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CLINICAL RESEARCH

Cross-Population Validation of the Pediatric CKD Risk-Prediction Tool

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Introduction: This study aimed to externally validate the performance of the kidney replacement therapy (KRT) risk prediction calculator for chronic kidney disease (CKD) in children in an ethnically distinct East Asian population.

Methods: We externally validated the KRT risk prediction calculator for CKD in children using data from the KoreaN Cohort Study on Outcomes in Pediatric CKD (KNOW-Ped CKD) cohort. Six parametric survival models from the generalized gamma family were tested, stratified into 2 groups as follows: change in glomerular filtration rate (GFR)-based (group 1) and cross-sectional (group 2). Missing data ($\leq$ 7.9%) were addressed via multiple imputations using chained equations. Outcomes were timed to KRT initiation. The model performance was evaluated based on goodness-of-fit, discrimination ability, calibration, and predictive ability.

Results: Overall, 533 children were included in the validation cohort. The median age and baseline estimated GFR (eGFR) were 10.8 years (interquartile range [IQR]: 5.3–14.5) and 57.6 ml/min per 1.73 m^2 (IQR: 34.8–81.4), respectively. Over a median follow-up of 4.8 years (IQR: 2.0–8.9), KRT was initiated in 171 participants (32.1%). Models in group 1 ($n = 433$) and 2 ($n = 533$) demonstrated excellent discrimination ability (C-statistic: 0.911–0.972). The calibration slopes exceeded 0.9 across all models, though the Greenwood-Nam-D'Agostino goodness-of-fit test indicated a miscalibration ($P < 0.001$). Enriched models incorporating the eGFR slope showed the closest alignment with the observed risks.

Conclusion: These findings underscore the potential utility of the calculator in improving prognostication and clinical decision-making in pediatric CKD.

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CKD is a progressive disorder associated with substantial morbidity and mortality, and is a major global burden.[1,2] Although children represent only a small proportion of all patients with CKD, the prolonged disease course and lifelong complications necessitate a multidisciplinary approach to improve long-term prognosis. Pediatric CKD is associated with diverse complications, including kidney failure, impaired growth and development, anemia, mineral and bone disorders, and cardiovascular diseases.[3–8] Because these complications become more pronounced with advancing CKD, the accurate prediction of disease progression in pediatric patients

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is critical for early recognition and optimal management.[9] Furthermore, risk stratification of CKD progression may help alleviate the considerable anxiety and distress experienced by patients and families, who often face uncertainty regarding the duration of residual kidney function and timing of KRT.[10,11]

The CKD in Children (CKiD) study is a large, prospective, multicenter cohort study established in the United States and Canada to improve our understanding of pediatric CKD.[12] Building on these data, CKiD investigators developed an adaptive web-based clinical prediction calculator for estimating the time to KRT in children with CKD.[13] Employing a random survival forest approach, they screened a wide array of sociodemographic metrics, laboratory results, and treatment variables drawn from baseline and longitudinal assessments. Six models were constructed, from elemental to enriched, according to variable availability. Internal validation was conducted via cross-validation, whereas the elementary model was externally validated using the European Study Consortium for Chronic Kidney Disorders Affecting Pediatric Patients dataset.[14] Across models, calibration was adequate, and discrimination was excellent, with a C-statistic of 0.880. External validation is indispensable for confirming the reliability, reproducibility, and generalizability of predictive models before their adoption in personalized clinical care; however, this is frequently underperformed. In pediatric CKD, a relatively rare condition, effective dissemination of a well-validated risk equation is critically important. Furthermore, because the existing models were developed predominantly in Caucasian cohorts, their applicability to East Asian populations remains uncertain. To bridge this knowledge gap, we aimed to validate the CKiD prediction algorithm using data from the KNOW-Ped CKD cohort.[15]

METHODS

Original Calculator

The original model was constructed using data obtained from 890 children enrolled in the CKiD study.[12] A total of 172 variables were incorporated, including sociodemographic factors, eGFR, urinary protein-to-creatinine ratio (UPCR), CKD duration, anemia, blood pressure stage, birth history, laboratory markers, medication use, and annualized changes in key variables such as eGFR. Using a random forest algorithm, the original team constructed 6 models ranging from an elementary model (which included the core predictors: CKD diagnosis type, eGFR, and UPCR) to an enriched model (Table 1). In the development cohort, optimism-corrected C-statistic ranged from 0.865 to 0.875, and the calibration slope for the enriched model was 1.019.

