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Enhancing newborn screening sensitivity and specificity for missed NICCD using selected amino acids and acylcarnitines

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Abstract

Purpose To enhance the detection rate of Neonatal Intrahepatic Cholestasis caused by Citrin Deficiency (NICCD) through newborn screening (NBS), we analyzed the metabolic profles of missed patients and proposed a more reliable method for early diagnosis.

Methods In this retrospective study, NICCD patients were classified into "Newborn Screening" (64 individuals) and"Missed Screening" (52 individuals) groups. Metabolic profles were analyzed using the non-derivatized MS/MS Kit, and genetic mutations were identifed via next-generation sequencing and confrmed by Sanger sequencing. Receiver Operating Characteristic (ROC) analysis evaluated the predictive value of amino acids and acylcarnitines in dried blood spots (DBS) for identifying missed patients including 40 missed patients and 17,269 healthy individuals, with additional validation using 12 missed patients and 454 healthy controls.

Results The age of diagnosis was signifcantly higher in the "Missed Screening" group compared to the "Newborn Screening" group (74.50 vs. 18.00 days, $P < 0.001$). ROC analysis revealed that citrulline had excellent diagnostic accuracy for missed patients, with an AUC of 0.970 and a cut-off value of 17.57 μ mol/L. Additionally, glycine, phenylalanine, ornithine, and C8 were signifcant markers, each with an AUC greater than 0.70. A combination of these markers achieved an AUC of 0.996 with a cut-off value of 0.00195. Validation demonstrated a true positive rate of 91.67% and a true negative rate of 96.48%. Common *SLC25A13* mutations in both groups were c.852_855del, IVS16ins3kb, and $c.615 + 5G > A$.

Conclusions Combining multiple metabolic markers during NBS signifcantly improves sensitivity and specifcity for detecting missed NICCD cases. However, the relationship between genetic mutations and missed cases remains unclear.

Keywords NICCD, Missed screening, Citrulline, Newborn screening, *SLC25A13*, Dried blood spots

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Introduction

Neonatal Intrahepatic Cholestasis caused by Citrin Deficiency (NICCD) is one of the most common inherited metabolic disorders in East Asia and a primary cause of intrahepatic cholestasis in infants. NICCD is typically diagnosed following elevated citrulline (Cit) levels during newborn screening (NBS). However, some children do not exhibit elevated Cit levels at birth but develop cholestasis within two to three months. The carrier rate of pathogenic variants in the *SLC25A13* gene in China is 1/65, leading to an estimated disease prevalence of $1/17,000$ [\[1](#page-8-0)]. However, the actual incidence of citrin defciency (CD) detected via NBS nationwide is only 1/68,000 [[2\]](#page-8-1), and in Zhejiang Province, it is as low as $1/82,352[3]$ $1/82,352[3]$ $1/82,352[3]$. The Zhejiang Neonatal Disease Screening Center, one of the largest centers for genetic metabolic disorders in China, has focused on collecting missed NICCD over the past decade. Despite this effort, only a few dozen cases have been clinically detected, suggesting that a signifcant number of missed patients remain undiagnosed. Some of these patients may still be asymptomatic, while a small fraction could progress to cirrhosis and liver failure, necessitating liver transplantation [\[4](#page-8-3)]. Research indicates that later-onset patients have a worse prognosis compared to those identified early $[5]$ $[5]$ $[5]$. Therefore, early identifcation, diagnosis, and treatment are critically important. However, since Cit levels during NBS in both missed screening and healthy newborns are within the normal range, identifying missed patients from tandem mass spectrometry (MS/MS) is challenging.

