ISPAD CLINICAL PRACTICE CONSENSUS GUIDELINES 2022:

The diagnosis and management of monogenic diabetes in children and adolescents

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Conflicts of interest:
Pr Michel Polak MD, PhD has acted as scientific advisor for the development of the glibenclamide-glyburide suspension named AMGLIDIA in the European Union. The other authors have declared no conflicts of interest.

**Keywords:**

Diabetes Mellitus classification, Genetics, Monogenic, Neonatal Diabetes, MODY
WHAT IS NEW OR DIFFERENT

- Addition of recently described subtypes of monogenic diabetes, including causes associated with diabetes in infancy (CNOT1, ONECUT1, YIPF5, EIF2B1, KCNMA1); and genetic causes associated with diabetes later in life (TRMT10A, DNAJC3, KCNK16, DUT).
- The expanding list of genes causing monogenic diabetes further emphasizes comprehensive next-generation sequencing (NGS) as the best approach to allow for early molecular diagnosis that can guide treatment, rather than phenotype-based targeted testing, particularly for neonatal diabetes (NDM).
- Use of increasingly available publicly accessible information about specific variants to allow for the appropriate classification of pathogenicity of gene variants according to ACMG/AMP guidelines, bolstered by the establishment of international Monogenic Diabetes Expert Panels for gene curation and variant curation with the elaboration of gene-specific rules (https://clinicalgenome.org/affiliation/50016).
- Further understanding of the neuroendocrine aspects of ATP-sensitive potassium channels (KATP) related neonatal diabetes (KATP-NDM) is now included.
- Clarification that a small fraction of NDM is likely to be autoimmune type 1 diabetes (T1D) and autoimmune etiology distinct from T1D occurring in Trisomy 21.
- Among young persons with diabetes with a clinical diagnosis of type 2 diabetes (T2D), a low but significant fraction can be found to carry pathogenic MODY mutations; highlighting the importance of considering a monogenic cause even when obesity may be present.
- The rate of diabetes-related complications may be lower in HNF1A diabetes who have been treated with sulfonylureas (SU).
- Liver (with or without pancreas) transplantation can improve the outcomes of individuals with Wolcott-Rallison syndrome.

EXECUTIVE SUMMARY AND RECOMMENDATIONS

General aspects of monogenic diabetes
- Monogenic diabetes is uncommon, but accounts for ~2.5–6.5% of pediatric diabetes. B
- NGS enables the simultaneous analysis of multiple genes at a lower cost per gene providing comprehensive testing. B
NGS is the recommended methodology for study of suspected monogenic diabetes, unless a very specific and highly suggestive clinical scenario is present distinct phenotype of asymptomatic and stable mild fasting hyperglycemia. B

Results of genetic testing should be reported and presented to families in a clear and unambiguous manner. E

Referral to a specialist in monogenic diabetes or an interested clinical genetics unit is suggested, to guide specific management considerations and/or facilitate genetic testing of other related affected or pre-symptomatic individuals. E

**Neonatal diabetes**

- All infants diagnosed with diabetes in the first 6 months of life are recommended to have immediate molecular genetic testing. B
- Genetic testing maybe be considered in infants diagnosed between 6-12 months, especially in those without islet antibodies or who have other features suggestive of a monogenic cause. C
- A molecular genetic diagnosis of NDM provides essential information regarding treatment options, associated features, and diabetes course that may have a significant clinical benefit. B
- Treatment with SU, especially glibenclamide, is recommended for NDM with ABCC abnormalities. B
- Permanent neonatal diabetes (PNDM) due to ABCC8 mutations have similar neurodevelopmental difficulties as KCNJ11-PNDM individuals. B
- KCNJ11-PNDM patient-derived induced pluripotent stem cells (iPSC) cerebral organoid studies suggesting significant disruption of early neural development. B
- ABCC8 encoded SUR1 protein is crucial for retinal function and SU confers direct retinal neuroprotection through SUR1 mediated mechanisms. A
- Glibenclamide significantly improved neurological and neuro-psychological abnormalities in individuals with neonatal-onset diabetes due to KCNJ11 or ABCC8 mutations. Earlier treatment initiation was associated with greater benefits. B

**Maturity onset diabetes of the youth (MODY)**
The diagnosis of MODY is recommended in the following scenarios:

- A family history of diabetes in a parent and first-degree relatives of that affected parent in persons with diabetes who lack the characteristics of T1D and T2D.  

Mild stable fasting hyperglycemia which does not progress is recommended testing for GCK-MODY, which is the commonest cause of persistent, incidental hyperglycemia in the pediatric population.

In familial autosomal dominant symptomatic diabetes, mutations in the HNF1A gene (HNF1A-MODY) should be considered as the first diagnostic possibility.

Specific features can suggest subtypes of MODY, such as renal developmental disease or renal cysts (HNF1B-MODY), macrosomia and/or neonatal hypoglycemia (HNF4A-MODY), exocrine pancreatic dysfunction or pancreatic cysts (CEL-MODY), or hearing impairment and maternal inheritance of diabetes (mitochondrial diabetes).

Obesity alone should not preclude genetic testing in young persons, especially if:

- family history is strongly suggestive of autosomal dominant inheritance of diabetes
- if some affected family members are NOT obese
- and/or, there are no other features of metabolic syndrome.

Some forms of MODY are sensitive to sulphonylureas, such as HNF1A-MODY and HNF4A-MODY.

Mild fasting hyperglycemia due to GCK-MODY is not progressive during childhood. These persons do not develop complications and do not respond to low-dose insulin or oral agents, so should not receive treatment.

Establishing the correct molecular diagnosis of MODY is suggested due to the following reasons:

- avoids misdiagnosis as T1D or T2D
- may offer more accurate prognosis of risk of complications
- may avoid stigma and limitation of employment opportunity (especially in the case of GCK-MODY)
- may enable prediction of risk in relatives, including offspring
- can be cost-effective when appropriately selected individuals are screened
Introduction
Monogenic diabetes results from one or more defects in a single gene or chromosomal locus. The disease may be inherited within families as a dominant, recessive, or non-Mendelian trait or may present as a spontaneous case due to a de novo mutation.

Monogenic diabetes has been categorized as neonatal or early infancy diabetes (Table 1), MODY (Table 2), diabetes associated with extra-pancreatic features, and monogenic insulin resistance syndromes (Table 3).

Clinical relevance of diagnosing monogenic diabetes
- Identification of children with monogenic diabetes usually improves their clinical care.\(^1\)
- Making a specific molecular diagnosis helps predict the expected clinical course of the disease and guides the most appropriate management in a particular person with diabetes, including pharmacological treatment.
- Characterizing the specific molecular diagnosis has important implications for the family as it enables genetic counseling. It also frequently triggers extended genetic testing in other family members with diabetes or hyperglycemia who may also carry a causal mutation, thereby improving the classification of diabetes.\(^2,3\)

Selecting candidates for molecular testing
In contrast to T1D and T2D, where there is no single definitive diagnostic test, molecular genetic testing is both sensitive and specific for diagnosing monogenic diabetes. Appropriate informed consent/assent must be prospectively obtained from the affected person and/or legal guardians and should be strongly considered in persons with a suspected monogenic cause. Genetic testing is currently available (and may be free of charge on a research basis in certain academic institutions) in many countries around the world: https://www.diabetesgenes.org; http://monogenicdiabetes.uchicago.edu; www.mody.no; http://euro-wabb.org; https://www.ospedalebambinogesu.it/test-genetici-89757/; https://robertdebre.aphp.fr/equipes-cliniques/pole-biologie/genetique/genetique-moleculaire/#1461944418-1-40 and several commercial laboratories.

NGS enables the simultaneous analysis of multiple genes at a lower cost per gene and has already replaced many single gene testing by Sanger sequencing or other methods.\(^4-8\) Such NGS panels
provide an efficient means of comprehensive testing; however, because they are still expensive it remains appropriate to use a judicious approach to selecting persons with diabetes for molecular testing. Moreover, some NGS panels include genes lacking robust evidence for a causal role in monogenic diabetes and this can result in a misdiagnosis with adverse consequences for the person with diabetes and any family members who undergo cascade testing.

In NDM, genetic testing may be cost saving because of improved cheaper treatment; testing for MODY in appropriate populations can also be cost-effective.\textsuperscript{2,3,9} Targeted gene sequencing, however, may still be appropriate for some persons with diabetes, for example, a pregnant female with mild fasting hyperglycemia, in whom a rapid test to identify a \textit{GCK} mutation will inform management of the pregnancy. For most people with diabetes suspected to have monogenic cause, NGS provides an optimal approach for clinical care as it provides a genetic diagnosis that often precedes the development of additional clinical features, informs prognosis, and guides clinical management.\textsuperscript{2,3,9}

\textbf{When to suspect a diagnosis of T1D in children may not be correct?}

Features that suggest monogenic diabetes in children initially thought to have T1D are listed below. Except for the age of diagnosis less than 6 months, none of these are pathognomonic and should be considered together rather than in isolation:

1. Diabetes presenting before 6 months of age (as T1D is extremely rare in this age group), or consider NDM if diagnosis between 6-12 months if there is no evidence of autoimmunity or if the person with diabetes has other features such as congenital defects, or unusual family history.\textsuperscript{10,11}
2. Family history of diabetes in one parent and other first-degree relatives of that affected parent.
3. Absence of islet autoantibodies, especially if checked at diagnosis.
4. Preserved β-cell function, with low insulin requirements and detectable C-peptide (either in blood or urine) over an extended partial remission phase (at least 5 years after diagnosis).

