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Childhood Adversity, Socioeconomic Instability, Oxytocin-Receptor-Gene Methylation, and Romantic-Relationship Support Among Young African American Men

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Abstract

Men's emerging adult romantic relationships forecast downstream relationship behavior, including commitment and quality. Accumulating evidence implicates methylation of the oxytocin-receptor-gene (*OXTR*) system in regulating relationship behavior. We tested hypotheses regarding the links between (a) childhood adversity and (b) socioeconomic instability in emerging adulthood on supportive romantic relationships via their associations with *OXTR* methylation. Hypotheses were tested using path analysis with data from 309 participants in the African American Men's Project. Consistent with our hypotheses, results showed that *OXTR* methylation proximally predicted changes in relationship support during a 1.5-year period. Childhood adversity was not directly associated with *OXTR* methylation but, rather, with contemporaneous socioeconomic instability, which in turn predicted elevated *OXTR* methylation. Findings suggest that early adversity is indirectly associated with *OXTR* methylation by links with downstream socioeconomic instability. Findings must be considered provisional, however, because preregistered replications are needed to establish more firmly the relations among these variables.

Keywords

African American men, early adversity, DNA methylation, oxytocin, romantic relationships

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Developmental theorists have identified the formation of increasingly intimate and nurturing bonds with a romantic partner as one of the critical tasks of emerging adulthood (Fincham & Cui, 2010). Although considerable diversity characterizes patterns of relationship growth during this developmental stage, the formation of nurturing, supportive romantic relationships appears to have prognostic significance for downstream adult relationship commitment and marital quality (Fincham & Cui, 2010). Young men, compared with young women, report greater difficulty in establishing such relationships (Rauer, Pettit, Lansford, Bates, & Dodge, 2013). Among the rural African American men who were the focus of the present study, a number of contextual challenges to the development of nurturing relationships have been documented. Disproportionate exposure to multiple stressors in rearing environments and contemporaneous settings have been linked to the quality of African Americans' relationships in adolescence and emerging adulthood (Kogan et al., 2013). These circumstances have also been implicated in the low rates of

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marriage that characterize African American populations (Barton & Bryant, 2016).

For the most part, investigations of the mechanisms linking contextual stressors to romantic-relationship behavior have been viewed in terms of stress-spillover and cognitive-mediation models. Spillover models emphasize individuals' immediate coping needs and the ways in which stressors undermine relationships by fostering negative emotionality and attributions that foment conflict and distrust (Conger et al., 2002). Cognitive-mediation models emphasize the capacity of relationships in childhood to form enduring cognitive schemas that organize future views of, and responses to, interpersonal behavior (Kogan et al., 2013). Recently, approaches to understanding the effects of challenging environments on romantic relationships have undergone a transformation in focus. Studies suggest that exposure to stressful social environments promotes biological changes, some with direct regulatory implications for contemporaneous and future behavior in close relationships (Meloni, 2014). Preclinical studies, as well as emerging evidence in humans, implicate epigenetic regulation of gene expression to explain how contextual factors affect relationship behavior (Meloni, 2014). Epigenetic regulation involves biochemical mechanisms that influence the genome to express (upregulate or downregulate) particular genes. Psychosocial stressors are known to alter epigenetic regulation of genes (Cunliffe, 2016). Epigenetic factors thus appear to be mechanisms whereby life experiences become biologically embedded, exerting a physiological influence on cognitive, emotional, and behavioral traits (Meloni, 2014).

DNA methylation, the addition of a methyl group to a DNA base, silencing gene expression, is the most well known and extensively studied example of an epigenetic modification (Meloni, 2014). Recent studies suggest that DNA methylation of the oxytocin receptor gene (*OXTR*) may be an important mechanism whereby exposure to stressful environments affects behavior in close relationships (Baker et al., 2017). *OXTR* codes for the oxytocin receptor; oxytocin is a neuropeptide with anxiolytic properties that plays an important role in social cognition and relationship behavior (Insel, 2010). Recent studies suggest that hypermethylation of *OXTR* may be an important mechanism whereby exposure to stressful environments affects general impairments in social, cognitive, and emotional functioning (Maud, Ryan, McIntosh, & Olsson, 2018). *OXTR* methylation has been shown to increase in response to maltreatment (Cecil et al., 2014; Unternaehrer et al., 2015) and conflicted or unsupportive social relationships in adulthood (Simons, Lei, Beach, Cutrona, & Philibert, 2017). Other studies have focused on the phenotypic consequences of *OXTR* methylation in humans, revealing links with a range of factors that affect close relationships. *OXTR* hypermethylation prospectively predicts maladaptive relationship cognitions in adults (Simons et al., 2017), callous and unemotional traits among adolescents (Cecil et al., 2014), and autistic traits (Gregory et al., 2009). Neuroimaging studies link *OXTR* methylation with performance on tasks germane to social cognition and perception (Jack, Connelly, & Morris, 2012; Puglia, Lillard, Morris, & Connelly, 2015). Taken together, these studies suggest that *OXTR* hypermethylation may serve as a biological mechanism linking challenging environments to difficulties in close relationships.

