

Isolated paternal age, not dual-advanced age, confers the highest SGA risk: a nationwide cross-sectional study, United States, 2014–2024

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Research Article

Keywords: small-for-gestational-age, advanced maternal age, advanced paternal age, additive interaction, RERI, population-based study

Posted Date: October 5th, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-10896387/v1>

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Additional Declarations: No competing interests reported.

Abstract

Background

The independent effects of advanced maternal age on small-for-gestational-age (SGA) are well studied, but the joint effect of maternal and paternal age remains unclear. Most prior research has evaluated parental ages separately rather than as interacting exposures. Our aim was to evaluate the joint effects of advanced maternal (≥ 35 years) and paternal (≥ 40 years) age on SGA using an additive interaction framework in a contemporary U.S. nationwide cohort.

Methods

This population-based cross-sectional study included 39,016,070 singleton live births from the U.S. National Vital Statistics System (2014–2024). Multivariable Poisson regression with robust standard errors estimated adjusted risk ratios (RR) for SGA by parental age categories and a four-category joint exposure. Additive interaction was quantified using the relative excess risk due to interaction (RERI), attributable proportion (AP), and synergy index (S). Sensitivity analyses included restriction to term deliveries, exclusion of ART conceptions, multiple imputation, and adjustment for metabolic covariates. E-values assessed unmeasured confounding.

Results

SGA prevalence was 9.9%. Maternal age showed a J-shaped association (highest RR at ≥ 45 years: 1.22, 95% CI 1.20, 1.23); paternal age also showed a J-shaped association (highest RR at ≥ 45 years: 1.36, 95% CI 1.36, 1.37). In joint analysis, "advanced paternal age only" carried the highest risk (RR 1.29, 95% CI 1.29, 1.30), while "dual-advanced age" risk was moderately elevated (RR 1.16, 95% CI 1.15, 1.16). A significant negative additive interaction was identified (RERI = -0.151 , 95% CI -0.157 , -0.145 ; AP = -0.131 ; S = 0.512 ; all $P < 0.001$). Results were robust across all sensitivity analyses.

Conclusions

Advanced parental ages exhibit a negative additive interaction on SGA, with the highest risk among younger mothers with older fathers. These findings support integrating paternal age into couple-based prenatal risk assessment.

Background

Small-for-gestational-age (SGA), defined as a birth weight below the 10th percentile for a given gestational age and sex, is a biometric classification rather than a pathological diagnosis [1, 2]. While SGA is sometimes used interchangeably with fetal growth restriction (FGR) in clinical settings, the two

are not synonymous: FGR refers to a failure to achieve growth potential due to underlying pathology [1, 3]. SGA includes both constitutionally small infants who are otherwise healthy and those with true growth restriction [3, 4]. SGA remains a well-established endpoint in perinatal epidemiology when the research question is framed appropriately [1, 5], and is a key indicator of perinatal morbidity [6] and a well-established predictor of long-term metabolic disorders [7] and neurodevelopmental impairment [8]. In high-income countries, the trend toward delayed childbearing has become increasingly prevalent [9], prompting substantial research interest in the impact of advanced parental age on perinatal outcomes [10]. Although the association between advanced maternal age (≥ 35 years) and SGA has been extensively investigated, the findings remain inconsistent. The role of advanced paternal age (≥ 40 years) is even more contentious, with studies reporting null, positive, or even protective associations [11].

A key limitation is that maternal and paternal ages are usually evaluated as isolated factors. Given the rising trend of both parents being older, assessing their joint effect is clinically relevant. However, few studies have formally tested interaction between parental ages on the additive scale, which is the most relevant scale for public health decision-making. A recent prospective multicenter cohort study in China examined the joint effects of parental age on perinatal outcomes including SGA [12], but did not formally evaluate additive interaction and had limited power ($n \approx 16,000$). Whether these findings generalize to a multiethnic Western population with a distinct risk profile remains unknown. A recent Chinese cohort study using a similar additive interaction framework reported a negative RERI for parental age on composite neonatal outcomes, though it did not identify a significant independent effect of paternal age on SGA specifically [13], raising further questions about the generalizability of these observations across populations.

Therefore, the objectives of the present study were: (1) to characterize the independent, potentially non-linear dose–response relationships of maternal and paternal age with SGA; (2) to evaluate the joint effects of advanced parental age using a four-category exposure variable; and (3) to formally test and quantify the additive interaction between advanced maternal and paternal age on SGA in a contemporary, nationwide U.S. birth cohort.

Methods

Study design and data source

This population-based cross-sectional study included 39,016,070 singleton live births from the U.S. National Vital Statistics System (2014–2024) [14]. Data were accessed via the publicly available Natality Public Use Files (National Bureau of Economic Research) [15]. Because this study used publicly available, de-identified data, it was exempt from Institutional Review Board review under U.S. Department of Health and Human Services regulations (45 CFR 46).

Study population

From a total of 39,016,070 singleton live births recorded between 2014 and 2024, a complete case dataset was constructed after applying the following exclusion criteria: multiple gestations, gestational age < 22 or > 42 completed weeks, birth weight < 300 g or > 6000 g, missing or ambiguous infant sex, maternal age < 12 or > 55 years, and paternal age < 12 or > 70 years. Births with missing data on paternal age (approximately 0.38%) were excluded from the primary analysis but were examined in sensitivity analyses.

Outcome definition

The primary outcome, small-for-gestational-age (SGA), was defined as a birth weight below the 10th percentile for a given gestational age and infant sex. To ensure consistency across calendar years and to avoid reliance on an external standard that may not fully reflect the contemporary U.S. birth weight distribution, an internal 10th percentile threshold was calculated from the study population. For each combination of gestational week (22–42 weeks) and infant sex (male/female), the 10th percentile of birth weight was determined within each calendar year. An infant was classified as SGA if its birth weight fell below this year-, sex-, and gestational age-specific threshold.

