL3 with GLIS3, thereby protecting GLIS3 protein from proteolytic degradation and enhancing the stability of GLIS3 protein (Fig. 1A) (ZeRuth et al. 2011).

Combining gel-enhanced liquid chromatography mass spectrometry and yeast two-hybrid analysis, they further reported that the ITCH protein, an itchy E3 ubiquitin ligase, interacted with GLIS3 through the WW domains with a PPxY motif located at N-terminus of GLIS3 and enhanced GLIS3 proteasomal degradation to reduce the GLIS3 stability. ITCH significantly increased GLIS3 protein turnover to inhibit the transactivation of GLIS3, resulting in the reduced expression of downstream targets including insulin (ZeRuth et al. 2015).

Long non-coding RNAs (lncRNAs) are non-protein coding transcripts longer than 200 nucleotides. LncRNAs are usually lineage specific and regulate multiple biological functions (Knoll et al. 2015). In an integrated sequence-based transcriptome and chromatin maps of human islets and β cells, Ferrer and coworkers identified a β cell-specific lncRNA HI-LNC25. They found that the mRNA expression of GLIS3 was significantly reduced in the HI-LNC25-knockdown human β cells, suggesting that GLIS3 is a regulatory target of HI-LNC25 (Moran et al. 2012). It, however, remains to be determined whether HI-LNC25-GLIS3 regulation correlates with the pathophysiology of diabetes as the expression of HI-LNC25 was unchanged in the islets from T2D donors (Moran et al. 2012).

GLIS3 and neonatal diabetes syndrome

In 2003, Taha and coworkers first described a rare clinical syndrome in a consanguineous Saudi Arabian family characterized by permanent neonatal diabetes, congenital hypothyroidism, polycystic kidneys, intrauterine growth retardation, facial anomalies, congenital glaucoma and hepatic fibrosis. Three affected children died at 10 days, 6 and 16 months of life, respectively (Taha et al. 2003, Senee et al. 2006). In 2006, Senée and coworkers identified a homozygous insertion (2067insC) in GLIS3 that underlies the neonatal diabetes syndrome in one family. In addition, they reported that affected individuals harbor homozygous large fragment (426 and 149 kb) deletions affecting the 5’ UTR of the GLIS3 gene in two other families (Senee et al. 2006). Recently, Dimitri and coworkers reported additional patients who carried homozygous or compound partial GLIS3 gene deletions or mutations. In addition to neonatal diabetes, congenital hypothyroidism and polycystic kidneys, they presented a broad spectrum of clinical phenotypes. These include craniosynostosis, hiatus hernia, atrial septal defect, splenic cyst, choanal atresia, sensorineural deafness and exocrine pancreatic insufficiency (Dimitri et al. 2011, 2015). They further described facial dysmorphism including bilateral low-set ears, depressed nasal bridge, elongated and upslanted palpebral fissures, persistent long philtrum with a thin vermilion border of the upper lip in some patients (Dimitri et al. 2016). Notably, one patient with compound heterozygous mutations in GLIS3 (p.Arg589Trp/exons 1–11 del) presenting with neonatal diabetes, but not congenital hypothyroidism or renal cysts, survived to adulthood. Interestingly, all patients present with neonatal diabetes, but with variable insulin sensitivity that is not associated with genotypes. For example, the patients with homozygous exons 1–2 deletion in GLIS3 may present with insulin resistance or high insulin sensitivity (Dimitri et al. 2015). Therefore, insulin therapy should be started with careful attention for this type of neonatal diabetes. The clinical features associated with the mutations in GLIS3 identified to date are summarized in Table 1.

As stated previously, human GLIS3 gene has multiple transcripts with differential expression profiles, which may contribute to the variability in phenotype (Senee et al. 2006). In addition, the severity of impaired function of GLIS3 mutants may also cause the variable phenotypes. For example, a homozygous insertion (2067insC) in GLIS3 leads to either a frameshift and a truncated protein that completely loses its transactivities (Senee et al. 2006, Yang et al. 2009) or likely no protein expression as a result of nonsense-mediated mRNA decay (Lykke-Andersen & Jensen 2015), whereas the compound heterozygous mutations (p.Arg589Trp/exons
1–11 del) might partially affect the function of GLIS3 (Dimitri et al. 2015).