Citrin, an aspartate-glutamate carrier (AGC) primarily expressed in the liver, is a component of the malate-aspartate shuttle $[6]$ $[6]$. AGC plays a crucial role in transporting aspartate into the cytoplasm and glutamate into the mitochondria, indirectly facilitating NADH transfer from the cytoplasm to the mitochondria. This balance is necessary for the synthesis of urea, proteins, and nucleotides^{[[7\]](#page-8-6)}. Citrin deficiency disrupts various metabolic pathways, including the urea cycle, aerobic glycolysis, gluconeogenesis, galactose metabolism, and fatty acid synthesis $[8-10]$ $[8-10]$. These disruptions cause biochemical abnormalities such as elevated transaminases, increased bilirubin, and hypercholesterolemia, as well as metabolic abnormalities like elevated levels of multiple amino acids, including Cit with or without methionine (Met), phenylalanine (Phe), tyrosine (Tyr), and ornithine (Orn), along with abnormal acylcarnitine profles [[11–](#page-8-9)[14](#page-8-10)]. However, current research primarily focuses on NICCD cases with evident metabolic abnormalities, while studies on the metabolic profles of missed cases during NBS are limited. Thus, it remains unclear whether certain metabolic indicators, which fall within normal ranges yet difer from those of healthy newborns, could serve as early markers for identifying these missed cases.

CD is a hereditary metabolic disorder caused by autosomal recessive mutations in the *SLC25A13* gene [\[15](#page-8-11)]. Four major mutations account for almost 80% of pathogenic alleles in the Chinese population $[16]$ $[16]$. These mutations exhibit geographic distribution diferences [\[17](#page-8-13)]. Beyond NICCD, CD presents with two additional agedependent clinical phenotypes: Failure to Thrive and Dyslipidemia caused by Citrin Defciency (FTTDCD), which occurs in older children and is characterized by growth retardation and abnormal blood lipids; and Adult Onset Type II Citrullinemia (CTLN2), which manifests in adolescence or adulthood [[18–](#page-8-14)[20](#page-8-15)]. However, genotype-phenotype correlations in CD remain unclear, and there is no defnite relationship between Cit concentration and genotype $[21]$ $[21]$. Therefore, we aim to investigate the genetic distribution in both NBS-positive and missed patients to determine if there is a correlation between specifc gene mutations and phenotype.

To enhance the positive detection rate of NICCD in NBS, we identifed multiple metabolic indicators to detect missed patients and analyzed the genetic distribution of both missed and NBS-positive patients.

Methods

Setting

We conducted a single-center retrospective study at the Children's Hospital, Zhejiang University School of Medicine. This study included patients diagnosed with NICCD for the frst time in the Department of Genetic Metabolism or Gastroenterology between January 2011 and September 2023. The Ethical Committee of Children's Hospital, Zhejiang University School of Medicine, approved this study, and written consents were obtained from parents for sample collection and data publication.

Study design and data collection

Our NBS protocol aligns with the standard practices followed by screening centers both in China and internationally. During NBS, some newborns showed elevated Cit concentrations in dried blood spots (DBS). They were recalled for another DBS testing and blood sample collection. If their Cit levels remained elevated and were confrmed genetically as NICCD, along with biochemical indicators, they were classifed into the "Newborn Screening" group, which included 64 individuals (Fig. [1A](#page-2-0)). Additionally, some patients were admitted to the hospital with symptoms such as prolonged jaundice and failure to thrive. Upon admission, DBS and blood samples revealed elevated Cit levels, bilirubin, or liver enzymes, clinically suggesting neonatal intrahepatic cholestasis. A retrospective review of these patients' DBS

Fig. 1 Flow diagram

results during NBS was conducted. Patients with normal Cit levels during NBS were classifed into the "Missed Screening" group while those with unavailable or unclear Cit levels were excluded. This group included 52 individuals (Fig. [1B](#page-2-0)). Sociodemographic information and metabolic indices during NBS were collected from electronic medical records.