Exposure variables

Maternal and paternal ages were extracted from the birth certificate as single-year ages. For categorical analyses, maternal age was grouped into seven categories (< 20, 20–24, 25–29 [reference], 30–34, 35–39, 40–44, ≥ 45 years), and paternal age was similarly grouped (< 20, 20–24, 25–29, 30–34 [reference], 35–39, 40–44, ≥ 45 years). The reference categories were chosen based on the lowest observed SGA rates in descriptive analyses and consistency with prior literature.

To evaluate the joint effects of parental ages, a four-category exposure variable was constructed: (1) reference group (mother 25–29 years and father 30–34 years); (2) advanced maternal age only (mother ≥ 35 years and father ≤ 39 years); (3) advanced paternal age only (father ≥ 40 years and mother ≤ 34 years); and (4) dual-advanced parental age (mother ≥ 35 years and father ≥ 40 years). The thresholds of ≥ 35 years for maternal age and ≥ 40 years for paternal age were selected based on widely used clinical definitions of advanced parental age.

For additive interaction analyses, two binary variables were created: advanced maternal age (≥ 35 vs. <35 years) and advanced paternal age (≥ 40 vs. <40 years).

Covariates

Covariates were selected a priori based on established associations with SGA and parental age. The primary model adjusted for maternal race/ethnicity (non-Hispanic White, non-Hispanic Black, Hispanic, Asian/Pacific Islander, American Indian/Alaska Native, other/not reported), maternal educational attainment ($\geq$ 8th grade, some high school, high school graduate, some college, associate degree, bachelor's degree, master's degree, doctorate, unknown), and calendar year (2014–2024). In a pre-specified additional analysis, the model was further adjusted for hypertensive disorders of pregnancy (yes/no/unknown), gestational diabetes (yes/no/unknown), pre-pregnancy body mass index (BMI; categorized as underweight [$< 18.5 \text{ kg/m}^2$], normal [$18.5\text{--}24.9 \text{ kg/m}^2$], overweight [$25.0\text{--}29.9 \text{ kg/m}^2$], obese [$\geq 30.0 \text{ kg/m}^2$], and unknown), and parity (primiparous vs. multiparous). Missing values for metabolic variables, which accounted for approximately 28% for hypertension and diabetes and 30% for BMI, were treated as a separate “unknown” category to retain the full sample. Missingness was largely due to non-collection of these variables in specific calendar years (2015, 2018, 2019).

Statistical analysis

All analyses were conducted in R (version 4.1.2) using the `data.table`, `speedglm`, and `ggplot2` packages. Baseline characteristics were summarized by SGA status, with continuous variables expressed as median and interquartile range (IQR) and categorical variables as frequency and percentage. Standardized mean differences (SMD) were used to assess between-group imbalance, with an SMD > 0.10 considered indicative of a meaningful difference.

Multivariable Poisson regression with a log link function and robust standard errors was used to directly estimate risk ratios (RR) and 95% confidence intervals (CI) for the association between parental age and SGA [16]. Poisson regression was chosen over logistic regression because SGA is not a rare outcome (approximately 10%), and the odds ratio from logistic regression would overestimate the risk ratio at this event rate [17]. Three models were fitted: (1) maternal age alone, (2) paternal age alone, and (3) the joint four-category parental age variable, all adjusting for the covariates listed above.

Additive interaction between advanced maternal and paternal age was evaluated on the additive scale using the relative excess risk due to interaction (RERI), the attributable proportion due to interaction (AP) [18], and the synergy index (S). These metrics were derived from a Poisson model containing the two binary parental age variables and their product term. The RERI is defined as $RR_{11} - RR_{10} - RR_{01} + 1$, where RR_{11} , RR_{10} , and RR_{01} denote the risk ratios for the joint exposure, maternal advanced age only, and paternal advanced age only, respectively, relative to the reference group (neither parent advanced age) [19]. A RERI > 0 indicates a superadditive (synergistic) interaction, a RERI < 0 indicates a subadditive (antagonistic) interaction, and a RERI = 0 indicates no additive interaction. The AP quantifies the proportion of risk in the jointly exposed group that is attributable to the interaction, and the S measures the strength of the interaction ($S = 1$ indicates exact additivity). The 95% CI for RERI was calculated using the delta method, based on the covariance matrix of the regression coefficients [20].

Sensitivity analyses

Several pre-specified sensitivity analyses were performed to assess the robustness of the primary findings. First, the analysis was restricted to term deliveries (≥ 37 weeks) to evaluate whether the observed interaction was confounded by preterm birth, which itself can lead to low birth weight and potential misclassification of SGA. Second, births conceived via assisted reproductive technology (ART) were excluded to examine whether the antagonistic interaction was driven by ART use, which is more common among older parents and has been independently associated with adverse perinatal outcomes [21]. ART status was identified using the `rf_artec` variable on the birth certificate. Third, the primary model was additionally adjusted for hypertensive disorders, gestational diabetes, pre-pregnancy BMI, and parity to determine whether the interaction was independent of metabolic pathways. Missing metabolic data were coded as a separate “unknown” category to preserve the full sample. Fourth, E-values were calculated to quantify the minimum strength of association that an unmeasured confounder would need to have with both the exposure and the outcome to fully explain the observed exposure-outcome association [22], conditional on the measured covariates. E-values were calculated for the two most prominent positive associations: maternal age < 20 years and isolated advanced paternal age. Fifth, to address missing data on metabolic covariates and parity ($\sim 28\text{--}30\%$), multiple imputation using random forest-based imputation (`missRanger`) was performed on a randomly selected, representative sub-sample of 200,000 births. Fifty imputed datasets were generated, and parameter estimates were pooled across datasets using Rubin's rules to account for both within- and between-imputation variance. The RERI from multiply imputed data ($\text{RERI} = -0.177$, 95% CI $-0.178, -0.176$) was reported as a sensitivity analysis to verify the robustness of findings under an alternative missing-data framework.