**GLIS3 and type 1 diabetes**

Common T1D is an autoimmune disorder that arises from the action of a combination of genetic and environmental factors (Herold et al. 2013). More than 50 regions of the human genome have been identified to confer the susceptibility for common T1D (Yang & Chan 2016). Barrett and coworkers first identified the association between a GLIS3 variant rs7020673 and common T1D in European populations. They found that the region of strong linkage disequilibrium at chromosome 9p24.2 that harbors only a single gene, GLIS3 (Barrett et al. 2009). This association was replicated recently in Pakistani T1D patients (Kiani et al. 2015).

The human leukocyte antigen (HLA) is the major susceptibility locus for T1D, with an estimated 30–50% of the genetic risk of this disease (Noble et al. 1996). Winkler and coworkers assessed the predictive power of 40 non-HLA gene single nucleotide polymorphisms (SNP) associated with T1D. They found that the combination of GLIS3 rs7020673 and other eight SNPs significantly improved the prediction accuracy of T1D, compared to that provided by HLA alone (Winkler et al. 2014). However, GLIS3 rs7020673 alone exhibited nominal association with the development of islet autoimmunity (IA) and failed to predict the progression from IA to T1D (Steck et al. 2014).

Interestingly, Awata and coworkers reported that low frequency GLIS3 A908V variant was associated with the resistance to T1D in Japanese population. The underlying mechanism remains elusive. Given that GLIS3 mRNA is also moderately expressed in human thymus, they proposed that the protective variant GLIS3 908V might more efficiently induce central or peripheral immune tolerance than wild-type GLIS3 908A (Awata et al. 2013). Additional functional studies are needed to prove or disprove this hypothesis.

**GLIS3 and type 2 diabetes**

Shortly after the report that the GLIS3 variant was strongly associated with common T1D, Dupuis and coworkers first identified the GLIS3 variant rs7034200 as one of nine newly identified loci associated with fasting glucose in T2D trait, but not associated with body mass index (BMI), blood pressure or lipid profile in participants of European descent (Dupuis et al. 2010). This finding has been replicated in Danes (Boesgaard et al. 2010), Chinese (Hu et al. 2010, Liu et al. 2011, Dou et al. 2016) and South Asians (Rees et al. 2011), with a borderline association with T2D in a Japanese population (Fujita et al. 2012). Furthermore, the glucose-raising allele GLIS3 rs7034200 A was also strongly associated with impaired β-cell function both in non-diabetic adults (Dupuis et al. 2010, Hong et al. 2014) as well as in healthy children and adolescents (Barker et al. 2011), which suggests an age-independent effect of this locus on inter-individual differences in glucose levels from childhood onward. It is worth mentioning that GLIS3 rs7034200, in common with other previously identified T2D risk loci, had no significant impact on diabetes incidence or interaction with preventive interventions such as metformin or lifestyle modifications in individuals at high risk of diabetes in the Diabetes Prevention Program (Florez et al. 2012).

In addition, two other GLIS3 variants, rs7041847 and rs10814916, were reported to confer the susceptibility to T2D in East Asians (Cho et al. 2012, Sakai et al. 2013) and in Chinese (Li et al. 2013), respectively. In contrast to GLIS3 rs7034200, a risk SNP for T2D in multi-ethnic populations, GLIS3 rs7041847, appears to confer T2D susceptibility only in East Asians. It would be of interest to address whether GLIS3 rs7041847 contributes to underlie the unique epidemic characteristics in East Asians, e.g., higher rates of T2D at lower average BMI, compared to those in Europeans.

Notably, GLIS3 rs2380949 was found to be associated with insulin clearance in Hispanic Americans (Goodarzi et al. 2013), which suggests that GLIS3 may play a dual role in regulating both insulin production and clearance. GLIS3 variants associated with T2D and related traits are summarized in Table 2.