Although current evidence is suggestive, the potential role of *OXTR* methylation in linking stressful environments to romantic-relationship behavior requires additional investigation. It is unclear whether *OXTR* methylation is modified specifically by stressful rearing environments or by any proximal stressors. Studies linking childhood adversity to *OXTR* methylation are inconsistent (Cecil et al., 2014; Gouin et al., 2017). Other studies suggest that proximal rather than distal forms of stress affect *OXTR* methylation. Simons et al. (2017) found a prospective link between conflictual relationships in adulthood and *OXTR* methylation. A recent experimental study (Unternaehrer et al., 2012) showed that *OXTR* methylation changes in response to acute stressors engendered in a laboratory setting. Whether methylation is a product of childhood stressors, recent stressors, or both is an open question. In addition, studies examining the effects of adversity on methylation and those investigating the consequences of *OXTR* methylation for relationships have been conducted separately. Only one study of which we are aware (Simons et al., 2017) has examined indirect-effects hypotheses and found that the effects of adversity on relationship cognitions were connected via *OXTR* methylation; however, the influence of childhood stressors was not considered in this study.

To address these research limitations, we tested complementary hypotheses regarding the associations of adversity in childhood and socioeconomic instability in emerging adulthood with supportive romantic relationships via links with *OXTR* methylation. Hypotheses are presented visually in Figure 1. Our first hypotheses stated that childhood adversity and contemporaneous socioeconomic instability (residential instability, economic distress, unemployment, and low attachment to work) would each contribute independently to *OXTR*-methylation levels. To address the inconsistencies discussed previously regarding the unique role of early stress, we conducted simultaneous examinations to determine whether childhood adversity undermines socioeconomic stability during the transition to adulthood. Past research has revealed considerable continuity in stressful environments from childhood through

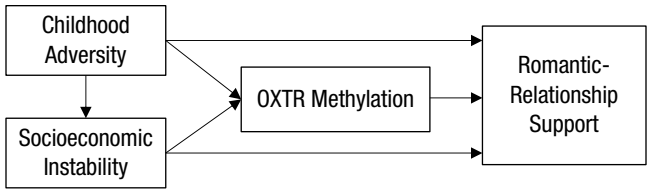

Fig. 1. Conceptual model used to test complementary hypotheses regarding the associations of adversity in childhood and socioeconomic instability in emerging adulthood with supportive romantic relationships via links with oxytocin-receptor-gene (*OXTR*) methylation.

adulthood (Pearlin, Schieman, Fazio, & Meersman, 2005). We reasoned that if no direct effects for early adversity emerged in the present study, then the indirect path might clarify the inconsistencies found for this variable in the literature.

Method

Participants

Hypotheses were tested with extant data from the African American Men's Project (AMP), a study of relationships and health-risk behavior among young African American men in the rural South. Rural African American young men experience elevated levels of poverty and community disadvantage as well as low rates of marriage; these factors underscore such men's importance for examining the effects of contextual disadvantages on relationship behavior. Participants resided in 11 rural counties in south Georgia, an area representative of a geographic concentration of rural poverty across the southern coastal plain (Crockett, Carlo, & Temmen, 2016). To be eligible, men must have been 19 to 22 years old (M = 20.18 years, SD = 1.08) and have designated themselves as African American or Black at the baseline interview (Time 1).

We recruited participants using respondent-driven sampling, which combines a prescribed chain-referral recruitment method designed to reduce biases commonly associated with network-based samples (Heckathorn, 1997). Community liaisons recruited 45 initial seed participants from targeted counties to complete a baseline survey. Each participant was then asked to identify three other men in his community from his personal network who met the criteria for inclusion in the study (self-reported African American or Black, age 19–22 years, and living in the targeted area). Project staff contacted the referred potential participants, and the referring participant received $25 for each person who completed the survey. After completing the survey, each referred participant, in turn, was asked to refer three men in his network. Recruitment ended after we reached a sample exceeding 500 (N = 505).