STROBE statement

This study was reported in accordance with the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) guideline for cross-sectional studies [23].

Results

Study population and baseline characteristics

A total of 39,016,070 singleton live births met the inclusion criteria, of whom 3,859,979 (9.89%) were classified as small-for-gestational-age (SGA). Baseline characteristics stratified by SGA status are presented in Table 1.

SGA mothers were younger (median 28.0 vs 29.0 years) and had higher proportions of non-Hispanic Black race, primiparity, and underweight, while differences in paternal age and gestational age were negligible (Table 1).

Compared with non-SGA infants, SGA infants had higher proportions of non-Hispanic Black mothers (19.1% vs. 12.6%) and primiparous mothers (35.5% vs. 27.5%), and lower maternal educational attainment. Metabolic profiles also differed: underweight was more common in the SGA group (4.3% vs.

2.1%), whereas obesity was more prevalent in the non-SGA group (20.3% vs. 17.2%). Detailed comparisons are shown in Table 1. Given the large sample size, we emphasize effect sizes (RRs) and their 95% confidence intervals throughout; all reported associations were statistically significant at $P < 0.001$ unless otherwise noted.

Table 1
Baseline characteristics of the study population stratified by SGA

Characteristic	Non-SGA (n = 35,156,091)	SGA (n = 3,859,979)	SMD
Maternal age, years, median [IQR]	29.00 [25.00, 33.00]	28.00 [24.00, 33.00]	0.164
Paternal age, years, median [IQR]	33.00 [28.00, 38.00]	33.00 [27.00, 40.00]	0.092
Gestational age, weeks, median [IQR]	39.00 [38.00, 40.00]	39.00 [38.00, 40.00]	0.002
Birth weight, g, median [IQR]	3,440 [3,180, 3,720]	2,630 [2,370, 2,790]	1.864
Maternal race/ethnicity, n (%)			0.246
Non-Hispanic White	18,698,121 (53.2)	1,678,993 (43.5)	
Non-Hispanic Black	4,431,060 (12.6)	737,256 (19.1)	
Hispanic	8,617,683 (24.5)	953,417 (24.7)	
Asian/Pacific Islander	1,969,863 (5.6)	331,941 (8.6)	
American Indian/Alaska Native	281,249 (0.8)	30,879 (0.8)	
Other/Not Reported	1,158,115 (3.3)	127,493 (3.3)	
Maternal education, n (%)			0.147
≤ 8th grade	1,158,115 (3.3)	127,493 (3.3)	
Some high school	3,058,593 (8.7)	428,842 (11.1)	
High school graduate	8,718,704 (24.8)	1,100,112 (28.5)	
Some college	6,714,814 (19.1)	737,256 (19.1)	
Associate degree	2,953,108 (8.4)	285,637 (7.4)	
Bachelor's degree	7,558,559 (21.5)	694,796 (18.0)	
Master's degree	3,480,453 (9.9)	328,098 (8.5)	
Doctorate	1,019,327 (2.9)	100,360 (2.6)	
Unknown	492,720 (1.4)	57,385 (1.5)	
Hypertensive disorders of pregnancy, n (%)			0.046
No	23,375,097 (66.5)	2,464,652 (63.9)	
Yes	1,865,994 (5.3)	311,042 (8.1)	

Characteristic	Non-SGA (n = 35,156,091)	SGA (n = 3,859,979)	SMD
Unknown	9,915,000 (28.2)	1,084,285 (28.1)	
Gestational diabetes, n (%)			0.057
No	23,395,461 (66.5)	2,598,891 (67.3)	
Yes	1,845,630 (5.3)	176,803 (4.6)	
Unknown	9,915,000 (28.2)	1,084,285 (28.1)	
Pre-pregnancy BMI category, n (%)			0.161
Underweight	738,859 (2.1)	164,167 (4.3)	
Normal	10,034,649 (28.5)	1,218,134 (31.6)	
Overweight	6,711,826 (19.1)	653,143 (16.9)	
Obese	7,144,764 (20.3)	663,010 (17.2)	
Unknown	10,525,993 (29.9)	1,161,525 (30.1)	
Parity, n (%)			0.230
Multiparous	15,704,723 (44.7)	1,422,804 (36.9)	
Primiparous	9,681,192 (27.5)	1,369,589 (35.5)	
Unknown	9,770,176 (27.8)	1,067,586 (27.7)	

Independent effects of maternal and paternal age

Maternal age showed a J-shaped association with SGA (Table S1, Fig. 1), with the highest risk at ≥ 45 years (RR 1.22, 95% CI 1.20, 1.23), followed by 40–44 years (RR 1.09, 95% CI 1.08, 1.09). The lowest risk was at < 20 years (RR 0.97, 95% CI 0.96, 0.97), suggesting that the crude excess risk in young mothers was largely explained by metabolic factors (low BMI and primiparity).

Paternal age also exhibited a J-shaped association (Table S1, Fig. 2), peaking at ≥ 45 years (RR 1.36, 95% CI 1.36, 1.37), with elevated risks at 40–44 years (RR 1.08, 95% CI 1.07, 1.08) and 20–24 years (RR 1.08, 95% CI 1.07, 1.08). The strong independent effect of advanced paternal age persisted after full adjustment.