**The molecular mechanisms that underlie the association between GLIS3 and diabetes**

These association studies between GLIS3 variants and diabetes in people are intriguing. However, the underlying mechanisms were largely unknown until Glis3 global and β cell-specific knockout mice were generated. To gain insight into the role of GLIS3 in diabetes, three groups independently generated Glis3-deficient mice with different strategies (Kang et al. 2009b, Watanabe et al. 2009, Yang et al. 2011) and identified three direct downstream targets of GLIS3, such as NGN3 (Yang et al. 2011), insulin
GLIS3 controls insulin gene transcription

A number of cis-acting regulatory sequences in the insulin promoter region, which bind the key β cell-restricted or ubiquitous transcription factors, have been identified to confer the transcriptional control of insulin expression. For example, PDX1, MAFA and NEUROD1 control insulin gene transcription through their binding to A boxes, C elements and E boxes, respectively (Hay & Docherty 2006). Early studies in rat insulinoma 832/13 cells revealed that stable overexpression of GLIS3 enhanced the expression of Ins2, whereas knockdown of GLIS3 drastically reduced the expression of Ins1 and Ins2. They further identified a GLIS3RE in the insulin gene promoter and found that GLIS3 physically and functionally interacts with PDX1, MAFA and NEUROD1 to control insulin gene transcription (Yang et al. 2009). Subsequent study showed that mutations in the GLIS3RE markedly attenuated the insulin promoter activation by a combination of PDX1, MAFA and NEUROD1, indicating that the direct binding of GLIS3 to the insulin promoter is required for the interaction of its partners with the promoter (ZeRuth et al. 2013). In agreement with these in vitro findings, Yang and coworkers found that tamoxifen-mediated β cell-specific inactivation of Glis3 in mice markedly downregulates insulin expression, leading to fulminant diabetes and death (Yang et al. 2013). Thus, both in vitro and in vivo data demonstrated that GLIS3 is a potent transactivator of the insulin gene.

Interestingly, the mRNA level of glucose transporter 2 (Glut2), the key β cell glucose transporter, was significantly reduced in adult islets of β cell-specific Glis3-deficient mice, compared to that in the control mice (Yang et al. 2013). In addition, the mRNA expression of ATP-binding cassette transporter sub-family C member 8 (Abcc8) encoding sulfonylurea receptor 1 (SUR1) was also decreased in the pancreata of Glis3−/− mice at postnatal day 3, compared to that in their wild-type littermates (Kang et al. 2009b). SUR1 is a sensor of intracellular levels of the nucleotides ATP and ADP to initiate insulin secretion in response to the sulfonylurea class of antidiabetic drugs (Yang & Chan 2016). These data suggested that in addition to controlling insulin gene transcription, GLIS3 may also play a role in insulin secretion in β cells. Given that the insulin production is markedly reduced by more than 80% (Yang et al. 2011), it is a challenge to assess the defect of insulin secretion per se in Glis3−/− mice.
GLIS3 is required for obesity-induced β cell proliferation and mass expansion

In states of insulin resistance, such as obesity and pregnancy, the expansion of β cell mass in accordance with the requirements for insulin is critical for maintaining glucose homeostasis and preventing diabetes. Increasing β cell proliferation is the primary mechanism underlying this β cell mass expansion, although neogenesis may also be involved (Ackermann & Gannon 2007). Failure of β cell mass expansion may be associated with T2D. Consistent with an autosomal recessive inheritance observed in humans, heterozygous Glis3-mutant (Glis3+/−) mice remained euglycemic while on a regular chow diet. However, when they were challenged with a high-fat diet (HFD), adult mice developed overt diabetes with hypoinsulinemia. Histology showed that Glis3+/− mice failed β cell mass expansion in response to HFD. Mechanistically, it has been shown that GLIS3 controls β cell proliferation in response to HFD feeding partly by direct regulation of Ccnd2 mRNA transcription (Yang et al., 2013).

CCND2 is essential for postnatal pancreatic β cell growth (Georgia & Bhushan, 2004, Kushner et al., 2005) and compensatory mass expansion in response to insulin resistance (Georgia et al., 2010). Interestingly, GWAS identified that the variant rs11063069 G in CCND2 confers susceptibility to T2D (Morris et al., 2012), whereas the variant rs76895963 G in CCND2 reduces risk of T2D by half and is correlated with increased CCND2 expression (Steinthorsdottir et al., 2014). Further research is needed to identify additional potential targets of GLIS3 to fully elucidate the molecular mechanisms that underlie reduced GLIS3 and defective β cell mass expansion.