External Validation Group and Outcome Assessment

For external validation, we used data from 533 children with CKD enrolled in the KNOW-Ped. KNOW-Ped CKD is a 10-year prospective observational cohort study conducted in Korea in 2011 to comprehensively characterize the clinical course and outcomes of pediatric CKD. The study was funded by the Korea Disease Control and Prevention Agency and was conducted in 2 phases: phase 1 (2011–2016) and phase 2 (2019–2023). The detailed study design and methods have been described previously.[16] In brief, this study enrolled children with CKD stages 1 to 5 from 7 major pediatric nephrology centers nationwide and prospectively collected standardized annual data, including medical history, anthropometric measurements, laboratory parameters, and imaging findings. The baseline characteristics of the KNOW-Ped CKD cohort were reported in our previous publication.[15]

We stratified the patients into 2 categories: group 1, with available change in GFR data required for the enriched model and partially enriched model 1; and group 2, which used only cross-sectional data and therefore could be modeled using the elementary model and partially enriched models 2 to 4. In group 1, change in GFR was calculated from eGFR values measured at baseline and at the 1-year follow-up visit; other variables were obtained from the 1-year follow-up visit. In group 2, change in GFR was not required, and validation was performed using only baseline variables. eGFR was estimated using the creatinine–cystatin C-based CKiD equation; when cystatin C was unavailable, the modified Schwartz equation was used instead. Given the low proportion of missing cystatin C values (< 5% in both groups), the potential impact on overall model performance was considered

Table 1. Explanatory variables required for each model

Variable	eGFR	UPCR	CKD cause	Elevated BP/HTN	Anemia	Albumin	Chloride	CO_2	ΔGFR
Elementary model	V	V	V						
PE model 1	V	V	V						V
PE model 2	V	V	V	V					
PE model 3	V	V	V	V	V				
PE model 4	V	V	V	V		V	V	V	
Enriched model	V	V	V	V	V	V	V	V	V

BP, blood pressure; CKD, chronic kidney disease; eGFR, estimated glomerular filtration rate; HTN, hypertension; PE, partially enriched; UPCR, urine protein-to-creatinine ratio; V, variable included in the analysis; ΔGFR, change in glomerular filtration rate.

minimal, and a separate sensitivity analysis was therefore not undertaken. All other variables were extracted directly from the cohort database. Participants missing essential predictors were excluded from the analysis (eGFR, UPCR, and cause of CKD). Information on KRT initiation was obtained from medical records or participant- or family-reported forms.

Statistical Analysis

Descriptive Statistics

Clinical and demographic characteristics were summarized, with continuous variables presented as median (IQR), representing the 25th to 75th percentile range, and categorical variables as frequency and percentage (%).

Missing Value Imputation

Observational studies, which are often conducted over long periods, are prone to missing data because of participant dropouts, incomplete measurements, or loss to follow-up, potentially affecting the validity and statistical power of the analysis. In this study, the proportion of missing values among the variables ranged from 0% to 7.9%. Missing data were handled using multivariate imputation by chained equations as originally proposed by Rubin, with predictive mean matching applied to continuous variables and binomial logistic regression to binary variables.[17,18] Five imputed datasets were generated, and the resulting parameter estimates were pooled according to Rubin's rules.

Survival Models

To validate our dataset, all 6 models were parametric survival models from the generalized gamma family as described previously.[13] The regression coefficients for each variable and the 3 parameters (location, scale, and shape) were used, as reported in the study.