Joint effects of parental age

In joint analysis (Table S2, Fig. 3), the highest SGA risk was in the “advanced paternal age only” group (RR 1.29, 95% CI 1.29, 1.30), while “advanced maternal age only” showed near-reference risk (RR 1.02, 95% CI 1.01, 1.02), and “dual-advanced” had moderate elevation (RR 1.16, 95% CI 1.15, 1.16). This

pattern confirms a negative additive interaction, as the joint effect (1.16) was less than the sum of independent effects ($1.02 + 1.29 - 1 = 1.31$).

Additive interaction

The additive interaction analysis confirmed a significant negative additive interaction between advanced maternal and paternal age on SGA (Table 2, Fig. 4). In the primary model, the RERI was -0.151 (95% CI $-0.157, -0.145$), the AP was -0.131 , and the S index was 0.512 . These metrics indicate that the joint effect of dual-advanced parental age was less than the sum of their independent effects, and that approximately 13.1% of the effect in the jointly exposed group was attributable to the negative interaction. The S index, substantially below 1, reflects a low efficiency of risk superposition—approximately half of that expected under a perfectly additive model.

In the model adjusting only for demographic factors (data not shown), the RERI was -0.182 . The attenuation to -0.151 after further adjustment for metabolic covariates suggests that a portion of the initially observed negative interaction is attributable to metabolic pathways associated with parental age. Nevertheless, the persistence of a significant negative RERI indicates that the interaction is not fully explained by measured metabolic confounders, supporting the existence of an independent biological mechanism.

For clarity, the 2×2 contingency table of the binary exposure variables and the corresponding RRs used in the RERI calculation are as follows: among births with neither parent of advanced age (reference), the RR = 1.00; with advanced maternal age only (mother ≥ 35 , father < 40), RR = 1.02; with advanced paternal age only (father ≥ 40 , mother < 35), RR = 1.29; and with both parents of advanced age (mother ≥ 35 , father ≥ 40), RR = 1.16. The RERI = $1.16 - 1.02 - 1.29 + 1 = -0.15$, confirming the negative additive interaction.

Sensitivity analyses

The negative additive interaction remained robust across all sensitivity analyses (Table 2). When the analysis was restricted to term deliveries (≥ 37 weeks), the RERI was further strengthened to -0.180 (95% CI $-0.186, -0.174$; AP = -0.156 ; S index = 0.465), confirming that the signal was not driven by preterm-related misclassification of SGA. After excluding births conceived via ART, the results were consistent with the primary analysis (RERI = -0.148 , 95% CI $-0.154, -0.142$; AP = -0.127 ; S index = 0.525), indicating that the interaction was independent of ART use. Furthermore, a sensitivity analysis using random forest-based multiple imputation (missRanger; 50 imputations) to address missing metabolic data yielded a comparable RERI of -0.177 (95% CI $-0.178, -0.176$; AP = -0.156 ; S index = 0.438), confirming the robustness of the findings under an alternative missing-data framework. The 200,000-subject imputation sample had an SGA prevalence of 9.8%, nearly identical to the full cohort (9.89%), supporting its representativeness.

Table 2
Sensitivity analyses — additive interaction between advanced maternal and paternal age on SGA

Analysis	RERI (95% CI)	AP	S index
Primary model	−0.151 (−0.157, − 0.145)	−0.131	0.512
Term deliveries (≥ 37 weeks)	−0.180 (−0.186, − 0.174)	−0.156	0.465
Multiple imputation	−0.177 (−0.178, − 0.176)	−0.156	0.438
Excluding ART	−0.148 (−0.154, − 0.142)	−0.127	0.525

E-value analysis

E-values were calculated for the two most prominent positive associations (Table S3). For maternal age < 20 years, the E-value was 1.18 (CI lower limit 1.16), indicating that the residual association was relatively sensitive to unmeasured confounding, which is consistent with the observation that metabolic factors explained a substantial portion of the excess risk in this group. For isolated advanced paternal age, the E-value was 1.66 (CI lower limit 1.65), suggesting that the independent effect of advanced paternal age was considerably more robust to unmeasured confounding. The relatively low E-value for young maternal age (1.18) further underscores the confounding role of metabolic factors in the association between young maternal age and SGA.

Comment

Principal findings

In this nationwide U.S. cohort of approximately 39 million singleton live births, we observed a clear negative additive interaction between advanced maternal and paternal age on SGA (RERI = − 0.151, 95% CI − 0.157, − 0.145). Notably, the highest SGA risk occurred not among couples with both parents older (RR = 1.16, 95% CI 1.15, 1.16), but rather in the 'advanced paternal age only' group (RR = 1.29, 95% CI 1.29, 1.30). This pattern persisted across multiple sensitivity analyses, including restriction to term births, exclusion of ART-conceived pregnancies, and multiple imputation for missing metabolic data. A recent population-based cohort study from China similarly reported a less-than-additive joint effect using the same additive interaction framework [13], though it did not find a significant independent association between paternal age and SGA. Our findings extend this line of inquiry to a multiethnic Western population and suggest that the role of paternal age may be more prominent in the U.S. context.

Strengths of the study

This study has several notable strengths. With approximately 39 million records, the nationwide, population-based design provided sufficient statistical power to detect subtle interaction effects that previous studies with smaller samples [12] could not reliably estimate. The use of additive interaction metrics, rather than conventional multiplicative terms, captured biological interactions on the most relevant scale for public health decision-making. The comprehensive suite of sensitivity analyses—

including restriction to term deliveries, exclusion of ART conceptions, multiple imputation, and E-value quantification—demonstrated the robustness of the primary findings under varying assumptions.