\textbf{When to suspect a diagnosis of T2D in children may not be correct?}

In young people, T2D often presents around puberty and the majority are obese. As there is no diagnostic test for T2D and because obesity has become so common in children, children and adolescents with monogenic diabetes may also be obese and can be very difficult to distinguish from T2D.\textsuperscript{1} One of these recent studies found that 3% of obese youth with presumed T2D in fact carried
pathogenic monogenic diabetes variants. Features that suggest monogenic diabetes in young people with suspected T2D are listed below:

1. Lack of consistent severe obesity among affected family members.
2. Lack of consistent acanthosis nigricans and/or other markers of metabolic syndrome (hypertension, low HDL, etc.) among affected family members.
3. Family history of diabetes in one parent and other first-degree relatives of that affected parent, especially if any affected family member lacks obesity and other markers of metabolic syndrome.
4. Unusual distribution of fat, such as central fat with thin or muscular extremities.

**Interpretation of genetic findings**

Despite the obvious clinical benefits derived from genetic diagnostic services:

- Care needs to be exercised in the interpretation of genetic findings. The way the clinician interprets the genetic report will have a major effect on the future clinical management of the person with diabetes and his/her family.
- Results should be presented in a clear and unambiguous way to ensure that both clinicians and person with diabetes and their families receive adequate and understandable information. Specific recommendations describing the information that should be included in the molecular genetics laboratory report for MODY testing have been published.\(^\text{12}\)
- This includes the method used for mutation screening, limitations of the test, classification of the variant as pathogenic/likely pathogenic or of uncertain significance (with supporting evidence included where appropriate), and information about the likelihood of the disease being inherited by the offspring.
- The laboratory reporting the results should adhere to the ACMG/AMP variant classification guidelines.\(^\text{13}\) Many genetic testing laboratories have been participating in the Monogenic Diabetes Variant Curation Expert Panel (https://clinicalgenome.org/affiliation/50016/), that has provided more definitive curation of hundreds of variants that are freely accessible and recognized by the US FDA. This resource can be utilized to check whether a variant in question has been deemed “pathogenic” or “likely pathogenic” in which case there should be confidence that this is the cause of diabetes, or if “benign” or “likely benign” that another cause should be considered. Whether or not the testing report follows ACMG/AMP guidelines, when testing reveals a variant of uncertain significance (VUS), or when predictive
testing of asymptomatic individuals is requested, consultation with an expert center with experience in monogenic diabetes can often provide additional insight on the interpretation and recommendations of how to proceed.

**Specific subtypes of monogenic diabetes and their management**

In children, the majority of cases of monogenic diabetes result from mutations in genes causing β cell loss or dysfunction, although diabetes can rarely occur from mutations resulting in very severe insulin resistance. From a clinical perspective, specific scenarios when a diagnosis of monogenic diabetes should be considered include:

1. Diabetes presenting before 6 months of age, which is known as neonatal diabetes, abbreviated here as NDM.
2. Autosomal dominant familial mild hyperglycemia or diabetes.
3. Diabetes associated with extra-pancreatic features (such as congenital heart or gastrointestinal defects, brain malformations, severe diarrhea, or other autoimmune conditions in a very young child, to name a few).
4. Monogenic insulin resistance syndromes (see below: characterized by high insulin levels or high insulin requirements; abnormal distribution of fat with a lack of subcutaneous fat, especially in extremities; dyslipidemia, especially high triglycerides; and/or significant acanthosis nigricans).

1.-**Neonatal diabetes diagnosed within the first 6-12 months of life.**

- The clinical presentation of autoimmune T1D may rarely occur before age 6 months, with a recent study suggesting approximately 4% of cases may be T1D (see section of autoimmune monogenic diabetes).
- All infants diagnosed under 6 months should have genetic testing for monogenic cause, regardless of antibody status.
- Some cases of NDM can be diagnosed between 6-12 months, although the vast majority of these older infants with diabetes have T1D. Reasons to consider genetic testing in those diagnosed between 6-12 months include: negative autoantibody testing, extra-pancreatic features such as gastrointestinal anomalies or congenital defects, unusual family history, or even the development of multiple autoimmune disorders at a young age.
- Approximately half will require lifelong treatment to control hyperglycemia and are
denominated as permanent neonatal diabetes (PNDM).

- In the remaining cases, known as transient neonatal diabetes (TNDM), will remit within a few weeks or months although it might relapse later in life.
- PNDM and TNDM presents more frequently isolated or is the first feature to be noted.
- Some infants with diabetes show a variety of associated extra-pancreatic clinical features that may point to a particular gene; however, because these features often are not apparent initially, they will not always be helpful in guiding genetic testing and instead, early comprehensive testing will often allow for the genetic testing result to precede the recognition of other features (Table 1).

Many infants with diabetes with NDM are born small for gestational age, which reflects a prenatal deficiency of insulin secretion as insulin exerts potent growth-promoting effects during intrauterine development.\(^{18}\)

1a Transient neonatal diabetes from imprinting anomalies on 6q24

- The genetic basis of TNDM has been mostly uncovered: approximately two thirds of cases are caused by abnormalities in an imprinted region on chromosome 6q24.\(^{19,20}\)
- Activating mutations in either of the genes encoding the two subunits of the ATP-sensitive potassium (K\(_{\text{ATP}}\)) channel of the \(\beta\)-cell membrane (\(KCNJ11\) or \(ABCC8\)) cause the majority of the remaining cases (KATP-NDM).\(^{21}\)
- A minority of cases of TNDM is caused by mutations in other genes, including \(HNF1B\)^{22}, \(INS\)^{23} amongst others.

Anomalies at the 6q24 locus, spanning two candidate genes \(PLAGL1\) and \(HYMAI\), are the single most common cause of NDM and always result in TNDM.\(^{24}\) In normal circumstances, this region is maternally imprinted so that only the allele inherited from the father is expressed. TNDM is ultimately associated with overexpression of the imprinted genes,\(^{25}\) with three different molecular mechanisms identified to date: 1) paternal uniparental disomy of chromosome 6 (UPD6) either complete or partial; it accounts for 50% of sporadic TNDM cases, 2) unbalanced paternal duplication of 6q24 (found in most familial cases), and 3) hypomethylation of the maternal allele (found in sporadic cases).\(^{26}\)

Methylation defects may result from an isolated imprinting variant affect only the 6q24 locus or may
arise in the context of a generalized hypomethylation syndrome causing by multiple imprinting alterations across the genome, i.e. multi-locus imprinting disturbance (MLIDs) along with other clinical features including congenital heart defects, brain malformations, etc.\textsuperscript{27} Some cases of TNDM secondary to multiple methylation defects are caused by recessively acting mutations in \textit{ZFP57}, a gene on chromosome 6p involved in the regulation of DNA methylation.\textsuperscript{28}

Neonates with diabetes with 6q24 abnormalities are born with severe intrauterine growth retardation (IUGR) and one third of them show macroglossia and, more rarely, an umbilical hernia is present. and develop severe but nonketotic hyperglycemia very early on, usually during the first week of life.\textsuperscript{26,29}

- Despite the severity of the initial presentation, the insulin dose can be tapered quickly so that most infants do not require any treatment by a median age of 12-14 weeks and the rate of remission is close to 1.0.\textsuperscript{30}
- Because most cases exhibit some degree of endogenous β-cell function, insulin therapy is not always necessary, and these infants may respond to oral SU or other drugs used for T2D.\textsuperscript{30-33}
- In some, a transition to remission has been observed with no need for insulin therapy or initial SU treatment.\textsuperscript{33}
- Some cases with TNDM have shown a positive response to SU.\textsuperscript{33,34}
- Following remission, a low proportion of affected infants and children will exhibit clinically significant hypoglycemia that in some cases requires long-term treatment.\textsuperscript{35,36} During remission, transient hyperglycemia may occur during intercurrent illnesses.\textsuperscript{37}
- Over time, diabetes relapses in at least 50-60\% of these young people and even in more than 85\% in one large cohort followed until 18 years of age,\textsuperscript{38} usually around puberty, although recurrences have been reported as young as 4 years of age.

Therefore, parents of children with TNDM should internalize the high risk of their child’s diabetes relapse and may benefit from annual HbA1c testing. Relapse clinically resembles early-onset T2D and is characterized by a loss of the first-phase insulin secretion.\textsuperscript{33} The long term metabolic and socio-educational follow-up has allowed to demonstrate that these persons have decreased educational attainment, and those with diabetes have lower insulin secretion capacity.\textsuperscript{39}

The phases described above do not present irremediably in every affected child. Interestingly, some
carrier relatives develop T2D or gestational diabetes in adulthood without any evidence of having had NDM, as well as in a small fraction of people with early-onset, non-obese, non-autoimmune diabetes without a history of NDM. This suggests significant variability in phenotype, possibly related to other genetic or epigenetic factors that may influence the clinical expression alterations of chromosome 6q24.19,30

The role of genetic counseling depends on the underlying molecular mechanism. Uniparental disomy of chromosome 6 is generally sporadic and therefore the risk of recurrence in siblings and offspring is low. When paternal duplication of the 6q24 region is found, affected newborn males have a 50% chance as adults of transmitting the mutation and the disease to their children. In contrast, newborn affected females will as adults pass on the duplication, but their children will not develop the disease. In this case, TNDM may recur in the next generation as their asymptomatic sons pass on the molecular defect to their own children. Some methylation defects (i.e. ZFP57 mutations) show an autosomal recessive inheritance and hence the recurrence risk is 25% for siblings and almost negligible for the offspring of an affected individual.