ROC analysis for predicting missed screening patients

We used Receiver Operating Characteristic (ROC) analysis to evaluate the predictive value of amino acids, free carnitines, and acylcarnitines during NBS for identifying missed NICCD patients. Using MedCalc, we estimated the required sample size for the healthy control group, setting $\alpha = 0.05$, Power=0.95, Area under ROC $curve = 0.7$, Null Hypothesis value $= 0.5$, and the ratio of sample sizes in negative/positive groups $=500$. The estimated sample size was 28 missed screening patients and 14,000 healthy individuals. Ultimately, we included 40 missed screening patients and 17,269 age- and sexmatched healthy individuals, all born in Zhejiang Province, in the ROC analysis. The remaining 12 missed screening patients and an additional 454 healthy controls were used to validate the ROC results.

Metabolic index detection and molecular testing

The DBS samples collected during NBS were obtained 3–7 days after birth using the heel prick method and then spotted onto the Whatman 903 flter paper. Amino acid and acylcarnitine profles were measured by the NeoBase non-derivatized MS/MS Kit (PerkinElmer, Finland). The procedure involved adding 100 μl of a working solution containing an internal standard to a U-bottom plate, vibrating at 650 rpm, and incubating at 45 °C for 45 min. Then, $75 \mu l$ of the liquid was transferred to a V-bottom plate and incubated at room temperature for 2 h before injecting 25 μl into MS/MS for metabolic analysis. Quality control includes low and high-level internal quality controls [[22\]](#page-8-17). MS/MS results were used to compare the metabolic characteristics of amino acids and acylcarnitines among diferent groups and to construct predictive models.

Detection of mutation

Genomic DNA was extracted from blood samples of the proband and their parents. Liquid-phase capture technology targeted 166 genes related to commonly inherited metabolic diseases, followed by next-generation sequencing and bioinformatics analysis. Suspected variants were confrmed by Sanger sequencing in the proband and family members, followed by genetic interpretation.

Treatment

Both groups received the same treatment regimen for NICCD, which includes: (1) Dietary therapy with lactosefree, medium-chain triglyceride formula milk; (2) Symptomatic treatment including liver protection treatment and arginine to reduce ammonia levels; (3) Supplementation of fat-soluble vitamins and other micronutrients; and (4) Introduction of a low-carbohydrate and high-fat, high-protein diet after complementary foods were added. All data in this study were collected before treatment began, ensuring that treatment had no impact on the results.

Statistical analysis

SPSS 26.0 software was used for statistical analysis of metabolic indices. Continuous variables were described as mean±standard deviation (SD). Continuous variables with a normal distribution were compared using Student's t-test, while variables with a non-normal distribution were compared using the Mann-Whitney or Kruskal-Wallis. Categorical variables were analyzed using the chi-square test. $P < 0.05$ was considered statistically signifcant. An AUC of the ROC curve between 0.70 and 0.90 indicates medium accuracy, and an AUC>0.90 indicates excellent test accuracy [[23\]](#page-8-18). Combined indicators from the ROC analysis were used for binary logistic regression. GraphPad Prism 8 software was used to draw gene distribution charts. The structure stability analysis of the novel missense variant was performed using Chimera ver 1.17.3.

Results

Sociodemographic of the "newborn screening" and "missed screening" group

Table [1](#page-3-0) shows that the age of diagnosis in the "Missed Screening" group was 74.50 (58.75,108.00) days, signifcantly greater than the "Newborn Screening" group 18.00 (14.00,21.00) days (P<0.001). There were no statistically signifcant diferences between the two groups in terms of gender, birth weight, and gestational age ($P > 0.05$).