Limitations of the data

We acknowledge several limitations. First, while the cross-sectional design prevents us from drawing causal conclusions, parental age is inherently determined before pregnancy, so reverse causation is not a concern. E-value analyses suggested that an unmeasured confounder would need to be quite strong—risk ratios of at least 1.66 for isolated advanced paternal age and 1.18 for young maternal age—to fully account for the observed associations. Second, the publicly available birth files lack data on maternal smoking during pregnancy and have substantial missingness for metabolic variables (BMI, hypertensive disorders, gestational diabetes) due to non-collection in certain calendar years. While these missing data are a limitation, our multiple imputation sensitivity analysis yielded results consistent with the primary complete-case analysis, suggesting that this is unlikely to be a major source of bias. ART status was available and explicitly excluded in a sensitivity analysis, which also showed consistent results. Third, using an internal 10th percentile threshold to define SGA ensured consistency across years, but it also means our definition is relative to this specific population rather than an external standard—a limitation shared by all vital statistics studies. Fourth, paternal age was missing for only 0.38% of records, but even this small fraction could introduce bias; reassuringly, multiple imputation yielded results consistent with the complete-case analysis. Fifth, the absence of state identifiers in the public-use files prevented us from adjusting for geographic clustering, which may make our confidence intervals somewhat too narrow, though it is unlikely to affect the point estimates themselves. Sixth, multiple imputation assumes that data are missing at random—an assumption we cannot verify directly. Still, the close agreement between imputed and complete-case analyses gives us confidence that this is not a major source of bias. Seventh, our use of SGA as the outcome measure warrants specific comment. While SGA is sometimes used interchangeably with fetal growth restriction (FGR) in clinical settings, the two are not synonymous: SGA is a biometric classification based on birth weight below the 10th percentile for gestational age [1, 2], whereas FGR refers to a pathological failure to achieve growth potential [1, 3]. SGA includes both constitutionally small infants who are otherwise healthy and those with true growth restriction [3, 4]. Our research question focuses on the association between parental age and birth size distribution at the population level, rather than on distinguishing these two groups. SGA remains a well-established endpoint in perinatal epidemiology when the research question is framed appropriately [1, 5]. Thus, we used SGA as an epidemiological measure of fetal size at birth, not as a clinical diagnosis of growth restriction, and our findings should be interpreted in this context.

Interpretation

One useful way to interpret this negative additive effect is through the lens of genomic imprinting [24, 25]. The idea, in essence, is that placental growth reflects a tug-of-war between paternal and maternal genes. Paternally expressed imprinted genes—like IGF2—push for greater placental growth and nutrient transfer to the fetus [26]. Maternally expressed ones—such as CDKN1C—put the brakes on placental invasion. As fathers age, sperm accumulate epigenetic changes that may dull the paternal 'pro-growth'

signal [27]. Meanwhile, advancing maternal age—whether through oocyte aging or changes in the uterine environment—may weaken the maternal 'growth-restraining' signal. When both parents are older, both signals may be dialled down together, shifting the system to a new equilibrium. That's exactly what we observed: the dual-advanced age group had a lower risk than an additive model would predict (1.16 vs. 1.31). But when only the father is older—and the mother is younger, so her restraining signal is likely still intact—the paternal 'go' signal weakens without any compensatory loosening of the maternal brake, tipping the balance toward restricted growth. We want to be clear: this is a hypothesis, not a proven mechanism, and it needs to be tested directly.

Other explanations also deserve consideration. For instance, older mothers have higher rates of miscarriage; if the fetuses that survive tend to be more robust, this could introduce selection bias and partly explain the pattern. However, the negative interaction was actually stronger in term births (RERI = - 0.180), which tells us that selection cannot be the whole story. Another possibility is placental adaptation—compensatory changes in uterine artery function in older mothers that somehow buffer the effects of paternal age. We also thought about assortative mating, but adjusting for maternal education and race—and seeing similar results after excluding ART—suggests it is unlikely to be a major confounder.

Most earlier studies examined maternal and paternal age separately [28, 29], or tested their interaction only on a multiplicative scale. By shifting our focus to the additive scale, we may have picked up a biologically meaningful signal that others had missed. And we believe this shift—combined with the sheer scale of 39 million records—is what made that possible.

Conclusions

From a clinical standpoint, our findings identify a specific high-risk subgroup—fathers aged ≥ 40 years with partners aged < 35 years—that is not currently captured by maternal-age-based screening alone (RR 1.29). This subgroup may warrant closer fetal growth monitoring, though the optimal age thresholds require confirmation in other cohorts. For older mothers, the observation that SGA risk in the dual-advanced age group was less than additive may offer some reassurance. Overall, these results suggest that consideration of paternal age in prenatal risk assessment, alongside maternal age, may improve the identification of higher-risk pregnancies.

Abbreviations

AP

Attributable proportion

ART

Assisted reproductive technology

BMI

Body mass index

CI
Confidence interval
FGR
Fetal growth restriction
IQR
Interquartile range
NBER
National Bureau of Economic Research
NCHS
National Center for Health Statistics
RERI
Relative excess risk due to interaction
RR
Risk ratio
S
Synergy index
SGA
Small-for-gestational-age
SMD
Standardized mean difference
STROBE
Strengthening the Reporting of Observational Studies in Epidemiology

Declarations

Ethics approval and consent to participate

Because this study used publicly available, de-identified data, it was exempt from Institutional Review Board review under U.S. Department of Health and Human Services regulations (45 CFR 46).

Consent for publication

Not applicable.

Availability of data and materials

The data underlying this article are publicly available from the National Center for Health Statistics (NCHS) via the U.S. National Vital Statistics System (https://www.cdc.gov/nchs/data_access/VitalStatsOnline.htm) and from the National Bureau of Economic Research (NBER) Vital Statistics Natality Birth Data repository (<https://www.nber.org/research/data/vital-statistics-natality-birth-data>). All analysis code used in this study is available from the corresponding author upon reasonable request.