1b Permanent neonatal diabetes and to mutations in the K\textsubscript{ATP} channel genes (KATP-NDM)
KATP-NDM is the commonest cause of PNDM\textsuperscript{40-44} and the second commonest cause of TNDM.\textsuperscript{21} The prevalence of KATP-NDM in a specific group depends on the degree of consanguinity. In outbred population the commonest known cause of PNDM are abnormalities in the K\textsubscript{ATP} channel or INS genes \textsuperscript{9,45}. If parents are related, Wolcott-Rallison syndrome or homozygous mutations in the GCK gene are the most common etiologies\textsuperscript{46}. Up to 20% of PNDM cases remain unknown.

- K\textsubscript{ATP} channels are hetero-octameric complexes formed by four pore-forming Kir6.2 subunits and four SUR1 regulatory subunits, encoded by the genes KCNJ11 and ABCC8 respectively.\textsuperscript{47} They regulate insulin secretion by linking intracellular metabolic state to the β-cell membrane electrical activity. Any increase in the intracellular metabolic activity induces a rise in the ATP/ADP ratio within the pancreatic β-cell. The high ATP/ADP ration closes the K\textsubscript{ATP} channels, and leading to the cell membrane depolarization which ultimately triggers insulin secretion.\textsuperscript{48}

- Activating mutations in KCNJ11 or ABCC8, prevent K\textsubscript{ATP} channel closure and hence reduce insulin secretion in response to hyperglycemia, resulting in diabetes\textsuperscript{41,40,42,44} (Figure 1).
loss-of-function nonsense mutation in \textit{ABCC8}, resulting in gain-of-channel function, has also been reported.\textsuperscript{49}

Approximately 90\% of persons with \textit{KCNJ11} mutations have PNDM while \textasciitilde10\% develop TNDM, whereas \textit{ABCC8} mutations cause TNDM more frequently (\textasciitilde66\%).\textsuperscript{41,50} There are no significant differences in the severity of IUGR or the age at diagnosis of diabetes between the two subtypes of NDM.\textsuperscript{21} \textit{K}_{\text{ATP}} channel mutations typically show milder IUGR and are diagnosed slightly later than infants with 6q24 abnormalities, indicating a less severe insulin deficiency during the last months of intrauterine development and at the time birth. In \textit{K}_{\text{ATP}}-TNDM, diabetes usually remits later and relapses earlier than in 6q24-TNDM.\textsuperscript{21}

The low or undetectable C-peptide levels and frequent presentation with diabetic ketoacidosis in KATP-NDM suggest insulin dependency.\textsuperscript{51} In addition to diabetes, about 20\% of affected children with \textit{KCNJ11} mutations present with associated neurological features\textsuperscript{40,52,53} in keeping with the expression of \textit{K}_{\text{ATP}} channels in neurons and muscle cells.\textsuperscript{48,54} The most severely damaging mutations are also associated with marked developmental delay and early-onset epilepsy, known as DEND (developmental delay, epilepsy and NDM) syndrome. An intermediate DEND syndrome characterized by neonatal diabetes and less severe developmental delay without epilepsy is more common. Neurological features have been reported less frequently in persons with \textit{ABCC8} mutations.\textsuperscript{41,42} Recent studies utilizing detailed testing have revealed that mild neurodevelopmental abnormalities occur even in those with milder mutations previously thought to cause only isolated diabetes. With some studies using sibling controls, mild but significant impairments were found in several domains including IQ, measures of academic achievement and executive function. Many of these children met criteria for developmental coordination disorder (particularly visual-spatial dyspraxia), attention deficit hyperactivity disorder, anxiety disorder, or autism, and/or had behavioral or sleep difficulties.\textsuperscript{38,55-57} In addition, those with PNDM due to \textit{ABCC8} mutations had a similar range of difficulties as those with \textit{KCNJ11} mutations.\textsuperscript{58}

- Approximately 90\% of children with activating mutations in the KATP channel genes can be switched from insulin to off-label SU tablets.\textsuperscript{59-61} A suspension of glibenclamide has shown to be safe and effective in individuals with NDM,\textsuperscript{62} and was authorization in the European Union.\textsuperscript{63}
• Treatment with SU dramatically improves glycemic management and appears to be durable long-term with only minimal mild hypoglycemia.\textsuperscript{64,65}

• The glibenclamide doses required when calculated per body weight are higher compared to the dose used in adults with T2D, typically needing around 0.5 mg/kg/day, although doses as high as 2.3 mg/kg/day have been occasionally reported.\textsuperscript{66-68} The dose required depends mostly on the age at which the person starts SU, as well as the specific mutation.\textsuperscript{69,70}

• Many persons have been able to progressively reduce the dose after transition while maintaining excellent glycemic management.\textsuperscript{71,72} The only side effects reported to date are transient diarrhea and staining of the teeth.\textsuperscript{73,74} Recently, it has been reported that celiac disease may cause secondary SU failure not explained by low compliance to therapy.\textsuperscript{75}

• Insulin secretion in children with diabetes treated with adequate SU doses seem to be driven mostly by food intake via non-KATP dependent pathways. Meals composed of either all carbohydrate or only protein/fat resulted in similar insulin response, highlighting the importance of carb intake with most meals to avoid post-prandial hypoglycemia.\textsuperscript{76}

• Some brain imaging studies have shown that SU may penetrate blood-brain barrier, but maintenance of levels may limit benefit.\textsuperscript{77-79}

• SU may partially improve some of the neurological symptoms, but the degree of improvement possible may also depend on how early treatment is started.\textsuperscript{80-83}

The \textit{ABCC8} encoded SUR-1 protein is crucial in retinal function and SU (glibenclamide) confers direct retinal neuroprotection through SUR-1 mediated mechanisms.\textsuperscript{84,85} A recent study utilized patient-derived iPSCs to generate cerebral organoids and found major defects in early development of cortical neuronal network in V59M mutants compared to controls, that could partially be rescued by the SU tolbutamide.\textsuperscript{86}

Activating mutations in \textit{KCNJ11} causing NDM are always heterozygous. Since about 90\% of these mutations arise \textit{de novo}, there is usually no family history of NDM\textsuperscript{87} but familial cases show an autosomal dominant inheritance. Recurrence risk for the offspring of an affected person is 50\%. This is also true for most people with activating mutations in \textit{ABCC8}. However, some persons are homozygous or compound heterozygous for two different mutations and NDM is recessively inherited.\textsuperscript{82} In this case, the risk of NDM for future siblings is 25\% but almost non-existent for the offspring of the affected person unless the other parent is also carrier for the same mutation. Germline
mosaicism (mutations present in the gonads but not detectable in blood) has been reported in several families and hence unaffected parents of a child with an apparently de novo mutation should be advised that the recurrence risk in siblings is low but not negligible.

**Neonatal diabetes due to mutations in INS gene.** Mutations in the proinsulin gene (INS) are the second most common cause of PNDM after KATP channel mutations. Individuals with diabetes due to INS mutations lack any extra-pancreatic features and are insulin dependent. Dominant heterozygous mutations are most common and usually result in a misfolded proinsulin molecule that is trapped and accumulated in sub-cellular compartments, leading to endoplasmic reticulum stress and beta-cell apoptosis. Recessive biallelic (homozygous or compound heterozygous) mutations lead to loss or inactivation of proinsulin. These mutations do not cause slowly progressive β-cell destruction but result in a lack of insulin biosynthesis before and after birth, which explains much lower birth weights and earlier presentation of diabetes in affected children. Since the disease is recessively inherited, there will be a 25% recurrence risk in siblings when each parent has been confirmed to be a carrier of a causal INS variant.

The severity of IUGR in children with heterozygous INS mutations is similar to those with KATP channel mutations, but they present at somewhat later ages.

- Although the diabetes is still diagnosed most often before 6 months of age, it can also occur up to a year of age or even later; therefore genetic testing should be considered in children with antibody-negative T1D presenting at early ages, as well as in those with a MODY-like phenotype.
- Most heterozygous INS mutations are sporadic de novo mutations but about 20% of probands have a family history of autosomal dominant NDM.

**Wolcott–Rallison syndrome (WRS).** This rare autosomal recessive syndrome is the commonest cause of PNDM in consanguineous population and characterized by early-onset diabetes mellitus, spondyloepiphyseal dysplasia, and recurrent hepatic and/or renal dysfunction. WRS is caused by biallelic mutations in the EIF2AK3 (eukaryotic translation initiation factor alpha 2-kinase 3) gene, which encodes a protein involved in the regulation of the endoplasmic reticulum (ER) stress response. Pancreatic development is rather normal in the absence of the functional protein, but misfolded proteins accumulate within the endoplasmic reticulum after birth and eventually induce β-cell apoptosis. Although diabetes usually manifests during infancy, it might not present until 3-4 years of
age. Diabetes may be the first clinical manifestation of the syndrome and therefore this diagnosis needs to be considered even in children with isolated PNDM especially if they were born to consanguineous parents or from a highly inbred population.\cite{99,100} Since the disease is recessively inherited, there is a 25% recurrence risk in siblings. Fulminant hepatic failure is the main cause of death in persons with WRS and currently there is no agent to reverse this abnormality\cite{101}; however, recent reports indicate that liver (with or without pancreas) transplantation can be life-saving and improve the outcomes of individuals with this syndrome.\cite{101-104}

**Neonatal diabetes due to GCK mutations** The enzyme glucokinase is considered the glucose sensor of the β-cells, as it catalyzes the rate-limiting step of glucose phosphorylation and therefore enables the β-cell to respond appropriately to the degree of glycemia.\cite{105}

- Complete glucokinase deficiency secondary to mutations in both alleles, either homozygous or compound heterozygous, prevents the β-cells from secreting insulin in response to hyperglycemia.\cite{106,107}
- Neonates present with severe IUGR, are usually diagnosed with diabetes during the first few days of life and require exogenous insulin therapy. Apart from diabetes, they do not show any relevant extrapancreatic features.\cite{106-113}

**GCK** is responsible for not more than 2-3% of cases of PNDM overall,\cite{46} but has an increased prevalence in regions with a high degree of consanguinity.\cite{114} This type of PNDM is inherited in a recessive manner so the recurrence risk for future siblings is 25%. This diagnosis should be strongly considered in probands born to parents with asymptomatic mild hyperglycemia; therefore, measuring fasting blood glucose in the parents of any child with NDM, even when there is no known consanguinity or family history of diabetes, is often recommended.