Evaluation of the 6 Models

First, we evaluated and compared the fit of the 6 candidate survival models using the Akaike Information Criterion, Bayesian Information Criterion, and log-likelihood. The Akaike Information Criterion balances the model's fit and complexity by penalizing the number of parameters,[19] whereas the Bayesian Information Criterion introduces a stronger penalty, which is useful when comparing models across different sample sizes.[20] Log-likelihood reflects the probability of the observed data given the specified model, with higher values indicating a better fit.[21] To further assess model adequacy, we examined standardized residual times, which under a correctly specified model should follow an exponential distribution with a mean of 1. The Kaplan-Meier estimate of the residual-time distribution was compared with the theoretical exponential survival curve; close agreement indicated an adequate fit, whereas systematic deviations suggested misspecification or overfitting.[22]

Second, model discrimination was assessed using the optimism-corrected C-statistic,[23] where values close to 1 indicate a better distinction between patients who experienced an event of interest. To evaluate model discrimination, the optimism-corrected C-index was calculated using an integrated approach combining multiple imputation and bootstrapping. First, multiple imputation was performed to handle missing data. Within each imputed dataset, a bootstrap procedure with 100 iterations was conducted to estimate optimism—defined as the average difference between the C-index obtained from the bootstrap sample and the original imputed sample. This optimism was then subtracted from the naive C-index of each dataset to obtain a bias-corrected estimate. Finally, these corrected C-indices were pooled using Rubin's rules to derive the final estimate and its associated standard error. This method simultaneously incorporates both the uncertainty from missing data imputation and the potential for model overoptimism. The Royston D statistic[24] quantifies the prognostic separation by measuring the standardized difference in the predicted risk between patients with and without an event, with higher values indicating better discrimination.

Third, the Greenwood-Nam-D'Agostino goodness-of-fit test[25] was used to assess the calibration at 2 (4 bins) and 5 years (6 bins). This test compares the observed and predicted survival probabilities across risk groups while accounting for censoring using Greenwood's formula. A chi-square statistic was computed, with higher *P*-values indicating good calibration. In addition, a visual assessment of calibration was performed using calibration plots that compared the predicted probabilities of the event with the observed event rates across the risk groups.[26,27] A calibration slope close to 1 indicates good agreement between the predicted and observed outcomes, reflecting adequate model calibration.

Finally, the integrated Brier score[28] was calculated to evaluate predictive accuracy over the follow-up period. It represents the average squared difference between the observed outcomes and the predicted survival probabilities at each time point, with lower values indicating better alignment with the actual outcomes.

Statistical testing was limited to the calculation of the Greenwood-Nam-D'Agostino *P*-value to evaluate model calibration, with a P-value > 0.05 indicating adequate fit. All analyses were conducted using R software (version 4.5.0; R Foundation for Statistical Computing, Vienna, Austria), specifically using the

flexsurv, survival, mice, and pec packages for statistical modeling and implementation of the tests.

Ethical Considerations

This study was reviewed and approved by the institutional review board of Seoul National University Hospital (No. H-1906068-1041). Written informed consent was obtained from each participant or, when applicable, from their legal guardians, depending on age.

RESULTS

Characteristics of the Cohort

In total, 533 children were included in the validation cohort. Of these, 436 participants were included in group 1, whereas all 533 children were included in group 2 (Table 2). In this study, the median age was 10.8 years (IQR: 5.3–14.5), and 69.8% were boys. All patients were East Asians, and 17.6% had a glomerular diagnosis. The median baseline eGFR was 57.6 ml/min per 1.73 m^2 (IQR: 34.8–81.4), and the median UPCR was 0.5 (IQR: 0.2–1.6). The median follow-up duration was 4.8 years (IQR: 2.0–8.9), during which KRT was initiated in 171 participants (32.1%). The cumulative incidence of KRT is shown in Figure 1. The detailed characteristics of groups 1 and 2 are summarized in Table 2. Compared with the original development cohort, there were no significant differences in most of the explanatory variables. However, the rate of eGFR decline was significantly faster in our validation cohort, with group 1 showing a median annual change of −3.9 (IQR: −10.3 to 1.4) ml/min per 1.73 m^2/yr compared with −0.4 (IQR: −4.6 to 3.4) in the development group ($P < 0.001$).