The respondent-driven-sampling protocols and weighting system were designed to attenuate the influence of biases common in chain-referral samples and to improve approximation of a random sample of the target population (Heckathorn, 1997). Analyses of network data related to substance use and other risky behavior at Time 1 (Kogan et al., 2017) indicated that the sample had negligible levels of common biases (often observed in chain-referral samples) arising from the characteristics of the initial seed participants, individual participants' recruitment efficacy, and differences in the sizes of participants' networks.

Data-collection procedures

African American research staff visited participants at their homes or at convenient community locations, and participants completed an audio computer-assisted self-interview on a laptop computer. This allowed participants to navigate the survey privately with the help of voice and video enhancements, eliminating literacy concerns. Approximately 18.30 months (SD = 4.19) after the baseline survey, when the sample's mean age was 21.85 years (SD = 1.27), a follow-up data collection visit (Time 2) was conducted in the same manner. A third visit (Time 3) took place 19.68 months later, when the sample's mean age was 23.49 years (SD = 1.21). Of the 505 men who participated at Time 1, 423 (83.8%) completed the Time 2 survey and 409 (81.0%) completed the Time 3 survey. Retention status from Time 1 to Time 3 was not associated with childhood adversity, socioeconomic instability, or relationship support; retention status also was not associated with *OXTR*-methylation status from Time 2 to Time 3. Participants received $100 at each time point for completing the survey. Participants provided written informed consent, and all study protocols were approved by the institutional review board of the University of Georgia, where the study was conducted.

At Time 2, participants provided saliva specimens for methylation assays. Unlike genetic modifications, epigenetic modifications are tissue specific, prompting preclinical studies of behavior to focus on DNA from brain tissues. Research with humans must rely on DNA extracted from proxy tissues, with blood typically the preferred medium. Accumulating evidence, however, indicates that high-quality methylation profiles can be generated from saliva for both genomewide (Langie et al., 2017) and candidate gene (Nishitani, Parets, Haas, & Smith, 2018) analyses. In recent years, the use of saliva in studies of methylation has become more common, in part, because of technical improvements in saliva sampling and storage (Wren, Shirtcliff, & Drury, 2015). A number of studies confirmed that genomewide DNA-methylation profiles from saliva are more than 90% comparable with those from blood (Langie et al., 2017).

Other evidence indicates that DNA extracted from saliva is more similar to the methylation patterns observed in brain tissues than is DNA from blood (Smith et al., 2015). Thus, saliva appears to be a good proxy tissue for methylation studies of human behavior. Participants provided saliva specimens using Oragene Discover OGR-500 kits (DNA Genotek, Ottawa, Ontario, Canada). Participants rinsed their mouths with tap water and then deposited 2 ml of saliva in the Oragene sample vial. The vial was sealed, inverted, and shipped via courier to a central laboratory in Iowa City, Iowa, where samples were prepared according to the manufacturer's specifications.

Of the 423 participants who completed survey data at Time 2, 374 (88.4%) agreed to provide a specimen, and for 358 participants (95.7%), valid information on *OXTR* methylation was obtained. Analyses comparing participants who declined to provide a specimen and participants who provided one revealed no differences in demographic variables (income, age, student status) or other study variables (childhood adversity, socioeconomic instability, relationship support). Of the 358 participants who provided DNA, we limited our sample to 309 young men who had a main partner either at Time 1 (n = 264, 85.4%) or at Time 2 (n = 262, 84.8%).

To ensure adequate power to detect hypothesized effects in our model, we considered statistical power estimates at the individual parameter and model levels. At the individual parameter level, we conducted a Monte Carlo simulation for mediational designs using Mplus Version 7.4 (Muthén & Muthén, 2012). We specified a sample size of 309 and data missing at random for a model with two exogenous variables (childhood trauma, Time 1 relationship support), two intermediate outcomes (socioeconomic instability, *OXTR*-methylation index), and one outcome (Time 2 relationship support). The simulation provides power estimates for individual parameters when the other parameters in the model are constrained. Power was .85 for detecting a small effect (Cohen's d = 0.10, $p < .05$) and for detecting indirect effects as small as .05. Using MacCallum, Browne, and Sugawara's (1996) model-based power-estimate protocols with a sample size of 309 and 14 degrees of freedom, we found that power would exceed .80 to detect a close-fitting model (root-mean-square error of approximation, or RMSEA = .05).