Few studies have evaluated the risk of microvascular complications in NDM, but one study showed that individuals with KATP/PNDM or abnormalities in the insulin gene (INS) do not seem prone to severe eye complications even after a median diabetes duration of 24 years.\cite{115}

1.d IPEX syndrome and other monogenic causes of autoimmune diabetes

- Mutations in at least 9 different genes are now known to cause autoimmune syndromes that can include neonatal and infancy-onset diabetes associated with pancreatic islet
autoantibodies: *AIRE, CTLA4, FOXP3, IL2RA, ITCH, LRBA, STAT1, STAT3 and STAT5B*.

- These monogenic conditions that do cause autoimmune diabetes share basic features with pediatric T1D\textsuperscript{15,116-118} and correspond to the previously mentioned rare cases of T1D in the first months of life.
- Rarely, some cases of diabetes with onset during the first six months of life have an autoimmune basis, it is now accepted that mutations in a range of genes related to immune function (such as *FOXP3, STAT3 or LRBA*) are at least as likely as T1D.

Mutations in the *FOXP3* gene are responsible for the immune dysregulation, polyendocrinopathy, enteropathy, X-linked (IPEX) syndrome.\textsuperscript{119,120} IPEX syndrome is clinically heterogeneous ranging from severe intrauterine forms to moderate phenotypes, as is described recently in different cohorts \textsuperscript{117,121,122}. Among male infants who present with diarrhea, eczema, autoimmune diabetes, immune deficiency, and/or life-threatening infection mutations in *FOXP3* should be considered.\textsuperscript{123,124} Treatment with immunosuppressive agents (sirolimus or steroids).\textsuperscript{123,124} Alternatively, allogeneic hematopoietic stem cell transplantation (HSCT) with reduced-intensity conditioning is recommended.\textsuperscript{125} Survival is similar with both immunosuppressant treatment and HSCT, but with HSCT higher rates of disease-free survival and improved quality of life are shown.\textsuperscript{126}

In addition to mutations in *FOXP3* “classic IPEX”, there is a group with an “IPEX-like” phenotype with defects in other genes. Examples include individuals with heterozygous mutations in *CTLA4* causing autoimmune lymphoproliferative syndrome which can include autoimmune diabetes, enteropathy, cytopenias and thyroiditis\textsuperscript{127}; individuals with recessive mutations in the ubiquitin ligase gene (*ITCH*) presenting multisystem autoimmune disease with facial dysmorphism\textsuperscript{128}; individuals with bi-allelic mutations in *IL2RA* (interleukin 2 receptor subunit alpha) resulting in immunodeficiency 41 syndrome, with lymphoproliferation, other autoimmunity and autoimmune diabetes\textsuperscript{129,130}), as well as individuals with recessively inherited mutations in *LRBA* reported as a cause of immunodeficiency-8 with autoimmune enteropathy, T1D, autoimmune hypothyroidism, and autoimmune hemolytic anemia.\textsuperscript{118}

The proteins encoded by the *STAT3, STAT1* and *STAT5B* genes are transcription factors involved in the cellular response to cytokines and growth factors. Activating mutations in *STAT3* cause multiple autoimmune disease as enteropathy, hematological autoimmune disorders, autoimmune cytopenia
and autoimmune diabetes which often presents in the neonatal period.\textsuperscript{116,131} Persons with gain of function mutations in \textit{STAT1} present with chronic fungal infections including respiratory tract infections with a subset of people developing severe organ specific autoimmunity including T1D.\textsuperscript{132} On the other hand, loss of function mutations in \textit{STAT5B} are associated with disorders characterized by allergic or autoimmune manifestations.

Loss of function mutations in \textit{AIRE} gene cause polyendocrine autoimmune syndrome type 1 (APS1), characterized by chronic mucocutaneous candidiasis, hypoparathyroidism and autoimmune adrenal insufficiency. In addition, 13\% of individuals present with diabetes by 30 years of age.\textsuperscript{128}

\textbf{1.d. Other causes of neonatal diabetes}

More than 30 genetic subtypes of neonatal diabetes have been described. The clinical features seen in the more common causes of neonatal and infancy-onset diabetes are shown in Table 1. Pancreatic scanning is unreliable in neonates and so it is best to use functional tests of exocrine pancreatic function (fecal elastase and fecal fats) when assessing if pancreatic aplasia is present.\textsuperscript{133,134} Apart from KATP-NDM and some persons with \textit{SLC19A2} mutations causing thiamine-responsive megaloblastic anaemia (TRMA) syndrome,\textsuperscript{135} all other causes need to be treated with subcutaneous insulin. Children with pancreatic aplasia/hypoplasia will also require exocrine pancreatic supplements.

\textit{Genetic testing should be performed as soon as diabetes is diagnosed in a child aged less than 6 months.}

- All infants diagnosed with diabetes in the first 6 months of life should have immediate molecular genetic testing to define their subtype of monogenic neonatal diabetes mellitus (NDM), as T1D is extremely rare in this subgroup.
- Genetic testing will allow diagnosis of a specific type of monogenic diabetes in over 80\% of children whose diabetes is diagnosed before the age of 6 months. As discussed above, this will influence treatment as well as prediction of clinical features.
- It is no longer necessary to wait to see if the diabetes resolves or for other features to develop, as major labs will offer comprehensive testing of all NDM subtypes as well as very rapid testing of subtypes that alters treatment.
2.- Autosomal dominant familial mild hyperglycemia or diabetes (MODY)

A familial form of mild diabetes presenting during adolescence or in early adulthood was first described many years ago.\textsuperscript{10,136} Even though diabetes presented in young people, the disease clinically resembled elderly-onset non-insulin dependent diabetes and the newly recognized subtype of familial diabetes became known by the acronym MODY (maturity-onset diabetes of the young).\textsuperscript{137} As MODY persons passed on the disease to their offspring following an autosomal dominant pattern of inheritance, it was quickly suspected that it might be a monogenic disorder.\textsuperscript{138} MODY is by far the commonest type of monogenic diabetes. All currently known subtypes of MODY are caused by dominantly acting heterozygous mutations in genes important for the development or function of β-cells. Over the last few years, however, a number of forms of monogenic diabetes clinically and genetically different from MODY have been identified.\textsuperscript{1} Individuals may harbor dominant mutations arising\textit{de novo}; in such cases, where family history suggesting a monogenic condition is lacking.\textsuperscript{40,89,139} These facts, along with a widespread lack of awareness, hinder clinical diagnosis so that the majority of children with genetically proven monogenic diabetes are initially misdiagnosed as having T1D\textsuperscript{140,141} or T2D.\textsuperscript{142,143} Although monogenic diabetes is uncommon, it accounts for 2.5–6% of pediatric diabetes cases.\textsuperscript{144-149}

- MODY syndromes are forms of monogenic diabetes characterized by impaired insulin secretion, with minimal or no defects in insulin action.\textsuperscript{150}
- Most cause isolated diabetes and therefore may be misdiagnosed as either familial T1D or T2D.\textsuperscript{142,151}
- Classic criteria for MODY include family history of diabetes; however, sporadic\textit{de novo} mutations in a number of causative genes have been reported.\textsuperscript{152}
- The different genetic subtypes of MODY differ in age of onset, pattern of hyperglycemia, and response to treatment.
- Three genes are responsible for the majority of MODY cases (\textit{GCK}, \textit{HNF1A} and \textit{HNF4A}) and will be described in some detail below.
- Most MODY subtypes will have a phenotype of isolated diabetes or stable mild fasting hyperglycemia, but some MODY genes have additional features such as renal cysts (see \textit{HNF1B} below) or pancreatic exocrine dysfunction.\textsuperscript{153}
At least 14 different genes have been reported to cause diabetes with a MODY-like phenotype (Table 2), and some panels will include all of these genes, or possibly also many other genes associated with exceedingly rare recessive causes. It is reasonable to consider including syndromic causes, such as mitochondrial, as diabetes can often be the first presenting feature and a molecular diagnosis can thereby guide monitoring and treatment of other associated features. In the modern era of expanded testing by many different laboratories, caution must be used when interpreting test results, as often there is very little information available to support the causality of rare variants in uncommon subtypes.