Competing interests

The authors declare that they have no competing interests.

Funding

The authors have nothing to report.

Authors' contributions

SL and JL contributed equally to this work as co-first authors. They jointly conceived the study design, performed the literature search, and led the data analysis. SL wrote the first draft of the manuscript and prepared all figures and tables. JL conducted the statistical analyses using R, including the Poisson regression models and the additive interaction calculations, and verified the underlying data. TZ and XT contributed to data interpretation and critical revision of the manuscript for important intellectual content. TC and JCL assisted with data cleaning, variable definition, and sensitivity analyses, and provided administrative support. LH and LW are co-corresponding authors. LH participated in the study concept and coordination, and provided clinical expertise on perinatal outcomes. LW supervised the entire project, obtained access to the data sources, and revised the final manuscript. All authors reviewed and approved the final version, and agree to be accountable for all aspects of the work.

Acknowledgements

We thank the National Center for Health Statistics (NCHS) and the National Bureau of Economic Research (NBER) for making the natality data publicly available. We also thank our colleagues at the Perinatal Medical Center of the Fifth Affiliated Hospital of Sun Yat-sen University for their support and clinical input during the study. This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

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Figures

Maternal Age and SGA

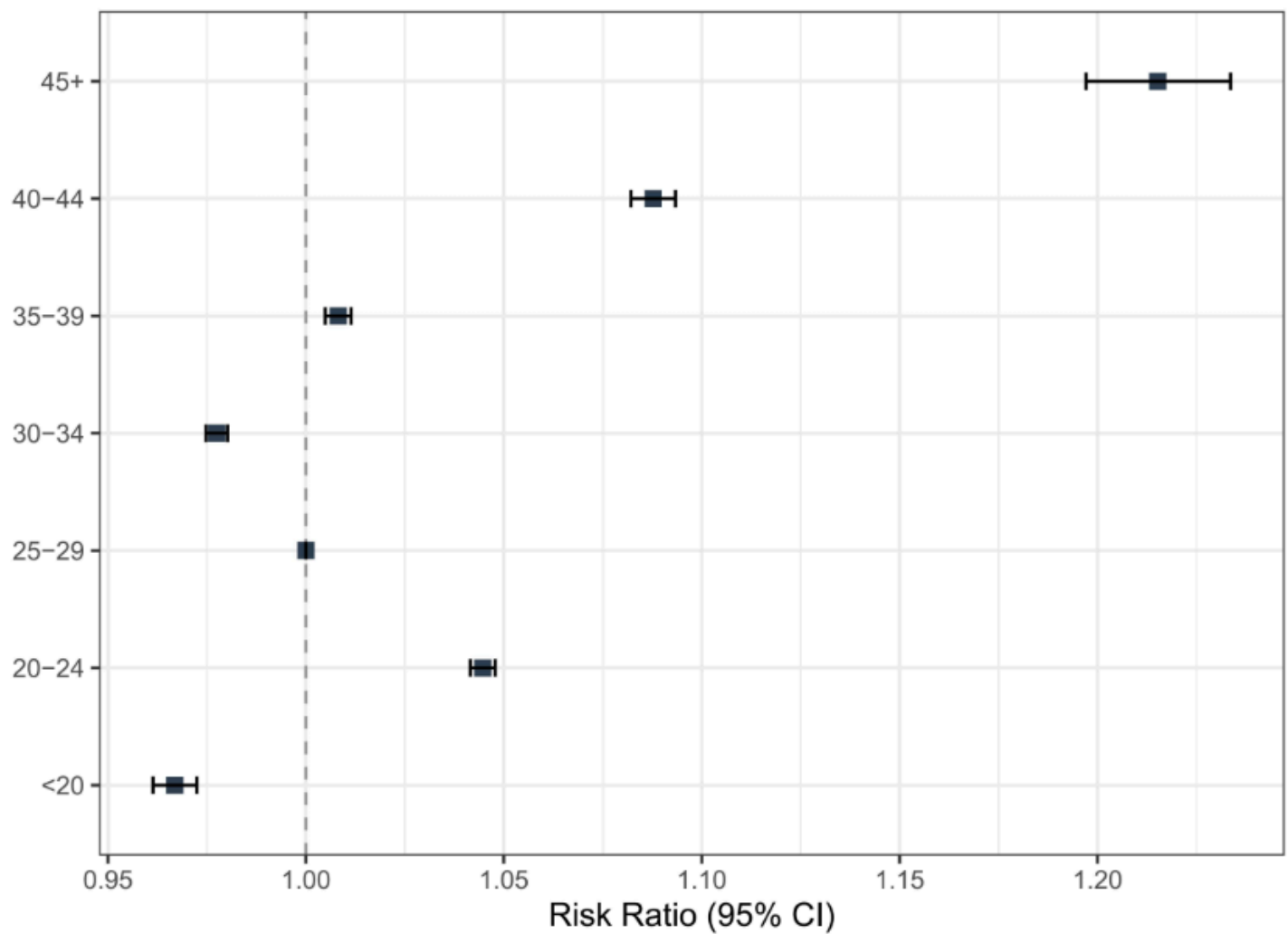


Figure 1

Adjusted risk ratios for SGA by maternal age categories.