OXTR-methylation assays

DNA was extracted using prepIT•L2P reagent (DNA Genotek) and was quantified with PicoGreen (Quant-iT PicoGreen dsDNA Assay Kit; Thermo Fisher Scientific, Pittsburgh, PA). Five hundred nanograms of DNA were treated with bisulfite using the EpiTect Bisulfite Kit (Qiagen, Germantown, MD). DNA methylation of 27 cytosine-phosphorus-guanine (CpG) sites in the promoter region, including the metallothionein 2 (MT2) region (Kusui et al., 2001) of the *OXTR* gene (chromosome 3: 8,792,095–8,811,300; human genome 19 build), were analyzed using EpiTYPER (MassARRAY system; Agena Biosciences, San Diego, CA) according to the manufacturer's instructions. Forward (AGGAAGAGAGGAGGTTTTAGTGAGAGATTTTAGTTTAG) and reverse (CAGTAATACGACTCACTATAGGGAGAAGGCTTCCCTACTAAAAAAACCCCTACCTC) primers were used corresponding to chr3: 8,810,604 to 8,811,075. Cycling conditions were denaturation (94° C for 15 min), 50 cycles of amplification (94° C for 30 s, 58° C for 60 s, and 72° C for 30 s), and a final extension step of 72° C for 10 min. Samples were electrophoresed using 2% agarose gel to confirm amplification. The mass-spectra methylation ratios were generated using EpiTYPER (Version 1.2; Agena Biosciences).

Measures

OXTR DNA-methylation index. Previous research has focused on methylation at individual CpG sites as well as mean methylation levels across sites in this region (Dadds et al., 2014). The present study focused on methylation across 14 consecutive CpG sites from chr3: 8,810,648 to 8,810,890. These sites are located in Intron 1, a region with demonstrated associations with social behavior and cognition (Gregory et al., 2009; Kumsta, Hummel, Chen, & Heinrichs, 2013). In two instances, sites covaried totally with each other (CpG 19 with CpG 20, CpG 25 with CpG 26) and were thus considered one data point, resulting in 12 data points under study. Mean levels of methylation for each site are presented in Figure S1 in the Supplemental Material available online. Using the SPSS scale to produce Cronbach's alpha, we found that the consecutive CpG sites resulted in reasonable convergence to a single scale (α = .58), which exceeds convergence found in prior research (Dadds et al., 2014). The reliability of the methylation assays was checked for each CpG site. EpiTect control DNA samples (Qiagen), known to be fully methylated and fully unmethylated, were assessed in triplicate in parallel to the study DNA to confirm the reproducibility and sensitivity (upper and lower limits of detection) for each assay (see Fig. S2 in the Supplemental Material).

Relationship support. At Time 1 and Time 2, men reported their relationships with a main partner (defined as "a woman or girl that you have a very special or committed relationship with, such as a girlfriend or a spouse"). Men reported the support they gave to this partner on a three-item subscale of the Network of Relationships Inventory (Furman & Buhrmester, 2009). The items were

"How often do you protect and look out for her?" "How often do you take care of her?" and "How often do you help her with things she can't do by herself?" The response set ranged from 0 (*never*) to 3 (*very often*). Items were summed, and higher scores reflected greater support ($\alpha = .81$).

Socioeconomic instability. We developed a composite index to assess the socioeconomic-instability construct using four indicators collected at Time 1. Men reported on the number of times they had moved in the past 6 months on a scale ranging from 0 (*none*) to 4 (*four or more times*) and their school enrollment or employment status (0 = *either enrolled in school or full time/part-time employed*, 1 = *neither enrolled in school nor employed*). Men reported their vocational engagement on a six-item scale (e.g., "I have trouble keeping jobs," "I am a dependable employee"; $\alpha = .80$). Economic distress was assessed with a five-item scale (e.g., "I have enough money to afford the kind of home I need," "I have enough money to afford the kind of food I need"; $\alpha = .79$). We conducted a principal component analysis to assess the unidimensionality of the four indicators, which revealed that the indicators tapped a single underlying factor (eigenvalue = 1.37) and factor loadings ranged from .49 to .65. We subsequently operationalized the socioeconomic-instability construct as the factor score from this analysis.