2.a Mild fasting hyperglycemia due to glucokinase gene mutations (GCK-MODY, MODY2)

- GCK-MODY is the commonest subtype of monogenic diabetes in the pediatric diabetes clinic and its clinical phenotype is remarkably homogeneous among affected persons.
- In contrast to other subtypes of monogenic diabetes, GCK-MODY persons regulate insulin secretion adequately but around a slightly higher set point than other people. As a result, they show non-progressive mild hyperglycemia from birth.\(^{154}\)
- HbA1c is mildly elevated but usually below 7.5%.\(^{155}\)
- Despite the mild fasting hyperglycemia, there is usually a small increment in blood glucose during an oral glucose tolerance test (OGTT) (<60 mg/dL or <3.5 mmol/L)\(^{156}\) although this should not be considered an absolute criterion because of the variability of the OGTT.
- Since the degree of hyperglycemia is not high enough to cause osmotic symptoms, most cases are usually diagnosed incidentally when blood glucose is measured for any other reason.
- The incidental finding of mild hyperglycemia (5.5-8 mmol/L or 100-145 mg/dL) in otherwise asymptomatic children and adolescents raises the possibility that these people subsequently develop T1D or T2D. In the absence of concomitant pancreatic autoimmunity, the risk of future T1D is minimal.\(^{157}\) and a significant proportion will have a heterozygous mutation in GCK.\(^{158}\) In peripubertal children and adolescents with a diagnosis of T2D, the lack of obesity or other signs of insulin resistance should raise concern about the diagnosis of MODY.
- Since blood glucose does not deteriorate significantly over time, this subtype of monogenic diabetes is rarely associated with chronic microvascular or macrovascular complications of
diabetes.\textsuperscript{159,160} and affected individuals do not generally require any treatment\textsuperscript{161} except in the setting of pregnancy where an affected mother has an unaffected fetus and there is \textit{in utero} evidence of accelerated growth.\textsuperscript{162}

- When the clinical features of asymptomatic, long standing, stable mild fasting hyperglycemia are present, specific testing of \textit{GCK} is be appropriate.

Very often, the affected parent remains undiagnosed or has been misdiagnosed with early-onset T2D. Measuring fasting glucose in apparently unaffected parents is important when considering a diagnosis of a \textit{GCK} mutation. GCK-MODY may first be diagnosed during pregnancy; it represents approximately 2-6\% of cases of gestational diabetes and can be differentiated from gestational diabetes on the basis of clinical characteristics and fasting glucose.\textsuperscript{163,164}

Of note, the presence of a \textit{GCK} mutation does not protect against the concurrent development of polygenic T2D later in life, which occurs at a similar prevalence than in the general population.\textsuperscript{165} \textit{GCK}-PNDM may manifest in \textit{GCK}-MODY families especially in the setting of consanguinity.

2.b Familial diabetes due to \textit{HNF1A-MODY} (MODY3) and \textit{HNF4A-MODY} (MODY1)

- The possibility of monogenic diabetes should be considered whenever a parent of a diabetic child has diabetes, even if they are thought to have T1D or T2D.
- Glucose intolerance associated with HNF1A- and HNF4A-MODY usually becomes evident during adolescence or early adulthood. In the early stages of the disease, fasting blood glucose may be normal, but there may be a large increment in blood glucose (>80 mg/dL or 5 mmol/L) after meals or at 2 hours during an OGTT.\textsuperscript{156}
- Over time, fasting hyperglycemia and osmotic symptoms (polyuria, polydipsia) present but they rarely develop ketosis because some residual insulin secretion persists for many years.
- Chronic complications of diabetes are frequent, and their development is related to the degree of glycemic management.\textsuperscript{166}
- HNF1A-MODY is the most common form of monogenic diabetes that results in familial \textit{symptomatic} diabetes, with heterozygous HNF1A mutations being about 10 times more frequent than heterozygous mutations in HNF4A.\textsuperscript{167} Therefore, HNF1A-MODY is the first diagnostic possibility to be considered in families with autosomal dominant symptomatic
diabetes.

- Persons with HNF1A-MODY demonstrate impaired incretin effect and inappropriate glucagon responses to OGTT.\textsuperscript{168}

- Despite the association of \textit{HNF1A} mutations with microvascular complications, recent data suggest that timely initiation of treatment with SUs is associated with lower rate of microvascular complications that T1D.\textsuperscript{169} \textit{HNF1A} mutations are also associated with an increased frequency of cardiovascular disease and mortality.\textsuperscript{170}

Mutations in \textit{HNF1A} show a high penetrance so that 63\% of mutation carriers develop diabetes before 25 years of age, 79\% before age 35 and 96\% before 55 years.\textsuperscript{1} The age at diagnosis of diabetes is partly determined by the location of the mutation within the gene.\textsuperscript{171,172} Persons with mutations affecting the terminal exons (8 to 10) are diagnosed, on average, 8 years later than those with mutations in exons 1 to 6. On the other hand, exposure to maternal diabetes \textit{in utero} (when the mutation is maternally inherited) brings forward the age at onset of diabetes by about 12 years.\textsuperscript{156} In the pediatric population, diabetes in \textit{HNF4A} mutation carriers tend to appear at a similar age to persons with mutations in \textit{HNF1A}.\textsuperscript{146}

Some differential clinical characteristics may be noted between persons with mutations in \textit{HNF4A} and \textit{HNF1A}; however, they would not often help in choice of genes to be sequenced and it would be preferable to test all genes simultaneously with NGS whenever possible.\textsuperscript{173}

- Persons with \textit{HNF1A} mutations typically have a low renal threshold for glucose reabsorption due to impaired renal tubular transport of glucose and may present postprandial glycosuria before developing significant hyperglycemia.\textsuperscript{174}

- In addition to diabetes, carriers of the p.Arg76Trp (R76W) mutation in \textit{HNF4A} present with an atypical form of Fanconi syndrome including hypercalciuria and nephrocalcinosis.\textsuperscript{175}

- About 50\% of \textit{HNF4A} mutation carriers are macrosomic at birth and 15\% have diazoxide-responsive neonatal hyperinsulinemic hypoglycemia.\textsuperscript{176} In this case, hyperinsulinism typically remits during infancy and individuals develop diabetes from adolescence.\textsuperscript{177,178} Hyperinsulinemic hypoglycemia has also been reported in \textit{HNF1A} mutation carriers\textsuperscript{179} but this is very uncommon.

Persons with both \textit{HNF1A} and \textit{HNF4A}-diabetes can initially be treated with diet although they will have marked postprandial hyperglycemia with high carbohydrate food.\textsuperscript{156}
• Most will need pharmacological treatment as they show progressive deterioration in glycemic management. They are extremely sensitive to SUs,\textsuperscript{180} which usually allow a better glycemic management than that achieved on insulin, especially in children and young adults.\textsuperscript{181}

• The initial dose of SUs should be low (one-quarter of the normal starting dose in adults) to avoid hypoglycemia. As long as there are no problems with hypoglycemia, they can be maintained on low-dose SUs (e.g. 20–40 mg gliclazide daily) for decades.\textsuperscript{182,183}

• If there is hypoglycemia despite dose titration of a once or twice daily SU preparation, a slow-release preparation or meal time doses with a short-acting agent such as a meglitinide may be considered.\textsuperscript{184} A randomized controlled trial comparing a glucagon-like peptide receptor agonist (GLP1RA) with a SU demonstrated lower fasting glucose in those treated with the GLP1RA.\textsuperscript{168}

3.- **Diabetes associated with extra-pancreatic features**

A monogenic disorder should be considered in any child with diabetes associated with multi-system extrapancreatic features,\textsuperscript{185} or in young-onset diabetes when consanguinity is known or suspected, even when syndromic features are not obvious.\textsuperscript{186} These syndromes may either cause NDM (Table 1) or present later in life (see below). The Online Mendelian Inheritance in Man website (www.ncbi.nlm.nih.gov/omim or www.omim.org) can help with clinical features and to know if the gene for a particular syndrome has been defined and hence molecular genetic testing is available. Genetic testing for some of these conditions is available on a research basis at www.euro-wabb.org.\textsuperscript{187} The most common syndromes usually presenting beyond infancy are described in some detail below. A number of rare syndromes that include diabetes may also be tested through a gene panel approach (for example, see https://www.diabetesgenes.org/).

**Diabetes insipidus, diabetes mellitus, optic atrophy and deafness (DIDMOAD) syndrome (Wolfram syndrome, WFS).** The combination of diabetes and progressive optic atrophy below 16 years of age is diagnostic of this autosomal recessive syndrome.\textsuperscript{188} Non-autoimmune, insulin requiring diabetes, presenting at a mean age of 6 years, is usually the first manifestation of the disease.\textsuperscript{189} Other reported features, including sensorineural deafness, central diabetes insipidus, urinary tract dysfunction and neurological symptoms develop later in a variable order even within the same family.\textsuperscript{190-192} Many individuals with WFS are initially diagnosed as having T1D and subsequent loss of vision, which occurs approximately four years after diabetes diagnosis, may be misdiagnosed
Persons with WFS die at a median age of 30 years, mainly from neurodegenerative complications. At least 90% of these people harbor biallelic mutations in the WFS1 gene. This gene encodes WFS1, which is an endoplasmic reticulum (ER) transmembrane protein important for the negative regulation of ER stress and the maintenance of cellular calcium homeostasis. Preclinical studies in cell and animal models suggest that therapeutic strategies targeting ER calcium homeostasis may be beneficial. However, a recent trial of using dantrolene sodium in 19 WFS subjects showed no significant improvement in β-cell, retinal or neurological function.

A second variant of the syndrome (WFS2) has been described in association with mutations in CISD2 gene. Persons with this rare variant do not develop diabetes insipidus but present with additional symptoms including bleeding diathesis and peptic ulcer disease.

The current management of WFS involve symptomatic treatment of the associated features with no agents to cure or slow the disease progression.