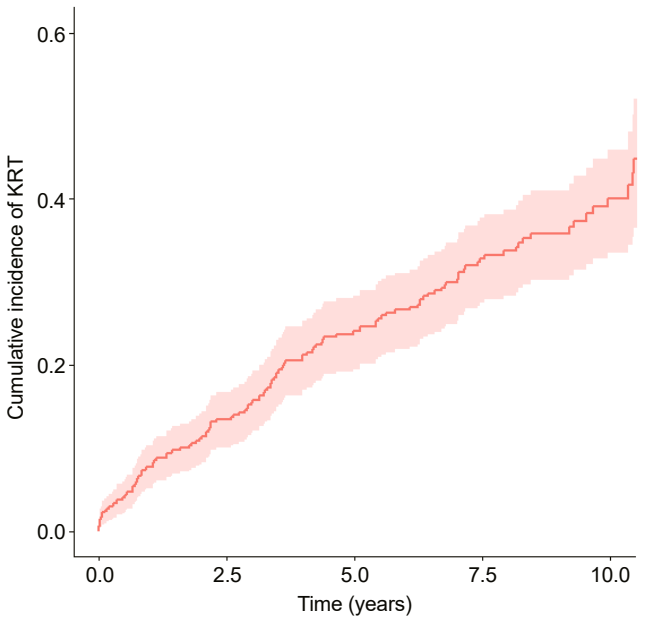

Figure 1. Cumulative incidence of kidney replacement therapy in the KNOW-PED CKD cohort. KRT, kidney replacement therapy. KNOW-PED CKD, KoreaN Cohort Study on Outcomes in Pediatric CKD cohort.

Table 2. Clinical and demographic characteristics of the development and validation cohorts

Variable	Development group (n = 890)	Validation group 1 (n = 436)	Validation group 2 (n = 533)
Age, yrs	11.4 (6.7–15.3)	11.9 (6.2–15.5)	10.8 (5.3–14.5)
Male sex	557 (62.6%)	310 (71.1%)	372 (69.8%)
Glomerular cause of CKD diagnosis	186 (20.9%)	70 (16.1%)	94 (17.6%)
eGFR[a], ml/min per 1.73 m^2	50.4 (35.0–64.6)	52.7 (33.4–80.3)	57.6 (34.8–81.4)
1-yr annualized change, ml/min per 1.73 m^2	−0.4 (−4.6 to 3.4)[a]	−3.9 (−10.3 to 1.4)	-
UPCR	0.3 (0.1–1.0)	0.4 (0.1–1.3)	0.5 (0.2–1.6)
HTN or elevated BP	331 (37.2%)	129 (30.2%)	157 (32.0%)
Serum albumin	4.4 (4.2–4.6)	4.3 (4.0–4.5)	4.3 (4.0–4.5)
Serum chloride	104 (102–107)	105 (103–107)	105 (103–108)
Serum bicarbonate	23 (21–25)	24 (22–26)	23 (21–26)
Anemia	228 (25.6%)	123 (28.3%)	175 (32.8%)
Duration of follow-up, yrs	5.2 (2.2–7.9)	6.3 (2.0–8.9)	4.8 (1.9–9.1)
Any kidney replacement therapy	261 (29.3%)	130 (29.8%)	171 (32.1%)

BP, blood pressure; CKD, chronic kidney disease; eGFR, estimated glomerular filtration rate; HTN, hypertension; IQR, interquartile range; UPCR, urine protein-to-creatinine ratio.
[a]Estimated median [IQR] derived via Monte Carlo simulation from the original summary data.

Prognostic Performance

In Figure 2, we present the calibration results for the elementary and fully enriched models in group 1, displaying the calibration plots for the bins of the predicted 5-year risk. In both models, the predicted and observed risks were closely aligned with the full model showing a calibration slope of 0.972 in the validation group (Table 3). The C-statistic ranged from 0.956 to 0.976 in group 1 and 0.911 to 0.941 in group 2, indicating excellent discrimination, and the Akaike Information Criterion for outcome prediction ranged from 652.41 to 704.16 in group 1 and 1007.50 to 1026.76 in group 2 (Table 4). However, the expected standardized residual times did not align perfectly with the standard exponential distribution over 5 years (6 bins), and the Greenwood-Nam-D'Agostino test indicated significant differences between the predicted and observed risks (P-value < 0.001 for both models). The models in group 2 and partially enriched models in group 1 also demonstrated acceptable calibration plots (Supplementary Figures S1 and S2).