Childhood adversity. At Time 3, men completed the short form of the Childhood Trauma Questionnaire (Bernstein, Ahluvalia, Pogge, & Handelsman, 1997), which includes 28 questions that assess sexual abuse (e.g., "Someone tried to touch me in a sexual way, or tried to make me touch them"), physical abuse (e.g., "People in my family hit me so hard that it left me with bruises or marks"), emotional abuse (e.g., "I thought that my parents wished I had never been born"), physical neglect (e.g., "I didn't have enough to eat"), and emotional neglect (e.g., "I felt loved"; reverse coded) prior to the age of 16 years. The response set ranged from 0 (*never true*) to 4 (*very often true*). The five subscales were standardized and summed to form a childhood-trauma index. The alpha for the total score was .78.

Demographic and other covariates. Past research has suggested that older age, educational attainment, and cohabitation are associated with greater supportive behavior in a relationship; cohabitation also covaries with opportunity to be of support to a partner (Larson & Holman, 1994). Thus, we controlled for these constructs. Targets' age at baseline was assessed as a continuous variable. At Time 1 and Time 2, the main partner's age and educational attainment and cohabitation with the main partner were assessed. Approximately one half of the participants had the same partner at Time 1 and Time 2. Because men's supportiveness may vary across partners, we also controlled for having the same main partnership across Time 1 and Time 2. In addition, we controlled for smoking frequency during the past 3 months at Time 1, which has been associated with DNA methylation in previous research (Sugden et al., 2019). The response set for the smoking item ("How many cigarettes did you smoke in the past 3 months?") ranged from 0 (*none at all*) to 7 (*more than two packs a day*).

Plan of analysis

The hypotheses visualized in Figure 1 were tested with path analyses implemented in Mplus Version 7.13 (Muthén & Muthén, 2012). We controlled for the influences of age, educational attainment, cohabitation, and having the same partner across waves on romantic-relationship support. Data missing because of attrition or lack of information on relationship support at one time point were not associated with any study variables. Missing data thus were managed with full-information maximum-likelihood estimation, which tests hypotheses with all available data; no cases are dropped. To assess goodness of fit, we used indices that Bollen (1989) recommended, which included the chi-square test, the RMSEA, and the comparative fit index (CFI). Close-fitting models are indicated by a nonsignificant chi-square value, a CFI greater than or equal to .95, and an RMSEA less than .06. The significance of indirect effects was assessed with bootstrapping, and effect sizes were calculated on the basis of the proportion of indirect effects to the total effects using a regression-based model protocol (Preacher & Kelley, 2011).

Results

Table 1 presents the sample's characteristics. At Time 1, approximately 40% of young men ($n = 119$) had moved more than once in the previous 6 months, and nearly 30% of the sample ($n = 91$) were neither enrolled in school nor employed. At Time 2, about 60% of the sample ($n = 154$) lived with their main partners, and 47% ($n = 145$) maintained romantic relationships with the same partners across Time 1 and Time 2. Correlations among all study variables are shown in Table 2. As expected, childhood adversity, socioeconomic instability, and *OXTR* methylation were negatively correlated with romantic-relationship support. Scatterplots showing correlations between the methylation index and the dependent variables are presented in Figure S3 in the Supplemental Material. Associations between individual CpG sites and dependent variables are presented in