Comparison of various amino acids and acylcarnitines during NBS among three groups

We compared indicators including amino acids and acylcarnitines during NBS between healthy control, "Newborn Screening" and "Missed Screening" groups. In the "Newborn Screening" group, indicators with an abnormal rate (proportion of values exceeding or falling below the normal range) greater than 10% included Cit, Met, Phe, Tyr, Arg, and Gly. Among these, Cit, Met, Phe, Tyr, and Arg were elevated compared to the healthy control group, while Gly was lower. Some additional metabolites were signifcantly diferent between the two groups but remained within the reference range. Although the abnormal rates of all amino acid and acylcarnitine indicators in the "Missed Screening" and healthy control group are within 10%, slight abnormalities were observed in some indicators between the two groups. Cit, Arg, Orn, Pro, Phe, Gly, C3, C6, C8, C16, and C18 showed statistically signifcant diferences compared to the control group ($P < 0.05$). These indicators are considered potential markers for missed NICCD (Table [2](#page-4-0)).

The diagnostic value of amino acids and acylcarnitines for missed screening patients

Table [3](#page-4-1) illustrates the diagnostic value of differential amino acids and acylcarnitines for detecting missed screening patients during NBS compared to a control group. The ROC curves for Cit exhibited excellent accuracy with an AUC of 0.970. In comparison, the ROC curves for Gly, Phe, Orn, and C8 demonstrated moderate accuracy, with AUC values of 0.806, 0.762, 0.703, and 0.729, respectively. The ROC curves for Pro, Arg, C6, C16, C18, and C3 showed lower accuracy, all with AUC values below 0.70. The cut-off levels of these indicators are Cit (17.57 μmol/L), Gly (480.5 μmol/L), Phe (51.36 μmol/L), Orn (126.8 μ mol/L), and C8 (0.07 μ mol/L). Additionally, the combination of Cit, Gly, Phe, Orn, and C8, which all had an AUC>0.70, signifcantly enhances diagnostic accuracy, achieving an AUC of 0.996, sensitivity of 97.5%, and specifcity of 97.4% with a cut-of level of 0.00195.

Prediction and validation of missed NICCD Patients using Cit, Gly, Orn, Phe, and C8

A binary logistic regression analysis of Cit, Gly, Orn, Phe, and C8 (Table 4), resulted in the following regression equation:

Total $score = 1.155 \times \text{Cit-0.021} \times \text{Gly-}$ $0.12 \times$ Phe + 0.044 \times Orn + 34.5 \times C8-17.77.

To validate the model's predictive ability, we retrospectively collected MS/MS data during NBS from an additional 12 missed patients and 454 healthy children. We applied Cit, Gly, Orn, Phe, and C8 to this regression equation. If the total score exceeded the cut-off value of 0.00195, determined by the ROC curve for the combined variables, the prediction was classifed as a missed

Table 1 Sociodemographic information of the "Newborn Screening" and "Missed Screening" group

The bold type means the abnormal rate is higher than 10%

The data in the "Newborn Screening" group are from the frst DBS during NBS

Table 3 The diagnostic value of DBS amino acids and acylcarnitines for missed patients

	Cut-off(umol/L)	AUC	P value	Sensitivity (%)	Specificity (%)
Cit	17.57	0.970	< .001	95	91.67
Gly	480.5	0.806	< .001	80	67.72
Phe	51.36	0.762	< .001	65	80.29
Orn	126.8	0.703	< .001	77.5	55.95
Pro	230.4	0.680	< .001	60	72.7
Arg	9.97	0.672	< .001	55	80.96
C8	0.07	0.729	< .001	72.5	72.77
C ₆	0.05	0.676	< .001	65	68.24
C16	2.87	0.670	< .001	67.5	62.88
C18	0.86	0.658	< .001	75	53.3
C ₃	1.55	0.628	< 0.01	72.5	52.05
A combination of Cit, Orn, Phe, Gly, C8	0.00195	0.996	< .001	97.5	97.4

The bold type means AUC>0.70

patient; otherwise, it was classifed as a healthy child (Fig. [2](#page-5-1)). The validation results demonstrated a True Positive rate (sensitivity) of 91.67% (11/12), a True Negative rate (specifcity) of 96.48% (438/454), a False Positive rate

of 3.52% (16/454), a False Negative rate of 8.33% (1/12), and a Positive Predictive Value (PPV) of 40.74% (11/27) (Fig. [3\)](#page-5-2).