**Renal cysts and diabetes (RCAD) syndrome (HNF1B-MODY or MODY5).** Although initially described as a rare subtype of familial diabetes, it is now clear that persons with heterozygous mutations in HNF1B rarely present with isolated diabetes. In contrast, renal developmental disorders (especially renal cysts and renal dysplasia) are present in almost all persons with HNF1B mutations or gene deletions and constitute the main presentation in children, even in the absence of diabetes. Genital-tract malformations (particularly uterine abnormalities), hyperuricemia and gout can also occur, as well as abnormal liver function tests. Diabetes develops later, typically during adolescence or early adulthood although TNDM has been reported in a few cases. In addition to insulin deficiency related to pancreatic hypoplasia, affected persons also show some degree of hepatic insulin resistance, which explains why they do not respond adequately to SU treatment and require early insulin therapy. Moreover, mutation carriers have lower exocrine pancreatic function with reduced fecal elastase; this involves both ductal and acinar cells. Therefore, the phenotype of RCAD is highly variable even within families sharing the same HNF1B mutation and therefore this diagnosis should be considered not only in the diabetes clinic but also in other clinics (nephrology, urology, gynecology, etc.). In people with diabetes found to have renal cysts, imaging of the pancreas is indicated, since the absence of the pancreatic body and/or tail is
highly indicative of HNF1B-MODY. Fecal elastase should also be measured, as this is always abnormal in persons with HNF1B-MODY. Importantly, a family history of renal disease or diabetes is not essential to prompt genetic testing, as de novo mutations and deletions of this gene are common (one-third to two-thirds of cases).

**Mitochondrial diabetes.** Diabetes due to mitochondrial mutations and deletions is rarely seen (<1%) in children and adolescents as the vast majority of persons develop diabetes as young or middle-aged adults. The most common form of mitochondrial diabetes is caused by the m.3243A>G mutation in mitochondrial DNA. Diabetes onset is usually insidious but approximately 20% may have an acute presentation, even in diabetic ketoacidosis. Although it typically presents in adulthood, some cases have been reported in adolescents with a high degree of heteroplasmy. Mitochondrial diabetes should be suspected in persons presenting with diabetes and sensorineural hearing loss inherited from mother's side, or diabetes and progressive external ophthalmoplegia. Interestingly, the same m.3243A>G mutation also causes a much more severe clinical syndrome known as MELAS (myopathy, encephalopathy, lactic acidosis and stroke).

Persons with mitochondrial diabetes may respond initially to diet or oral hypoglycemic agents but often require insulin treatment within months or years. Metformin should be avoided as it interferes with mitochondrial function and may trigger episodes of lactic acidosis.

The penetrance of diabetes in mutation carriers depends on the age considered, but is estimated to be above 85% at 70 years. Affected males do not transmit the disease to their offspring. In contrast, females transmit the mutation to all their children, although some may not develop the disease. In addition to the m.3243A>G mutation, early-onset diabetes (even in infancy) has been reported in other less common mitochondrial disorders such as Kearns-Sayre syndrome and Pearson syndrome.

**Diabetes secondary to monogenic diseases of the exocrine pancreas.** Heterozygous mutations in CEL, which encodes a pancreatic lipase, cause CEL-MODY or MODY8, an autosomal dominant disorder of pancreatic exocrine insufficiency and diabetes. Importantly, the exocrine component of the syndrome is initiated already in childhood, 10-30 years before diabetes develops, and can be revealed by lowered fecal elastase and/or pancreatic lipomatosis. Diabetes typically develops in
the 30-40s together with pancreatic cysts. The \textit{CEL} gene is highly polymorphic and extremely difficult to sequence. A recent paper by El Jellas et al describes how to correctly diagnose CEL-MODY. The disease mechanism of CEL-MODY involves protein misfolding/aggregation, endoplasmic reticulum stress and proteotoxicity. Other autosomal dominant monogenic diseases affecting mainly the exocrine pancreas that can lead to diabetes sooner or later include cystic fibrosis (\textit{CFTR}), hereditary pancreatitis (\textit{PRSS1} and \textit{SPINK1}) and pancreatic agenesis/hypoplasia (\textit{GATA6}).

\textbf{Syndromic diabetes due to TRMT10A and DNAJC3 deficiencies: oxidative stress, apoptosis in β-cells.} Mutations in TRMT10A, a nuclear tRNA methyltransferase, are associated with a novel syndrome of young-onset diabetes mellitus or impaired glucose metabolism, microcephaly, intellectual disability, short stature, and delayed puberty [OMIM 616013]. To date, 5 families were described in the literature with a total of 11 people with a mutation. Phenotypes were heterogeneous with most individuals presenting impaired glucose homeostasis, microcephaly, short stature, seizures, and intellectual disability.

DNAJC3 mutation, which is associated with DM and multisystemic neurodegeneration, have been described. Familial case of DNAJC3 mutation manifesting as juvenile-onset DM, hypothyroidism, multisystemic neurodegeneration, short-stature, and sensorineural hearing loss with the new finding of pancreatic fibrosis and atrophy.

\textbf{4.- Monogenic insulin resistance syndromes}

- The cardinal features of insulin resistance (IR) syndromes include moderate to severe acanthosis nigricans in association either with markedly increased insulin concentrations (fasting insulin >150pmol/l) or, where there is diabetes, increased insulin requirements, usually in the absence of a corresponding degree of obesity.
- Three different subtypes are described, based on the underlying pathogenic mechanism: primary insulin signaling defects, insulin resistance secondary to adipose tissue abnormalities, and insulin resistance as a feature of complex syndromes.
- Clinical and biochemical characterization of persons with severe insulin resistance may be used to guide genetic testing (Table 3).
• In contrast with monogenic syndromes of \( \beta \)-cell failure, hyperglycemia and diabetes tend to occur later in the genetic syndromes of severe insulin resistance and may not be a feature before the onset of puberty,\(^{228}\) except for Donohue syndrome.

The phenotypes of monogenic insulin resistance syndromes tend to be more pronounced in females, who may present during adolescence with significant ovarian hyperandrogenism. The physical appearance of the partial lipodystrophies can also be less pronounced in males and so the presentation is more common in females who can present with features similar to those seen in polycystic ovarian syndrome.

**Primary insulin signaling defects due to mutations in the insulin receptor (INSR) gene.** \( \text{INSR} \) mutations are responsible for a number of rare IR syndromes.\(^{229,230}\) Leptin levels are low, but adiponectin levels are paradoxically normal or elevated since insulin normally inhibits adiponectin secretion.\(^{231}\) There is a spectrum of severity, depending on the effect of the mutation on the signaling function of the receptor. The most severe forms are associated with either homozygous or compound heterozygous mutations in the \( \text{INSR} \) gene responsible for Donohue and Rabson-Mendenhall Syndromes. In Donohue Syndrome this leads to almost complete loss of insulin action at the cellular level and in Rabson-Mendenhall Syndrome, where there is some residual insulin signaling, the phenotype can be milder.\(^{232}\) Infants with Donohue Syndrome are born small for gestational age and develop diabetes in infancy with insulin concentrations over 1000 pmol/l, often in association with cardiomyopathy and hypertrichosis. Postprandial hyperglycemia may be severe, and present early in life, but is usually accompanied by fasting hypoglycemia. There is no effective treatment, and the majority of infants sadly succumb to infection, or cardiac complications during the first year of life. Children with Rabson-Mendenhall Syndrome may not present until later in childhood, with failure to thrive, gingival hyperplasia, acanthosis nigricans and hyperandrogenism, with insulin resistant diabetes requiring very high doses of insulin developing during adolescence.\(^{229,233}\)

Type A IR Syndrome is the mildest form and results most commonly from a heterozygous mutation in the \( \text{INSR} \) gene and is inherited in an autosomal dominant manner.\(^{229}\) Diabetes is rare before adolescence, but there can be significant ovarian hyperandrogenism and acanthosis nigricans during puberty.

The management of hyperglycemia in persons with \( \text{INSR} \) mutations can be challenging as insulin is
largely ineffective even at high does. Insulin sensitizers such as metformin may be tried initially but most will need extraordinarily high doses of insulin, with limited effect.\textsuperscript{229} As an alternative therapeutic method for young children, recombinant human IGF-I has been reported to improve both fasting and postprandial glycemia although long-term effects on survival remain unclear.\textsuperscript{234,235} Recently, a trial showed benefits of long-term treatment with metreleptin in persons with Rabson-Mendenhall Syndrome.\textsuperscript{236} Use of SGLT2i has also been reported to be beneficial on improving hyperglycemia.\textsuperscript{237,238} For females, the hirsutism resulting from ovarian hyperandrogenism should be managed using similar strategies as for polycystic ovarian syndrome.\textsuperscript{239}

\textbf{Monogenic lipodystrophies.} Lipodystrophies are characterized by a partial or complete reduction in adipose tissue, which results in decreased adipokine levels and insulin resistance.\textsuperscript{240,241} Mutations in either \textit{AGPAT2} or \textit{BSCL} account for approximately 80\% of cases of congenital generalized lipodystrophy (Berardinelli–Seip syndrome).\textsuperscript{242} These are recessively inherited disorders characterized by an almost complete absence of subcutaneous and visceral fat. The clinical features are often apparent at birth. An ability to store excess dietary fat safely results in ectopic fat deposition in the liver, with hepatic steatosis which may progress to cirrhosis.\textsuperscript{241} Diabetes can manifest in early infancy, but there then can be a period of remission until late childhood.