Table 1. Sample Characteristics

Variable	*n* (%)	*M* (*SD*)	Range
Childhood adversity		0.22 (4.13)	−5.38 to 12.57
Socioeconomic instability (Time 1)		0.00 (1.00)	−1.85 to 3.65
Residential instability			
No or one move	190 (61.5)		
More than one move	119 (38.5)		
Not enrolled in school and not employed			
No	218 (70.6)		
Yes	91 (29.4)		
Vocational engagement		33.91 (3.95)	21 to 40
Economic distress		10.58 (3.00)	5 to 19
OXTR methylation (Time 2)		0.24 (0.03)	
Romantic-relationship support (Time 1)		4.58 (3.41)	0 to 9
Romantic-relationship support (Time 2)		4.40 (3.32)	0 to 9
Target age (Time 1)		20.18 (1.08)	19 to 22
Main partner age (years; Time 1)[a]			
18 or younger	62 (23.5)		
19–20	103 (39.0)		
21–22	55 (20.8)		
23–25	27 (10.2)		
26 or older	17 (6.4)		
Main partner age (years; Time 2)[b]			
18 or younger	19 (7.3)		
19–20	75 (28.6)		
21–22	71 (27.1)		
23–25	68 (26.0)		
26 or older	29 (11.1)		
Main partner education (Time 1)[a]			
< High school	35 (13.3)		
High school/GED	153 (58.0)		
> High school	76 (28.8)		
Main partner education (Time 2)[b]			
< High school	23 (7.3)		
High school/GED	124 (47.3)		
> High school	115 (43.9)		
Living arrangement with a main partner (Time 1)[a]			
Living together	117 (44.3)		
Not living together	147 (55.7)		
Living arrangement with a main partner (Time 2)[b]			
Living together	154 (58.8)		
Not living together	108 (41.2)		
Same main partnership (Time 1–Time 2)			
With same main partner	145 (47.1)		
Not with same main partner	163 (52.9)		
Smoking frequency (Time 1)			
None at all	181 (58.6)		
Less than one cigarette a day	27 (8.7)		
One to five cigarettes a day	50 (16.2)		
About a half pack a day	27 (8.7)		
About a pack a day	21 (6.8)		
About one and a half packs a day	2 (0.6)		
About two packs a day	1 (0.3)		

Note: *OXTR* = oxytocin receptor gene; GED = general equivalency diploma.
[a]Values for this variable were obtained only from respondents who had a main partner at Time 1 ($n = 264$).
[b]Values for this variable were obtained only from respondents who had a main partner at Time 2 ($n = 262$).

Table 2. Correlations Among the Study Variables

Variable	1	2	3	4	5	6	7	8	9	10	11	12	13
1. Childhood adversity													
2. Socioeconomic instability (Time 1)	.24**												
3. *OXTR* methylation (Time 2)	−.03	.15**											
4. Romantic-relationship support (Time 1)	−.07	−.09	−.15**										
5. Romantic-relationship support (Time 2)	−.17**	−.06	−.21**	.36**									
6. Target age (Time 1)	.04	.15**	−.04	−.03	−.01								
7. Main partner age (Time 1)	.05	.08	−.04	.11	.12	.49**							
8. Main partner age (Time 2)	.06	.05	.06	.02	.04	.30**	.44**						
9. Main partner education (Time 1)	−.04	−.14*	−.06	.11	.03	.16**	.25**	.26**					
10. Main partner education (Time 2)	−.14*	−.25**	−.08	.07	.15*	−.13*	−.10	.14*	.54**				
11. Living arrangement (Time 1)	.05	.15*	−.10	.26**	.17**	.25**	.33**	.19**	.09	−.09			
12. Living arrangement (Time 2)	−.05	.08	−.05	.11	.11	.06	.20**	.20**	.04	−.07	.35**		
13. Same main partnership (Time 1–Time 2)	.01	.01	−.19**	.32**	.38**	−.02	−.07	−.12	.01	.04	.14*	.09	
14. Smoking frequency (Time 1)	.21**	.17**	−.03	.04	.04	.29**	.29**	.15*	−.01	−.10	.19**	.14**	.01

Note: Time 2 was approximately 18 months after Time 1. *OXTR* = oxytocin receptor gene.
*$p < .05$. **$p < .01$.

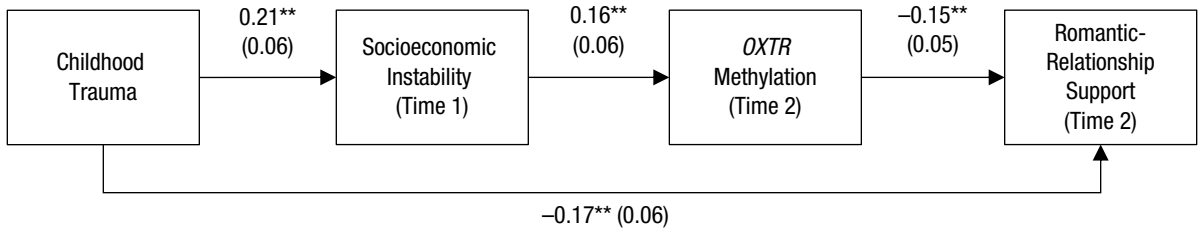

Fig. 2. Final model used to test the effect of childhood trauma on adult romantic-relationship support through socioeconomic instability at Time 1 and oxytocin-receptor-gene (*OXTR*) methylation at Time 2. Standardized coefficients are shown (standard errors are in parentheses). The model included controls for target's age, romantic partner's age and education, living arrangement with a romantic partner, maintaining a relationship with the same romantic partner across 18 months (from Time 1 to Time 2), and baseline romantic-relationship support. Asterisks indicate significant paths ($p < .01$).