Table 4 Binary logistic regression of predictor variables

* We expanded the C8 variable by 100 times to address the extremely large ORs and CIs from the original variable

Fig. 2 Flowchart for predicting using combined indicators' cut-off

Genetic fndings

A total of 29 *SLC25A13*(NM_014251.3) mutations were detected, with 22 in the "Newborn Screening" group and 16 in the "Missed Screening" group. In both groups, c.852_855del, IVS16ins3kb, and $c.615+5G>A$ were the most frequent mutations. In the "Newborn Screening" group, the mutation frequencies were 41%, 15%, and 10%, respectively, while in the "Missed Screening" group, they were 48.08%, 13.46%, and 11.54%, respec-tively (Fig. [4](#page-6-0)). The $c.1638_1660$ dup mutation accounts for 10% in the "Newborn Screening" group but only 1.92% in the "Missed Screening" group. The *SLC25A13* mutations in both groups were primarily concentrated in these four mutations, accounting for 76% and 75%, respectively. A novel mutation c.392C>T was found in the "Newborn Screening" group and its protein model is presented in the supplement fle.

Discussion

Missed NICCD cases are fagged as normal during NBS because their Cit levels are below the screening cutof, resulting in many false-negative results. To address this, we retrospectively identifed diferential metabolisms between missed cases and healthy controls, assessing their sensitivity and specifcity. We validated these markers as predictors of missed NICCD and compared the genetic distribution between missed and NBS-positive patients.

Consistent with previous fndings [\[24](#page-8-19), [25](#page-8-20)], the onset age of the "Missed Screening" group was approximately 2-3 months, older than the "Newborn Screening" group. The Cit level of "Missed Screening" patients during NBS was normal, likely due to early blood sampling before metabolic profles had fully manifested [[26](#page-8-21)]. Late referral and failure to switch to a high-MCT or lactose-free formula were associated with poor prognosis in NICCD [[27\]](#page-8-22). In later-onset symptomatic patients, fatty acid oxidation, liver function, and cholestasis were more severely impaired compared to those identifed through NBS, as evidenced by higher transaminase, direct bilirubin, bile

	Actual missed patients	Actual healthy children	Total
Predict positives (missed patients)	11	16	27
Predict negatives (healthy children)		438	439
Total	12	454	466

Fig. 3 Validation with missed patients and healthy controls

Fig. 4 Mutation frequency in *SLC25A13* (NM_014251.3): Newborn Screening (A) vs. Missed Screening (B)

acids, dyslipidemia, and lower protein levels [[3](#page-8-2)]. Among the missed patients in our study, two were not diagnosed with NICCD until they were 9-10 months old, at which point liver cirrhosis was detected, ultimately necessitating liver transplantation. These findings emphasize the importance of early diagnosis and management.

Citrin defciency disrupts multiple metabolic pathways, leading to abnormalities in amino acids and acylcarnitines. The deficiency impairs the synthesis of argininosuccinate, resulting in the accumulation of intermediate products of the urea cycle such as Cit, Arg, and Orn [\[3](#page-8-2)]. Additionally, aromatic amino acids (AAA) like Phe, Tyr, and tryptophan, as well as Met, increase due to cholestatic liver injury [\[28](#page-9-0)]. Glycogenic amino acids like Gly are signifcantly reduced, which may indicate enhanced gluconeogenic activity. This is consistent with previous studies showing that impaired gluconeogenesis from lactate caused by an increased NADH/NAD+ratio that inhibits the conversion of lactate to pyruvate[[29](#page-9-1)], leads to greater reliance on glycogenic amino acids like glycine, serine, and alanine, ultimately resulting in their decreased levels[[3,](#page-8-2) [26,](#page-8-21) [30](#page-9-2)].