Paternal Age and SGA

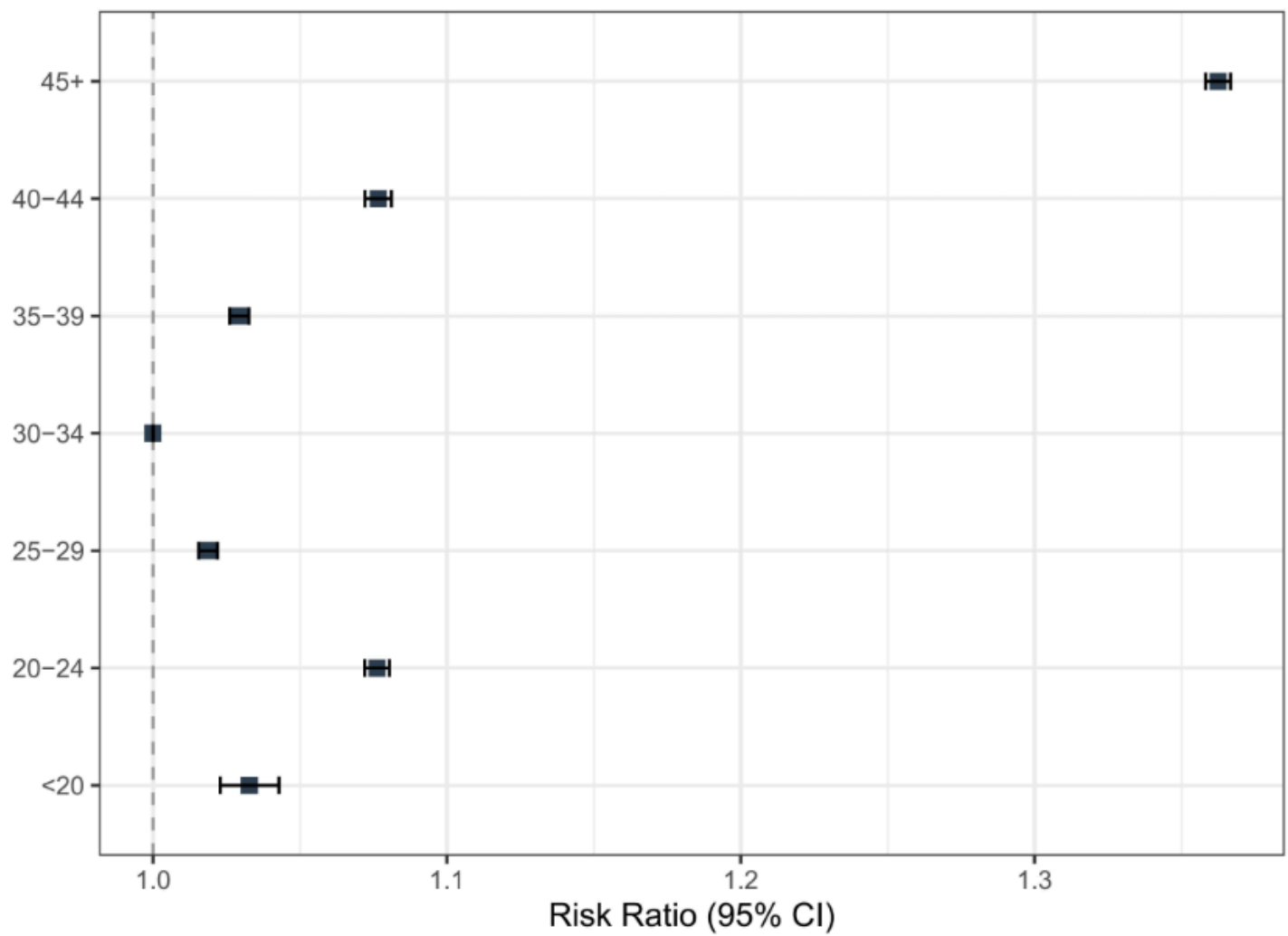


Figure 2

Adjusted risk ratios for SGA by paternal age categories.