Table S1 and Figures S4 to S6 in the Supplemental Material.

The results of the study hypotheses are presented in Figure 2 and in Table S2 in the Supplemental Material (nonsignificant paths and control variables are not pictured in Fig. 2). The model fitted the data as follows: $\chi^2(10, N = 309) = 12.41$, $p = .26$, RMSEA = .03, CFI = .98. Childhood adversity was significantly associated with young African American men's contemporaneous socioeconomic instability ($\beta = 0.21$, $p < .01$), which in turn was significantly associated with *OXTR* methylation ($\beta = 0.16$, $p < .01$). *OXTR* methylation predicted decreases in romantic-relationship support at Time 2 ($\beta = -0.15$, $p < .01$) after we controlled for baseline levels ($\beta = 0.20$, $p < .01$). Although childhood adversity was not significantly associated with *OXTR* methylation, it evinced a significant direct effect on romantic-relationship support at Time 2 ($\beta = -0.17$, $p < .01$). Indirect-effects analyses are presented in Table 3. The total indirect effect of childhood adversity on romantic-relationship support through socioeconomic instability and *OXTR* methylation was significant ($p < .05$; $b = -0.01$, 95% confidence interval, or CI = [−0.019, −0.001], effect size = .07). Childhood adversity was associated with *OXTR* methylation indirectly through participants' socioeconomic instability ($b = 0.04$, 95% CI = [0.008, 0.071], effect size = .38). Also, the indirect path linking socioeconomic instability to romantic-relationship support via *OXTR* methylation was significant ($b = -0.03$, 95% CI = [−0.054, −0.003], effect size = .31).

Discussion

In the present study, we investigated the potential role of DNA methylation in *OXTR* as a mechanism linking childhood adversity and socioeconomic instability in young adulthood to changes in relationship support among young African American men. Consistent with our hypotheses, results showed that *OXTR* methylation was associated with changes in relationship support during a 1.5-year period. Despite previous evidence that early adversity may become physiologically embedded via *OXTR* methylation (Unternaehrer et al., 2015), we found no evidence for a direct association of self-reported childhood adversity with *OXTR*-methylation status. Rather, contemporaneous socioeconomic instability was associated with elevated methylation, ostensibly resulting in reduced expression of *OXTR* (Kusui et al., 2001). Findings suggest that early adversity may be indirectly associated with *OXTR* methylation via links with downstream socioeconomic instability.

Accumulating evidence implicates aspects of the oxytocin system in the manifestation of supportive, nurturing relationships (Algoe, Kurtz, & Grewen, 2017). Consistent with this research, our results showed that *OXTR* methylation forecast decreases in relationship

Table 3. Indirect Effects

Predictor	Mediator	Outcome	*b*	Effect size
Childhood adversity	Socioeconomic instability	*OXTR* methylation	0.04* [0.008, 0.071]	.38 [.174, .569]
Socioeconomic instability	*OXTR* methylation	Romantic-relationship support	−0.03* [−0.054, −0.003]	.31 [.110, .521]
Childhood adversity	Socioeconomic instability and *OXTR* methylation	Romantic-relationship support	−0.01* [−0.019, −0.001]	.07 [.001, .159]

Note: Values in brackets are 95% confidence intervals. *OXTR* = oxytocin receptor gene.
*$p < .05$.

support that participants provided to their main romantic partners. This effect was noteworthy, given that we controlled for relationship support at baseline, the influence of childhood adversity, and various demographic characteristics. An independent effect with these variables controlled for suggests that *OXTR* expression may operate directly on relationship functioning. Research on proximal phenotypes of *OXTR* methylation that mediate its influence on reported relationship support is warranted. Related research suggests that oxytocin expression influences cooperation as well as emotional recognition and processing (Maud et al., 2018). This may result in greater sensitivity in responding to a romantic partner, thus enhancing support and intimacy in the present study.