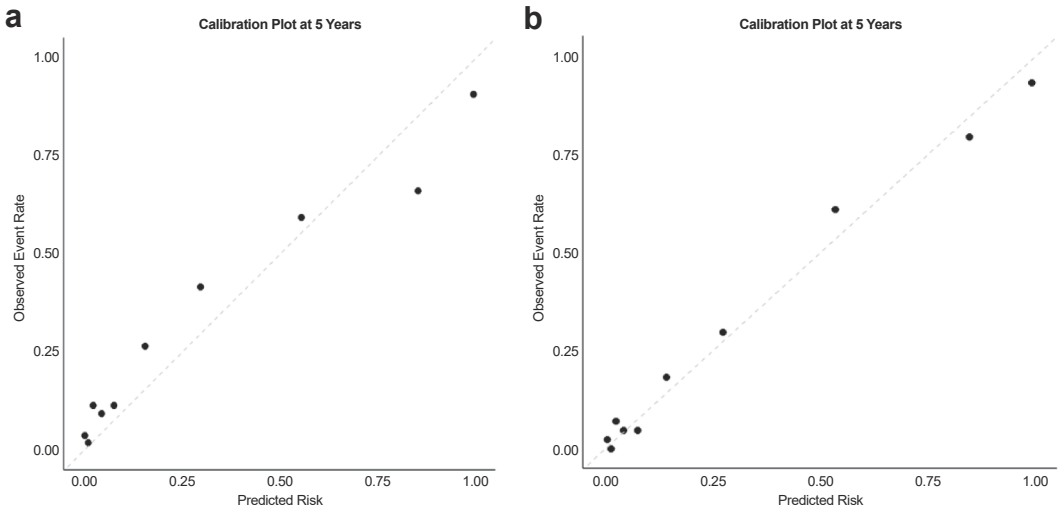

Figure 2. Calibration plot depicting observed risk on predicted risk from a 5-year risk of kidney replacement therapy in (a) the elementary model and (b) the enriched model in group 1.

Sensitivity Analysis Using Different Outcome Definitions

Because KRT initiation practices may vary across centers and cultural contexts, we conducted a sensitivity analysis using kidney failure, defined as eGFR < 15 ml/min per 1.73 m^2 or KRT initiation, as the outcome of interest. This analysis yielded similar calibration and discrimination results, confirming that the model maintained a good predictive performance under this alternative definition (Supplementary Tables S1 and S2).

DISCUSSION

Our study aimed to externally validate the CKiD risk prediction model, which has been widely applied in clinical practice worldwide, by using data from the KNOW-Ped CKD cohort to assess its performance in an ethnically distinct East Asian pediatric population. KNOW-Ped CKD is a unique, prospective cohort encompassing all age groups of pediatric patients with CKD, representing Asian populations, providing essential insights into disease progression and regional characteristics.[29]

Through the KNOW-Ped CKD study, important insights were gained regarding key determinants of pediatric CKD progression. Earlier investigations have primarily focused on the prevalence and clinical impact of major comorbidities, revealing conditions, such as cardiovascular disorders, short stature, neurocognitive impairment, anemia, mineral bone disorders, and impaired quality of life in children and their families, as highly prevalent and clinically significant.[4,7,10,30–34] Subsequent analyses examined factors associated with disease progression and demonstrated that nephrotic-range proteinuria and poorly controlled total cholesterol level were independently associated with a more rapid decline in kidney function.[35,36] Most recently, KNOW-Ped CKD investigators applied a

Table 3. Model performance in the validation cohort group 1

Performance metric	Elementary	PE model 1	PE model 2	PE model 3	PE model 4	Enriched
Model fit						
AIC	704.16	684.50	692.09	663.89	663.51	652.41
BIC	716.40	696.74	704.32	676.12	675.74	664.65
LL	−349.08	−339.25	−343.04	−328.94	−328.76	−323.21
Discrimination						
C-statistic	0.894	0.899	0.899	0.904	0.906	0.908
RD statistic	0.385	0.358	0.365	0.365	0.352	0.381
Calibration						
GND test, *P*-value	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001
Calibration slope	0.956	0.969	0.973	0.976	0.976	0.972
Prediction ability						
IBS	0.199	0.199	0.202	0.196	0.199	0.199

AIC, Akaike Information Criterion; BIC, Bayesian Information Criterion; GND, Greenwood-Nam-D'Agostino; IBS, integrated Brier score; LL, log-likelihood; PE, partially enriched; RD, Royston D.