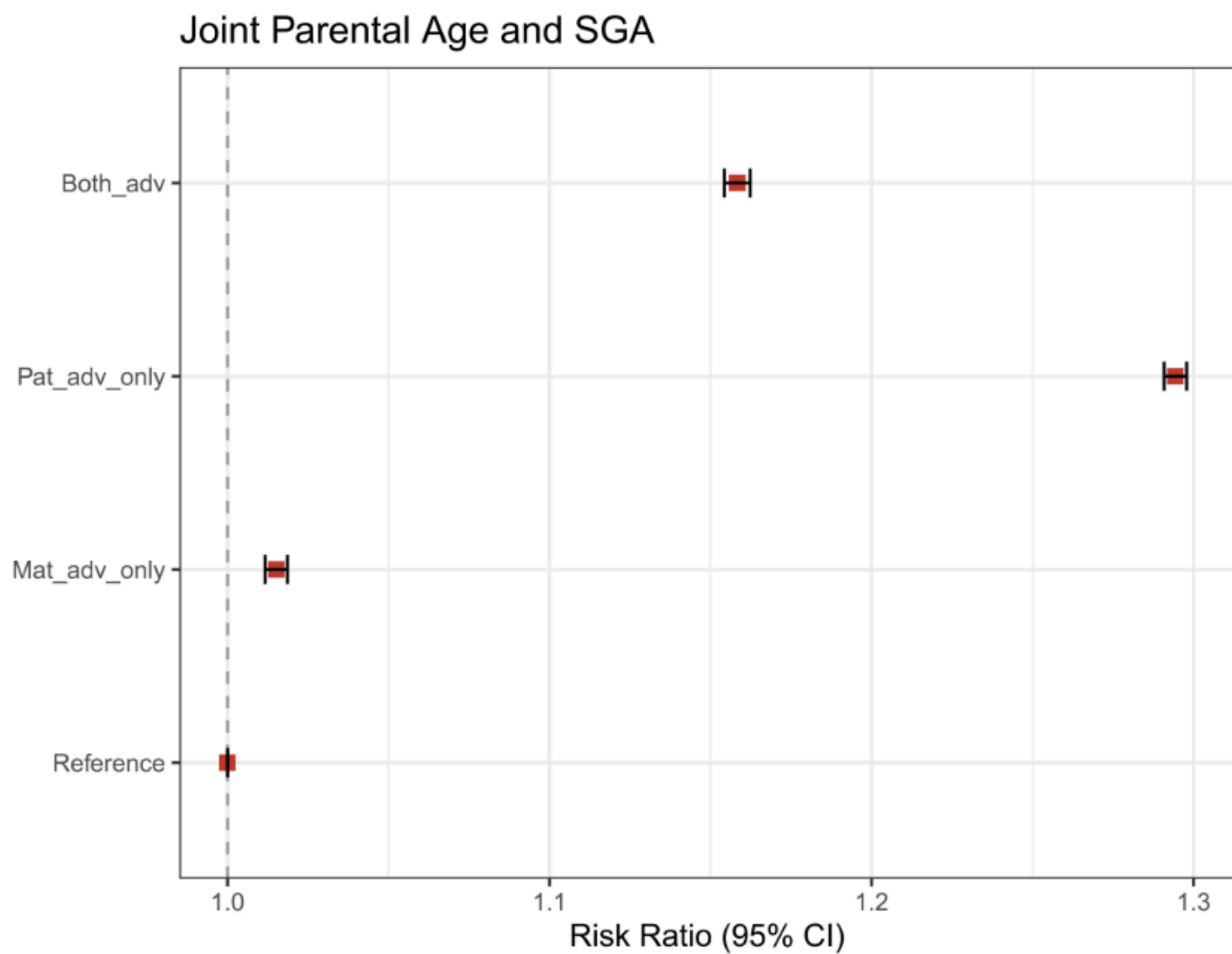


Figure 3

Adjusted risk ratios for SGA by joint parental age categories.

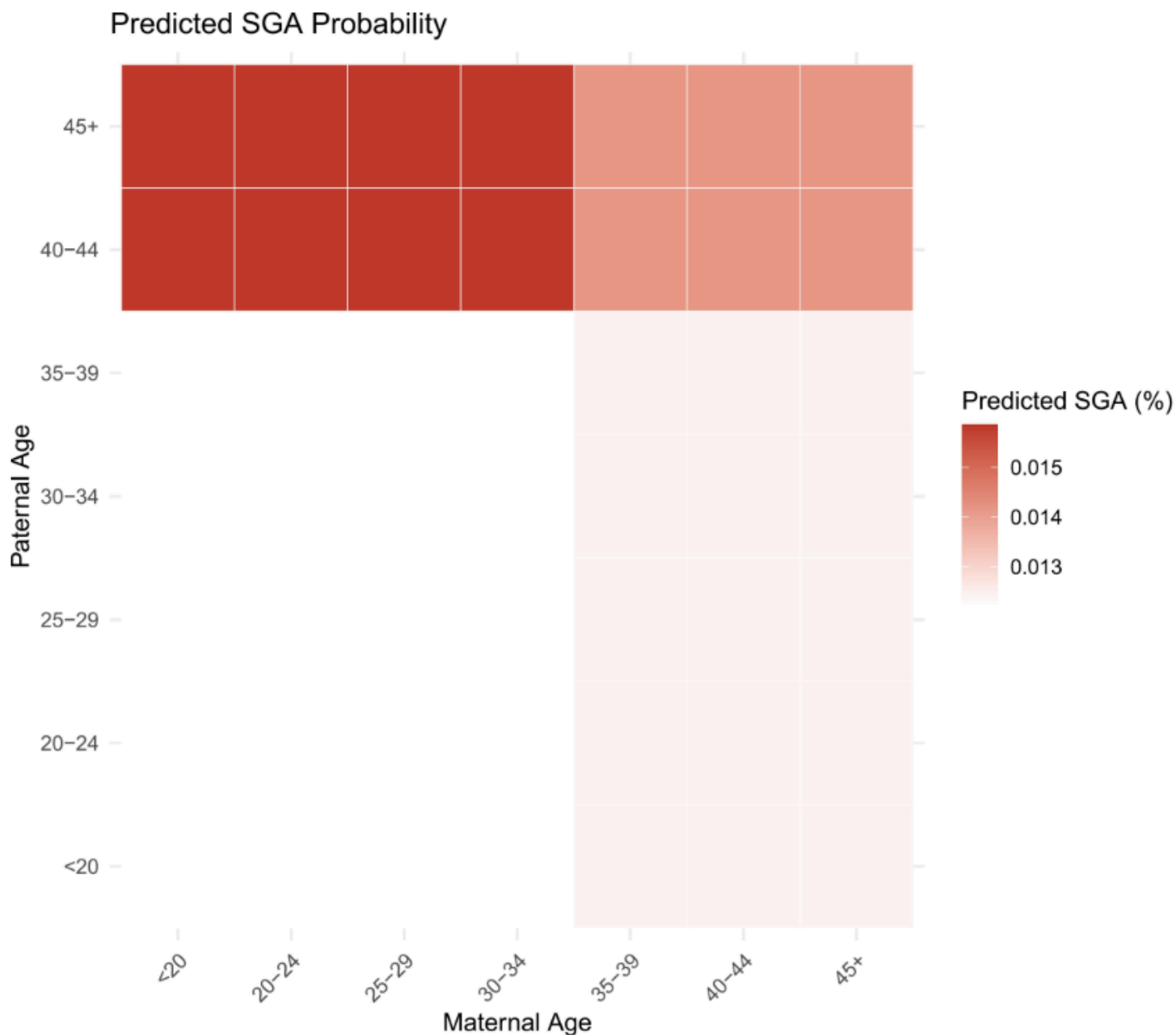


Figure 4

Additive interaction between advanced maternal and paternal age on SGA risk

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