In contrast, a clinical diagnosis of familial partial lipodystrophy (FPLD) is usually made after puberty where there is failure to gain subcutaneous fat in the extremities and lower trunk during puberty, in combination with progressive accumulation of subcutaneous adipose tissue in the face and around the neck.\textsuperscript{241,243} Heterozygous mutations in \textit{LMNA} or \textit{PPARG} account for approximately 50\% of cases.\textsuperscript{240} Visceral fat is greatly increased in addition to hyperinsulinemia, hypertriglyceridemia, and decreased HDL cholesterol.\textsuperscript{244} Diabetes usually appears in late adolescence or early adulthood. More recently, there has been opportunity to make a genetic diagnosis in the offspring of persons with FPLD. This in theory permits early intervention with lifestyle recommendations and screening for co-morbidities in the hope that the development of co-morbidities can be delayed but is too early to tell whether this approach will be effective.

More rarely, lipodystrophy may occur as part of a multi-system disorder. A mutation in \textit{POLD1}, a universal DNA polymerase causes subcutaneous lipodystrophy in combination with diabetes, deafness, mandibular hypoplasia and hypogonadism in males.\textsuperscript{245} SHORT syndrome (short stature,
hypermobility of joints, ocular depression, Rieger’s anomaly, teething delay) with partial lipodystrophy, is caused by a hot spot mutation in \textit{PIK3R1} which has a central role in the insulin-signaling pathway and growth factor resistance.\textsuperscript{246-248} Mutation carriers of the dominant-negative mutation in \textit{PIK3R1} seem to be protected from obesity and hepatic steatosis but not diabetes,\textsuperscript{249} and the disease mechanisms is associated with unfolded protein response and reduced sensitivity to ER stress-dependent apoptosis.\textsuperscript{250}

The mainstay of therapy for lipodystrophy is dietary intervention with a low-fat, calorie neutral diet\textsuperscript{241} and, as such, access to an expert dietician as part of the multidisciplinary team is paramount. In partial lipodystrophy, insulin sensitizers such as metformin and glitazones may be initially effective\textsuperscript{251} but glitazones may exacerbate accumulation of ectopic fat in the face and neck.\textsuperscript{228} More recently, therapy with recombinant leptin, given by daily subcutaneous injection, has been shown to be well tolerated, with sustained improvements in hypertriglyceridemia, glycemic management, and liver volume.\textsuperscript{252} Efficacy in the partial forms of lipodystrophy is less clear, but where conventional therapy for diabetes and hypertriglyceridemia have not been successful, adjunctive therapy with metreleptin should be considered.\textsuperscript{253}

\textbf{Ciliopathy-related insulin resistance and diabetes. Alström syndrome (ALMS).} This autosomal recessive disorder shares symptoms with Bardet-Biedl syndrome (see below), including progressive visual impairment related to cone-rod dystrophy, sensorineural hearing loss, obesity, and diabetes mellitus. It can be distinguished from the latter syndrome by the lack of polydactyly and hypogonadism and by the absence of cognitive impairment.\textsuperscript{254} More than 60\% of individuals with ALMS develop cardiomyopathy. The syndrome is caused by mutations within the \textit{ALMS1} gene of unknown function.\textsuperscript{255} Persons with Alström syndrome usually show many features of the metabolic syndrome including acanthosis nigricans, hyperlipidemia, hyperuricemia, hypertension, and slowly-progressive insulin-resistant diabetes.\textsuperscript{256} Lifestyle intervention can initially ameliorate the metabolic abnormalities.\textsuperscript{257}

\textbf{Bardet-Biedl syndrome (BBS).} This disorder is characterized by intellectual disability, progressive visual impairment due to cone-rod dystrophy, polydactyly, obesity, diabetes mellitus, renal dysplasia, hepatic fibrosis, and hypogonadism. Obesity is found in almost every affected
individual, while diabetes affects less than 50%. While the syndrome shares some similarities with Lawrence-Moon syndrome, these two disorders can be distinguished by the presence of paraplegia and the absence of polydactyly, obesity, and diabetes mellitus in Lawrence-Moon syndrome. Terms such as Lawrence-Moon-Bardet-Biedl or Lawrence-Moon-Biedl syndrome should therefore be avoided. Bardet-Biedl syndrome has been linked to 18 different genetic loci, referred to as $BBS1$ to $BBS18$. The majority of cases are autosomal recessive, but triallelic inheritance has been reported. Genetic diagnostic laboratories and detailed clinical recommendations for persons with ALMS and BBS are present at [http://www.euro-wabb.org](http://www.euro-wabb.org).

**Conclusions**

Advances in molecular genetics have led to the identification of genes associated with many clinically identified subgroups of diabetes. Molecular genetic testing should now be considered an essential clinical diagnostic tool that can help define the diagnosis and treatment of children with diabetes. Although the cost of NGS continues to drop, diagnostic genetic testing should be limited to those person with diabetes who are likely to harbor a mutation based on the suggestive clinical features described above.
Figure 1: Insulin secretion from the pancreatic beta cell in (a) normal cell in a high plasma glucose environment and (b) in a cell with a K-ATP channel mutation - adapted from 263.

(a) Glucose enters the cell and is metabolized, causing an increase in ATP, K-ATP channel closure is induced via ATP binding, the membrane is depolarized, and calcium influx is triggered resulting in the release of insulin from its storage vesicles.

(b) A gain of function mutation in the K-ATP channel results in the failure of ATP to bind to the channel, causing the channel to remain open, the membrane stays hyperpolarized and no insulin is released.
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<td>6p22.1</td>
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<td>TNDM (multiple hypomethylation syndrome) ± macroglossia ± developmental delay ± umbilical defects ± congenital heart disease</td>
<td>28</td>
</tr>
<tr>
<td><em>PDX1</em></td>
<td>13q12.1</td>
<td>Recessive</td>
<td>PNDM + pancreatic agenesis (steatorrhoea)</td>
<td>264</td>
</tr>
<tr>
<td><em>PTF1A</em></td>
<td>10p12.2</td>
<td>Recessive</td>
<td>PNDM + pancreatic agenesis (steatorrhoea) + cerebellar hypoplasia/aplasia + central respiratory dysfunction</td>
<td>265</td>
</tr>
<tr>
<td><em>PTF1A enhancer</em></td>
<td>10p12.2</td>
<td>Recessive</td>
<td>PNDM + pancreatic agenesis without CNS features</td>
<td>133</td>
</tr>
<tr>
<td><em>HNF1B</em></td>
<td>17q21.3</td>
<td>Dominant</td>
<td>TNDM + pancreatic hypoplasia and renal cysts</td>
<td>22</td>
</tr>
<tr>
<td><em>RFX6</em></td>
<td>6q22.1</td>
<td>Recessive</td>
<td>PNDM + intestinal atresia + gall bladder agenesis</td>
<td>266,267</td>
</tr>
<tr>
<td><em>GATA6</em></td>
<td>18q11.1-q11.2</td>
<td>Dominant</td>
<td>PNDM + pancreatic agenesis + congenital heart defects + biliary abnormalities</td>
<td>134</td>
</tr>
<tr>
<td><em>GATA4</em></td>
<td>8p23.1</td>
<td>Dominant</td>
<td>PNDM + pancreatic agenesis + congenital heart defects</td>
<td>268</td>
</tr>
<tr>
<td><em>GLIS3</em></td>
<td>9p24.3-p23</td>
<td>Recessive</td>
<td>PNDM + congenital hypothyroidism + glaucoma + hepatic fibrosis + renal cysts</td>
<td>269</td>
</tr>
<tr>
<td><em>NEUROG3</em></td>
<td>10q21.3</td>
<td>Recessive</td>
<td>PNDM + enteric anendocrinosis (malabsorptive diarrhea)</td>
<td>270</td>
</tr>
<tr>
<td>Gene</td>
<td>Chromosome</td>
<td>Inheritance</td>
<td>Clinical Features</td>
<td>Reference</td>
</tr>
<tr>
<td>----------</td>
<td>------------</td>
<td>-------------</td>
<td>-----------------------------------------------------------------------------------</td>
<td>-----------</td>
</tr>
<tr>
<td>NEUROND1</td>
<td>2q32</td>
<td>Recessive</td>
<td>PNDM + cerebellar hypoplasia + visual impairment + deafness</td>
<td>271</td>
</tr>
<tr>
<td>PAX6</td>
<td>11p13</td>
<td>Recessive</td>
<td>PNDM + microphthalmia + brain malformations</td>
<td>272</td>
</tr>
<tr>
<td>MNX1</td>
<td>7q36.3</td>
<td>Recessive</td>
<td>PNDM + developmental delay + sacral agenesis + imperforate anus</td>
<td>4</td>
</tr>
<tr>
<td>NKX2-2</td>
<td>20p11.22</td>
<td>Recessive</td>
<td>PNDM + developmental delay + hypotonia + short stature + deafness + constipation</td>
<td>273</td>
</tr>
<tr>
<td>CNOT1</td>
<td>16q21</td>
<td>Spontaneous</td>
<td>PNDM + pancreatic agenesis + holoprosencephaly</td>
<td>274</td>
</tr>
<tr>
<td>ONECUT1</td>
<td>15q21.3</td>
<td>Recessive</td>
<td>PNDM + pancreatic hypoplasia + gall bladder hypoplasia</td>
<td>275</td>
</tr>
</tbody>
</table>