Socioeconomic instability at baseline predicted *OXTR* methylation at Time 2. This finding is consistent with recent research by Simons et al. (2017) linking stressful social and economic environments to *OXTR* methylation among African American adults. Similarly, research links aspects of conflict and support in spousal and other close relationships to circulating oxytocin levels, generally finding that supportive relationships are associated with increases in oxytocin production (Algoe, et al., 2017; Schneiderman, Zagoory-Sharon, Leckman, & Feldman, 2012). In contrast, childhood adversity did not directly predict *OXTR*-methylation status. Preclinical research suggests that harsh parenting may be transmitted across generations through methylation at *OXTR* (Perkeybile et al., 2019). To date, however, clinical studies linking aspects of adversity to *OXTR* methylation are inconsistent. Findings from the present study suggest that rather than exerting a direct effect on methylation, childhood adversity may contribute to problems with social stability, which in turn affect methylation status. Support for this thesis is evident in research indicating that *OXTR* methylation can fluctuate in response to day-to-day social interactions (Unternaehrer et al., 2012). Alternately, one study found that *OXTR* methylation moderated the influence of a history of physical abuse (Smearman, Winiarski, Brennan, Najman, & Johnson, 2015). Taken together, these findings suggest that *OXTR* methylation may act as a vulnerability factor, increasing the impact of stressful experiences.

Consistent with past research (Umberson, Thomeer, Williams, Thomas, & Liu, 2015), results showed that childhood adversity exhibited a robust direct effect on relationship support. This effect was in evidence despite the fact that we modeled the influence of socioeconomic instability and *OXTR* methylation on relationship support. This suggests that childhood adversity exhibits effects that are not wholly explained by *OXTR* methylation or contemporaneous stressors. Alternative biological and psychosocial mechanisms must be considered to document more fully the mechanisms through which childhood adversity exerts such powerful effects. Biological mechanisms may include other CpG islands in the oxytocin gene system or on *OXTR*, as well as other neuropeptides such as vasopressin and testosterone.

Caution is necessary in interpreting this study's findings. Childhood adversity was retrospectively self-reported and may be subject to recall and social-desirability biases. In addition, our socioeconomic-instability index relied on four indicators available in our data; other socioeconomic-instability factors could have been considered. *OXTR* methylation was assayed using DNA from saliva samples. The social-support measure was limited conceptually to providing care; other dimensions of social support should be assessed in future studies. Concordance of methylation in peripheral tissue with tissues found centrally is a core issue in epigenetic research on behavior (Langie et al., 2017). Validation of this procedure and concordance with sera-based methods, however, suggest that saliva samples yield reliable information on *OXTR* methylation in both central and peripheral systems (Langie et al., 2017; Nishitani et al., 2018; Smith et al., 2015). Cellular heterogeneity can act as a confounding factor for epigenetic studies of saliva-derived DNA; however, our targeted sites were located in a CpG island that exhibits relatively consistent methylation levels among cell types (Smith et al., 2015). This feature could minimize the impact of differences in cell type for between-groups comparisons. *OXTR* data were available at only one time point. Future studies with repeated assessments of *OXTR* methylation are needed to identify more clearly the directions of effects between methylation and social relationships. Finally, findings obtained in a single sample must be considered provisional, especially given the complexity of the model. Preregistered replications are needed to establish more firmly the relations between these variables.

In conclusion, our findings provide evidence that *OXTR* methylation is linked to romantic-relationship support and may act as a mechanism to explain how socioeconomic instability influences relationship quality. We also found support for the conjecture that childhood adversity affects *OXTR* methylation via current socioeconomic instability, rather than as a stable effect that is biologically embedded during childhood.

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James K. McNulty served as action editor for this article.

Author Contributions

S. M. Kogan conceptualized the study, formulated the hypotheses, supervised data collection and analysis, and drafted

most of the manuscript. D. Bae contributed to hypothesis development, conducted statistical tests of the hypotheses, and wrote the methodological portion of the manuscript. J. Cho conducted psychometric analyses of oxytocin-receptor-gene-methylation indices and provided substantive feedback on the manuscript. A. K. Smith developed and supervised all methylation assays and provided substantive feedback on the manuscript. S. Nishitani conducted all methylation assays and provided substantive feedback on the manuscript. All the authors approved the final manuscript for submission.

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The author(s) declared that there were no conflicts of interest with respect to the authorship or the publication of this article.

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Supplemental Material

Additional supporting information can be found at http://journals.sagepub.com/doi/suppl/10.1177/0956797619854735

Open Practices

Data and materials for this study have not been made publicly available, and the design and analysis plans were not preregistered.

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