The current Cit cutoff for screening NICCD is inadequate, as many missed patients have Cit levels below this threshold, resulting in numerous false negative results [[31\]](#page-9-3). Using amino acids and acylcarnitines from established NBS systems to identify missed patients is a highly feasible, straightforward, and cost-efective method. Zhang et al. [\[3](#page-8-2)] found that Cit, Arg, Met, Orn, Phe, Ala, Leu, Val, C0, C3, C16:1OH, C18:1, C18:2, ammonia, aspartate transaminase, and total bile acids contributed most to the diferentiation between the "newborn screening group" and the "clinical diagnosis group". Our study found Cit, Arg, Orn, Pro, Phe, Gly, C3, C6, C8, C16, and C18 to be potential diferential markers for missed NICCD. Cit was the frst abnormality detected after birth. To address the issue of false negatives, Chen et al. [[32](#page-9-4)] used Cit levels > 20 μ mol/L as the first tier and gene analysis as the second tier for detection. By simultaneously evaluating Cit and the Cit/tAA ratio, MS/MS demonstrates high sensitivity for detecting NICCD, identifying nearly 80% of previously missed patients [[31\]](#page-9-3). Consistent with previous studies, Cit remained the best indicator with high sensitivity and specificity in our cohort. Specifically, a Cit value of 17.57 μmol/L was the optimal diagnostic cutoff for missed patients, approximately half of the upper limit (min-max: $7.14-37 \mu$ mol/L). This was also consistent with the hypothesis we previously formulated based on clinical experience [[33\]](#page-9-5). In addition, Gly, Phe, Orn, and C8 also served as moderate accuracy indicators $(AUC > 0.7)$ for identifying missed patients. Therefore, we propose a combined evaluation using Cit, Gly, Phe, Orn, and C8 levels (combined $AUC=0.996$) to improve the detection rate for NICCD. This approach offers higher accuracy, sensitivity, and specifcity, with a lower false positive rate compared to using a single amino acid or acylcarnitine.

Previous studies have developed a combined evaluation method for detecting newborns who later develop NICCD, which uses a scoring system based on five biomarkers (Arg, Cit, Ile+Leu, Tyr, and C0/C5-DC), where exceeding specifc thresholds for these biomarkers results in a score; a total score of 4 or more indicates a high risk of developing NICCD [[34](#page-9-6)]. Despite its high specifcity (98.7%), it has a low sensitivity (66.7%), resulting in a high rate of missed diagnoses and limited predictive power. In our study, we developed a new predictive formula using binary logistic regression. This formula requires only the values for Cit, Gly, Phe, Orn, and C8 from the NBS, making it especially useful for large samples of 10,000 or

more without additional steps or tests. Validation with 12 confrmed missed patients and 454 healthy children demonstrated high sensitivity and specifcity, both exceeding 90%. This indicates that our formula is simple, efficient, and highly predictive. Our study achieved a false negative rate below 10% and a false positive rate below 5%. To further reduce false positives or false negatives, we propose combining this predictive method with a highthroughput iPLEX genotyping assay to detect *SLC25A13* mutations [\[33](#page-9-5)]. Additionally, our ongoing non-targeted metabolomics research on NICCD will offer new approaches for screening missed patients. Notably, the PPV in our study was relatively low. For rare diseases like NICCD, a lower PPV is expected, even with a highly sensitive and specifc screening tool, because PPV is infuenced by both test accuracy and the disease's prevalence. Therefore, the low PPV observed in this study is largely due to the low prevalence of confrmed missed NICCD cases in our sample.

Delayed diagnosis and treatment of NICCD imposes a signifcant burden on patients and their families, often leading to unnecessary tests and, in some cases, prolonged hospitalization. Early identifcation of citrin defciency through NBS is associated with better outcomes compared to diagnoses made after symptoms have appeared $[5]$ $[5]$. The predictive scoring formula proposed in this study can reduce the false-negative rate and improve the sensitivity for detecting citrin defciency, minimizing missed cases and facilitating an earlier diagnosis. As a result, early intervention and treatment can be implemented, improving overall clinical outcomes and alleviating the long-term burden on both the healthcare system and afected families.