Table 4. Model performance in the validation cohort group 2

Performance metric	Elementary	PE model 2	PE model 3	PE model 4
Model fit				
AIC	1024.88	1026.76	1008.38	1007.50
BIC	1037.71	1039.59	1021.21	1020.34
LL	−509.44	−510.38	−501.19	−500.75
Discrimination				
C-statistic	0.860	0.865	0.872	0.874
RD statistic	0.376	0.383	0.37	0.369
Calibration				
GND test, *P*-value	< 0.001	< 0.001	< 0.001	< 0.001
Calibration slope	0.920	0.941	0.912	0.911
Prediction ability				
IBS	0.207	0.383	0.37	0.369

AIC, Akaike Information Criterion; BIC, Bayesian Information Criterion; GND, Greenwood-Nam-D'Agostino; IBS, integrated Brier score; LL, log-likelihood; PE, partially enriched; RD, Royston D.

machine learning–based approach to predict eGFR decline by integrating multidimensional clinical variables to enhance prognostic accuracy. The model revealed that UPCR was the strongest predictor of eGFR decline, followed by baseline eGFR and serum albumin, chloride, and hemoglobin levels, thereby highlighting their importance in assessing disease progression in pediatric CKD.[37] Taken together, these studies have enhanced our understanding of the underlying mechanisms of pediatric CKD progression and validated observations reported in Western cohorts, including CKiD and cardiovascular comorbidities in children with CKD.[38]

The baseline characteristics of the KNOW-Ped CKD and CKiD cohorts exhibited notable differences.[12,15] The CKiD cohort initially enrolled children with mild to moderate CKD (eGFR: 45–90 ml/min per 1.73 m^2) and later expanded to include patients with nonglomerular etiologies early in the disease course. The median age at enrollment was 11.4 years, and 63% of the participants were male. The cohort included 21% African Americans and 14% Hispanic participants. Congenital anomalies of the kidney and urinary tract accounted for 56% of the underlying etiologies, and the median eGFR was 50.4 ml/min per 1.73 m^2. In contrast, the KNOW-Ped CKD cohort included children across all CKD stages. The median age at enrollment was 10.9 years, and 68% of the participants were male. The cohort exclusively consisted of Korean children (from an East Asian population). The leading causes of CKD were congenital anomalies of the kidney and urinary tract (42.6%), followed by glomerulopathies (25.6%) and cystic kidney diseases (14.2%), with a median eGFR of 53.1 ml/min per 1.73 m^2. Compared with the CKiD cohort, the KNOW-Ped CKD cohort demonstrated a distinct racial composition, a lower prevalence of congenital anomalies of the kidney and urinary tract, and a higher proportion of advanced CKD stages at enrollment. In addition, Korean children exhibited a steeper decline in eGFR and a greater cumulative incidence of KRT (32% in KNOW-Ped CKD vs. 20%–25% in the earlier CKiD reports).

Proteinuria, hypertension, and anemia were major determinants of CKD progression and were comparable in both cohorts, with median values of 0.5 (IQR: 0.2–1.6) g/gCr, 32.0%, and 32.8% in the KNOW-Ped CKD cohort and 0.3 (IQR: 0.1–1.0) g/gCr, 37.2%, and 25.6% in the CKiD cohort. These findings indicated a similar overall burden of systemic complications between the 2 populations (Table 2).

Despite these differences, the CKiD risk prediction calculator performed robustly when applied to the KNOW-Ped CKD data, with model fit, discrimination, and calibration each evaluated using multiple complementary approaches. By incorporating additional validation methods beyond those used in the original study, the model demonstrated consistently good performance across all specifications, from the elementary to the enriched model. In the KNOW-Ped CKD cohort, the C-statistics ranged from 0.85 to 0.90, with the enriched model exceeding 0.90, indicating excellent discriminative ability, well above the conventional benchmark of 0.75, which is generally considered acceptable, and notably higher than the C-statistic of approximately 0.8, as observed when the international IgA prediction tool was externally validated using Korean data.[39] Although the calibration slopes did not fully replicate those observed in the original validation, and the standardized residual curve showed suboptimal fitting, all slope values remained > 0.9, demonstrating a consistent trend with the curve from the enriched model, thus reflecting strong agreement between predicted and observed risks. These findings underscore the generalizability and reliability of the CKiD risk calculator in the ethnically distinct Korean population, thereby supporting its potential clinical applicability to East Asian children with CKD.