**Abnormal β-cell function:**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Chromosome</th>
<th>Inheritance</th>
<th>Clinical Features</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>KCNJ11</td>
<td>11p15.1</td>
<td>Spontaneous or dominant</td>
<td>PNDM/ TNDM ± DEND</td>
<td>40</td>
</tr>
<tr>
<td>ABCC8</td>
<td>11p15.1</td>
<td>Spontaneous, dominant or recessive</td>
<td>TNDM/PNDM ± DEND</td>
<td>41</td>
</tr>
<tr>
<td>INS</td>
<td>11p15.5</td>
<td>Recessive</td>
<td>Isolated PNDM or TNDM</td>
<td>23</td>
</tr>
<tr>
<td>GCK</td>
<td>7p15-p13</td>
<td>Recessive</td>
<td>Isolated PNDM</td>
<td>107</td>
</tr>
<tr>
<td>SLC2A2 (GLUT2)</td>
<td>3q26.1- q26.3</td>
<td>Recessive</td>
<td>Fanconi-Bickel syndrome: PNDM + hypergalactosemia, liver dysfunction</td>
<td>276</td>
</tr>
<tr>
<td>SLC19A2</td>
<td>1q23.3</td>
<td>Recessive</td>
<td>Roger’s syndrome: PNDM + thiamine-responsive megaloblastic anemia, sensorineural deafness</td>
<td>277</td>
</tr>
<tr>
<td>KCNMA1</td>
<td>10q22.3</td>
<td>Spontaneous</td>
<td>PNDM (not all cases) + developmental delay + intestinal malformations + cardiac malformations + bone dysplasia + dysmorphic features</td>
<td>278</td>
</tr>
<tr>
<td>Gene</td>
<td>Chromosome</td>
<td>Inheritance</td>
<td>Phenotype</td>
<td>Reference</td>
</tr>
<tr>
<td>--------</td>
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<td>---------------------------------------------------------------------------</td>
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</tr>
<tr>
<td>INS</td>
<td>11p15.5</td>
<td>Spontaneous or dominant</td>
<td>Isolated PNDM</td>
<td>89</td>
</tr>
<tr>
<td>EIF2AK3</td>
<td>2p11.2</td>
<td>Recessive</td>
<td>Wolcott-Rallison syndrome: PNDM + skeletal dysplasia + recurrent liver dysfunction</td>
<td>98</td>
</tr>
<tr>
<td>IER3IP1</td>
<td>18q21.2</td>
<td>Recessive</td>
<td>PNDM + microcephaly + lissencephaly + epileptic encephalopathy</td>
<td>279</td>
</tr>
<tr>
<td>FOXP3</td>
<td>Xp11.23- p13.3</td>
<td>X-linked, recessive</td>
<td>IPEX syndrome (autoimmune enteropathy, eczema, autoimmune hypothyroidism, elevated IgE)</td>
<td>280</td>
</tr>
<tr>
<td>WFS1</td>
<td>4p16.1</td>
<td>Recessive</td>
<td>PNDM* + optic atrophy ± diabetes insipidus ± deafness</td>
<td>189</td>
</tr>
<tr>
<td>WFS1</td>
<td>4p16.1</td>
<td>Dominant</td>
<td>PNDM or infancy-onset diabetes + congenital cataracts + deafness</td>
<td>281</td>
</tr>
<tr>
<td>EIF2B1</td>
<td>12q24.31</td>
<td>Spontaneous</td>
<td>PNDM + episodic hepatic dysfunction</td>
<td>282</td>
</tr>
<tr>
<td>YIPF5</td>
<td>5q31.3</td>
<td>Recessive</td>
<td>PNDM + severe microcephaly + epilepsy</td>
<td>283</td>
</tr>
<tr>
<td>STAT3</td>
<td>17q21.2</td>
<td>Spontaneous</td>
<td>PNPM + enteropathy + other autoimmunity such as cytopenias</td>
<td>116</td>
</tr>
<tr>
<td>CTLA4</td>
<td>2q33.2</td>
<td>Spontaneous</td>
<td>Lymphoproliferative syndrome + enteropathy + cytopenias + diabetes + thyroiditis</td>
<td>127</td>
</tr>
<tr>
<td>ITCH</td>
<td>20q11.22</td>
<td>Recessive</td>
<td>PNDM + facial dysmorphism + multi-system autoimmunity</td>
<td>128</td>
</tr>
<tr>
<td>IL2RA</td>
<td>10p15.1</td>
<td>Recessive</td>
<td>Lymphoproliferation + multi-system autoimmunity + diabetes</td>
<td>129</td>
</tr>
<tr>
<td>LRBA</td>
<td>4q31.3</td>
<td>Recessive</td>
<td>PNDM + enteropathy + hypothyroidism + autoimmune hemolytic anemia</td>
<td>118</td>
</tr>
</tbody>
</table>
*The mean age of diagnosis among persons with WFS1 mutations is approximately 5 years*
Table 2. Common and/or treatment-relevant subtypes of MODY and associated clinical features.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Locus</th>
<th>Clinical features</th>
<th>Treatment</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>GCK</td>
<td>7p15-p13</td>
<td>Mild asymptomatic hyperglycemia</td>
<td>None</td>
<td>284</td>
</tr>
<tr>
<td>HNF1A</td>
<td>12q24.2</td>
<td>Renal glucosuria</td>
<td>Sulphonylurea</td>
<td>285</td>
</tr>
<tr>
<td>HNF4A</td>
<td>20q12-q13.1</td>
<td>Macrosomia and neonatal hypoglycaemia, renal Fanconi syndrome (mutation specific)</td>
<td>Sulphonylurea</td>
<td>286</td>
</tr>
<tr>
<td>HNF1B</td>
<td>17q12</td>
<td>Renal developmental abnormalities, genital tract malformations</td>
<td>Insulin</td>
<td>287</td>
</tr>
<tr>
<td>KCNJ11</td>
<td>11p15</td>
<td>Proband or relatives may have history of transient neonatal diabetes and/or neuropsychological difficulties</td>
<td>High-dose sulphonylurea</td>
<td></td>
</tr>
<tr>
<td>Gene</td>
<td>Chromosome</td>
<td>Description</td>
<td>Treatment</td>
<td></td>
</tr>
<tr>
<td>--------</td>
<td>------------</td>
<td>-------------------------------------------------</td>
<td>--------------------</td>
<td></td>
</tr>
<tr>
<td>ABCC8</td>
<td>11p15</td>
<td>Proband or relatives may have history of transient neonatal diabetes and/or neuropsychological difficulties</td>
<td>High-dose sulphonylurea</td>
<td></td>
</tr>
</tbody>
</table>
Table 3. Classification of Syndromes of Severe Insulin Resistance (modified from Parker et al\textsuperscript{228})

<table>
<thead>
<tr>
<th>IR syndrome subtype</th>
<th>Gene (inheritance)</th>
<th>Leptin</th>
<th>Adiponectin</th>
<th>Other clinical features</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Primary insulin signalling defects</strong></td>
<td>Receptor defect</td>
<td></td>
<td></td>
<td>No dyslipidemia or hepatic steatosis</td>
</tr>
<tr>
<td></td>
<td>INSR (AR or AD)</td>
<td>Decreased</td>
<td>Normal or elevated</td>
<td></td>
</tr>
<tr>
<td>Post receptor defects</td>
<td>AKT2, TBC1D4 (AD)</td>
<td></td>
<td></td>
<td>Elevated fasting triglycerides and LDL, hepatic steatosis, diabetes (AKT2)</td>
</tr>
<tr>
<td><strong>Adipose tissue abnormalities</strong></td>
<td>Monogenic obesity</td>
<td></td>
<td>Increased (low in LEP)</td>
<td>Tall stature (MC4R) Hypogonadism (LEP) Hypoadrenalism (POMC)</td>
</tr>
<tr>
<td></td>
<td>MC4R (AD)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LEP, LEPR, POMC (AR)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Others</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Congenital generalized lipodystrophy</td>
<td>AGPAT2, BSCL2 (AR)</td>
<td>Decreased</td>
<td>Decreased</td>
<td>Severe dyslipidemia (high triglycerides, low HDL cholesterol) Hepatic steatosis</td>
</tr>
<tr>
<td></td>
<td>Others</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Partial lipodystrophy</td>
<td>LMNA, PPARG, PIK3R1 (AD)</td>
<td>Variable</td>
<td></td>
<td>Myopathy and cardiomyopathy (LMNA) Pseudo-acromegaly (PPARG) SHORT syndrome with partial lipodystrophy, and diabetes (PIK3R1)</td>
</tr>
<tr>
<td>Complex syndromes</td>
<td>Gene</td>
<td>Description</td>
<td></td>
<td></td>
</tr>
<tr>
<td>-------------------</td>
<td>------</td>
<td>-------------</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Alström</td>
<td>ALMS1 (AR)</td>
<td>Cone-rod dystrophy leading to blindness, sensorineural hearing loss, diabetes and cardiomyopathy</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bardet-Biedl</td>
<td>BBS1 to BBS18 (mostly AR)</td>
<td>Cone-rod dystrophy, obesity, renal dysfunction, polydactyly, learning disabilities, hypogonadism and diabetes</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DNA damage repair disorders</td>
<td>WRN (AR)</td>
<td>Scleroderma-like skin changes, cataracts, increased cancer risk, atherosclerosis and diabetes; Sun-sensitive, telangiectatic skin changes; increased cancer risk and diabetes</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Primordial dwarfism</td>
<td>PCNT (AR)</td>
<td>Microcephalic osteodysplastic primordial dwarfism and diabetes</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

AR: autosomal recessive, AD: Autosomal dominant

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