GLIS3 may protect pancreatic β cells against apoptosis

The loss of β cell mass is a critical feature for both T1D and T2D. Pro-inflammatory cytokines, such as interleukin 1β (IL1β) and interferon γ (IFNγ), and the saturated nonesterified fatty acid palmitate, may contribute to the β cell loss in T1D and T2D, respectively (Donath et al., 2005, Santin & Eizirik 2013). An in vitro study showed that Glis3 knockdown in INS-1 cells increased basal and inflammatory cytokine (IL1β + IFNγ)- or palmitate-induced β cell apoptosis. Reduced GLIS3 expression was found to modulate the alternative splicing of the pro-apoptotic BH3-only protein Bim, promoting the expression of the pro-death variant BimS and β cell death (Nogueira et al., 2013). These data suggest that proper GLIS3 expression could be required for β cell survival. This notion was
supported by a recent study in Glis3+/- mice on NODβ genetic background.

NODβ mice harbor congenic replacement of the potent Idd1 major histocompatibility complex susceptibility locus, a genetic model used to dissect the components of diabetes susceptibility without spontaneous autoimmunity against islets. Compared to C57BL/10, NODβ mice are more prone to islet β cell failure due to increased susceptibility to endoplasmic reticulum stress. Dooley and coworkers found that Glis3+/- mice developed glucose intolerance and increased level of proinsulin secretion on NODβ genetic background. These mice developed diabetes upon aging. They further reported that reduced GLIS3 expression results in enhanced susceptibility to apoptosis probably due to poor induction of a critical antiapoptotic factor, mesencephalic astrocyte-derived neurotrophic factor (MANF) during the unfolded protein response (Dooley et al. 2016).

Moreover, studies in adult mouse models reveal that GLIS3 is required for the maintenance of proper adult β cell function. GLIS3 also plays an essential role in obesity-induced β cell proliferation via the transactivation of Ccld2 (Yang et al. 2013). These may underlie the GWAS finding that the GLIS3 locus is also linked to T2D in people. Of note, the variations of GLIS3 associated with T1D and T2D are unique and do not overlap, likely because they confer their susceptibility effects via different mechanisms. Continued research into GLIS3 gene will provide new insights into disease pathogenesis and potential therapeutic target identification to combat the global epidemic of T1D and T2D.

**Conclusions**

Candidate gene studies and GWAS have identified over 50 and 100 susceptibility loci for common T1D and T2D, respectively (Todd 2010, Bonnefond & Froguel 2015, Yang & Chan 2016). Among the repertoire of susceptibility loci associated with diabetes, GLIS3 and insulin are the only two known monogenic diabetes genes whose variations are strongly associated with both common T1D and T2D (Yang & Chan 2016). These unique characteristics differentiate GLIS3 from other pancreatic transcription factors and highlight its roles in neonatal diabetes (Table 1) as well as in T1D and T2D (Table 2).

Glis3 global and β cell-specific knockout models, together with the data from β cell lines, provide the mechanistic basis for the genetic associations of the GLIS3 gene and neonatal diabetes, common T1D and T2D (Fig. 2). GLIS3 potently controls insulin gene transcription (Yang et al. 2009, 2013, ZeRuth et al. 2013) as well as likely insulin secretion (Kang et al. 2009b, Yang et al. 2013) and β cell survival (Nogueira et al. 2013, Dooley et al. 2016), which perturbations may underlie all three forms of diabetes. Mutations or deletions in GLIS3 impair the proper expression and/or function of GLIS3 and its direct downstream target NGN3, causing severely abnormal β cell development in utero and marked impairment in insulin production at birth, culminating in permanent neonatal diabetes (Yang et al. 2011). A new report further unveiled that the differential gene dosage of GLIS3 largely determines the expression levels of NGN3 and insulin, leading to variable phenotypes (Yang et al. 2016).

**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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