To further elucidate the predictive behavior of the model, we assessed the model fit for each specification and inferred the contributions of the individual variables. The elementary model tended to overestimate risk at lower predicted probabilities and underestimate it at higher levels, whereas the enriched model demonstrated more accurate predictions across the entire risk spectrum. Given that the decline in eGFR was more pronounced among our patients, incorporating the eGFR slope (as implemented in the partially enriched model 1 or the enriched model) appears preferable for clinical application. Notably, the model performance improved substantially with the inclusion

of additional variables, all of which are readily obtainable in routine CKD care and do not require specialized testing, thereby enhancing the practicality of the model for real-world clinical use. Furthermore, the model remained robust even when alternative outcome definitions were applied to account for potential variations in clinical practice patterns of KRT initiation, suggesting that it can be reliably applied across diverse healthcare settings.

In our study, although the Greenwood–Nam–D'Agostino tests yielded statistically significant results indicating formal miscalibration, the calibration slopes and calibration plots demonstrated strong agreement between predicted and observed risks. This discrepancy can be attributed to the high sensitivity of goodness-of-fit tests in large sample sizes, where even minor, clinically insignificant deviations can lead to statistical significance. From a clinical perspective, the model maintains high discriminative and descriptive value. However, considering the faster eGFR decline and higher incidence of KRT in our validation cohort, simple recalibration, such as adjusting the baseline hazard, may be beneficial for optimizing the model's performance for specific clinical settings before widespread implementation.

This study has some limitations. The relatively small sample size may have limited our ability to fully optimize the predictive performance. Furthermore, whereas CKiD investigators recently adopted the U25 eGFR equation, we were constrained from using the Schwartz equation because of database limitations. In addition, although some variables, such as blood pressure levels, had approximately 8% missing data and were imputed, all core variables were included in the analysis. Finally, our cohort exclusively consisted of Korean children; therefore, our findings may not be generalizable to all Asian populations.

Nevertheless, this study has several notable strengths. Although the current Kidney Disease: Improving Global Outcomes guidelines recommend the use of prediction models such as the Kidney Failure Risk Equation in adults, no validated prognostic tools have yet been endorsed for children.[40] Continued external validation efforts, such as ours, may contribute to the refinement and standardization of prediction models applicable to pediatric CKD and ultimately enhance their clinical utility. Importantly, this study externally validated the CKiD risk-prediction calculator using the KNOW-Ped CKD cohort, which included a population with a broad range of kidney functions and centrally measured, standardized biomarker data, which is an important methodological strength.

In conclusion, this first cross-population validation of the CKiD risk-prediction tool for KRT in a Korean pediatric population with CKD demonstrated excellent discrimination and acceptable calibration, confirming its generalizability beyond Caucasian populations. These findings support the broader application of this tool across diverse pediatric CKD populations and highlight its potential to enhance prognostication, facilitate individualized clinical decision-making, and ultimately improve outcomes in children with CKD. Because genetic susceptibility and health care practices likely influence disease progression in pediatric CKD,[41,42] our team is currently working to refine and adapt the CKiD risk-prediction calculator for KRT to develop a population-tailored model optimized for East Asian children with CKD.

DISCLOSURE

HGK has received consulting fees from Bayer, Kyowa Kirin, Medicine Pharma Korea, and Samsung Bioepis; speaker honoraria from Alexion, Kyowa Kirin, AstraZeneca, and Handok; and research grants from Bayer, Kyowa Kirin, Boehringer Ingelheim, Amgen, Apellis Pharmaceuticals, and AstraZeneca. EP has received consulting fees from Samsung Bioepis.

All the other authors declared no competing interests.

PATIENT CONSENT

Written informed consent was obtained from each participant or, when applicable, from their legal guardians, depending on age.

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DATA AVAILABILITY STATEMENT

The data used in this study are available from the board of KNOW-Ped CKD investigators upon request.

SUPPLEMENTARY MATERIAL

Supplementary File (PDF)

Figures S1. Calibration plot depicting observed risk on predicted risk from at 5-year risk of kidney replacement therapy in partially enriched model among group 1.

Figure S2. Survival function of standardized residual times for participants in partially enriched model among group 1.

Table S1. Model performance in the validation cohort group 1 using an alternative outcome definition.

Table S2. Model performance in the validation cohort group 2 using an alternative outcome definition.

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