At least 100 *SLC25A13* variations have been described, with diferences in high-frequency regions of variations among diferent countries. In Japan, 11 mutations such as c.851_854del, c.1019_1177del, c.1231_1311del, and c.675C>A account for approximately 95% of the total mutations $[35]$ $[35]$. The hotspot mutation in Korea is IVS-16ins3kb [\[36\]](#page-9-8). In our cohort, we found twenty-eight known and one novel *SLC25A13* variants, expanding the mutational spectra of CD. Previous studies have indicated that homozygous $c.1177+1G>A$ or $c.852_855$ delTATG mutations correlate with low birth height/weight, elevated transaminases, cholestasis, hypoproteinemia, and prolonged prothrombin time [[12\]](#page-8-23). However, in our study, the distribution characteristics of gene mutations in both the "Newborn Screening" and "Missed Screening" groups were mostly represented by c.852_855del, IVS16ins3kb, and $c.615+5G>A$. This indicates that our data do not support a signifcant relationship between genotype and clinical manifestations or outcomes. It might be quite challenging to determine whether someone is a missed patient based solely on genetics. However, it is noteworthy that the frequency of c.1638_1660dup in the "Newborn Screening" group is signifcantly higher than in the "Missed Screening" group. Given the limited sample size, further validation is needed to establish the relationship between genotype and phenotype.

The present study has several strengths. First, we collected data on the characteristics of missed NICCD cases in Zhejiang Province, a high-incidence region, providing a theoretical basis for improving NICCD detection in other similar regions. Second, we identifed and validated metabolites from MS/MS that can reduce the rate of missed screenings, ofering a simple and feasible method. Third, we identified a gene mutation with a slight difference between missed and NBS-positive patients. However, our data only represented NICCD cases missed in Zhejiang Province. Future research could extend to multiple regions with both high and low NICCD incidence rates, with regular data collection (e.g., quarterly or annually) to create a time-series dataset. Using machine learning to dynamically adjust cut-off values based on diferent time periods and population characteristics may further improve NICCD detection.

In conclusion, we propose a novel predictive scoring formula incorporating levels of Cit, Gly, Phe, Orn, and C8, which demonstrates high sensitivity in identifying missed NICCD cases in our retrospective study. This method provides a simple and cost-efective approach to assist clinicians in the early detection of NICCD patients.

Abbreviations

Supplementary Information

The online version contains supplementary material available at [https://doi.](https://doi.org/10.1186/s13023-025-03532-7) [org/10.1186/s13023-025-03532-7](https://doi.org/10.1186/s13023-025-03532-7).

Additional fle 1

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Author contributions

WPY, HLW, and CYH should be considered joint frst authors. WPY, HLW, and CYH designed the research, analyzed the data, and wrote the manuscript; ZD and ZT carried out the genetic tests and mutation analysis; ZSS and CZY revised the manuscript; HQM, WBQ, and HXW supervised the research study and should be considered joint corresponding authors. All authors approved the fnal manuscript to be published.

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Availability of data and materials

The data supporting the fndings of this study are available at [https://doi.](https://doi.org/) [org/](https://doi.org/)[https://doi.org/10.6084/m9.fgshare.27628812.](https://doi.org/10.6084/m9.figshare.27628812)

Declarations

Ethics approval and consent to participate

This study was approved by the Institutional Review Board of the Ethics Committee in Children's Hospital, Zhejiang University School of Medicine (reference number: 2021-IRB-292). Written consents were obtained from parents for sample collection and data publication.

Consent for publication

We confrm that the family has signed a written informed consent for the publication of their children's genetic data, clinical details, and/or any accompanying images.

Competing interests

The authors declare no competing interests.

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