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Is a happy marriage a double-edged sword for biological aging? Preliminary evidence for the moderating role of couples' health behaviors

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ABSTRACT

While happily married couples may age more slowly, the effect's magnitude varies widely. This variation could stem from partners' reinforcing each other's healthy and unhealthy behaviors. Grounded in symptom-system fit theory, we examined associations of marital quality (marital satisfaction and behavior) with biological aging in 107 middle-aged and older mixed-gender couples both cross-sectionally and over two years, assessing the moderating role of couples' health behaviors. Cross-sectionally, happier couples had lower T cell $p16^{INK4a}$ expression ($B = -0.131$, $SE = 0.060$, $p = 0.0298$). Nevertheless, slowed peripheral blood mononuclear cell (PBMC)-based DNA methylation (DNAm) aging and lower $p16^{INK4a}$ emerged only among happier couples who were more active (e.g., $B_{region} = -0.122$, $SE = 0.059$, $p < 0.05$), slept better (e.g., $B_{region} = -0.136$, $SE = 0.064$, $p < 0.05$), or ate healthier diets ($B_{region} = -0.080$, $SE = 0.040$, $p < 0.05$). However, findings with marital satisfaction attenuated with multiple-test correction. Longitudinally, better marital quality predicted smaller rises in $p16^{INK4a}$ ($B = -0.182$, $SE = 0.069$, $p = 0.009$), but also shorter telomeres (B = -0.089, SE = 0.031, p = 0.006). Further, shortening telomeres and accelerated DNAm aging were driven by couples with both high satisfaction and poorer diet (e.g., $B_{region} = -0.046$, $SE = 0.023$, $p < 0.05$) or sleep quality (e.g., $B_{region} = -0.050$, $SE = 0.024$, $p < 0.05$). These longitudinal patterns persisted with multiple-test correction. The same patterns arose with inflammation: better marital quality predicted lower inflammation among couples with higher diet ($B_{region} = -0.075$, $SE = 0.037$, $p < 0.05$) and sleep quality ($B_{region} = -0.280$, $SE = 0.139$, $p < 0.05$), but higher inflammation among less active couples ($B_{region} = 0.140$, $SE = 0.070$, $p < 0.05$) and those with poorer sleep (e.g., $B_{region} = 0.297$, $SE = 0.149$, $p < 0.05$). These results begin to shed light on the literature's mixed findings—raising questions about the double-edged nature of happy marriages for immune health and aging, depending on the health behaviors they reinforce.

1. Introduction

On average, happily married people live longer, healthier lives. They have lower rates of chronic conditions such as cardiovascular disease, lower risk of breast cancer metastasis and recurrence, fewer functional limitations, and ultimately, delayed mortality (Robles et al., 2014; Yu and Zhang, 2020; Yuan et al., 2023; Azizi et al., 2024; King and Reis, 2012). Early evidence points to slowed biological aging as a possible

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mechanism. For instance, older adults in a large national U.S. sample who reported more spousal support also had younger biological ages as measured by PhenoAge, GrimAge, and DunedinPACE DNA methylation (DNAm) clocks (Rentscher et al., 2023). In another national sample, older adults who received some social support from their spouse within the last year had longer telomeres compared to those who lacked spousal support (Barger and Cribbet, 2016). This association remained after accounting for health risk factors, chronic disease, and the number of supportive ties outside the marital relationship. Further, among 73 young and middle-aged married adults, those who endorsed that they ever argued or fought with their spouse also had elevated expression of the cellular senescence marker $p16^{INK4a}$ (Rentscher et al., 2019). These studies join a large literature linking marital quality to inflammation (e.g., Donoho et al., 2013; Kiecolt-Glaser et al., 2015), an established potential pathway to heightened risks for age-related diseases (Furman et al., 2019).

In a 126-study meta-analysis, the beneficial associations between marital quality and better health were significant but small in magnitude, with large, unexplained variation across studies (Robles et al., 2014). This heterogeneity raises a key question: could certain factors alter the impact of marital satisfaction on health? We reasoned that health behaviors may help to determine marriage's risks and benefits for healthy aging. According to symptom-system fit theory, indulging together in unhealthy behaviors—e.g., substance use, sedentary behavior, excessive media use, unhealthy diet—promotes shared positive affect, bolstering connectedness and relationship satisfaction (Rohrbaugh et al., 2002). In a landmark study, couples—one or both of whom smoked cigarettes and had a lung or heart condition—began discussing a marital disagreement then continued while one or both smoked a cigarette (Shoham et al., 2007). Among dual smokers, lighting up a cigarette buoyed their moods and made the partners feel more in sync, whereas the opposite was true for single-smoker couples. In sum, the boost to couple well-being provided by health-impairing behaviors may help to explain why the impact of marital happiness on health is so variable.

Since that groundbreaking work, additional studies have documented similar patterns with other unhealthy behaviors, and outside of the laboratory. For instance, in two separate daily diary samples, when couples smoked together or when they both engaged in more sedentary behavior, they experienced greater relationship satisfaction on that day and the following day (Pauly et al., 2024). The latter sample showed that parallel engagement in unhealthy behaviors can contribute to a sense of couple identity and, thus, to relationship satisfaction, which may in turn reinforce unhealthy routines (Pauly et al., 2024).

Over time, the combination of relationship satisfaction and unhealthy couple behavior may erode physical health. Suggestive of this pattern, a cross-sectional study of 43 couples found that body mass index (BMI) was highest among women in couples who were emotional eaters, but only when the couple also thought of themselves as a single unit (i.e., used more 'we-talk') with their health routines (Skoyen et al., 2014). Another analysis in the same sample showed similar results: women's BMI was higher in satisfied couples who engaged in unhealthy behaviors compared to couples with fewer unhealthy behaviors (Skoyen et al., 2018). Among dissatisfied couples, women's BMI was higher regardless of the couple's health behaviors. It remains unknown whether this pattern of symptom-system fit, the dyadic engagement in unhealthy behaviors, also accelerates biological aging.

Just as the mutually reinforcing effects of unhealthy behaviors and marital quality may form a vicious, risky cycle, early evidence suggests that *healthy* behaviors could foster relationship satisfaction in a *virtuous* cycle. In a daily diary study, couples rated their marriage as more satisfying on days when they exercised together (Yorgason et al., 2018). Similarly, a study that tracked couples' sleep minute-by-minute found couples with more concordant sleep were more satisfied in the relationship (Gunn et al., 2015). Another daily diary study using accelerometry revealed that moments of greater synchrony—either in moderate-vigorous physical activity or in sedentary behavior—strengthened couple closeness (Pauly et al., 2020). Further, among community couples, daily activities such as eating, relaxing, and sleeping were rated as more enjoyable with the partner rather than alone (Sullivan et al., 1996). Broadly, when couples align in the health behaviors that anchor their daily lives—sleep, activity, meals—it may foster a sense of cohesion, create opportunities for connection, and thus reinforce both positive and negative health routines, with possible implications for biological aging.

2. Current study

A key objective of this study was to extend existing cross-sectional evidence linking self-rated marital support and strain to immune-based measures of biological aging using a multi-method approach, with marital quality indexed by both self-report and observed marital behavior alongside an array of established and cutting-edge biomarkers. Further, we sought to determine how the links between marital quality and biological aging unfold over time, a necessary step to establish temporal precedence. Finally, we examined couple-level averages of health behaviors—sleep, activity, and diet—as moderators of the associations between marital quality and biological aging (Fig. 1). This allowed us to evaluate whether couples' health behaviors help to explain the risks or benefits of marital quality for biological aging, in accordance with marriage-health frameworks and symptom-system fit theory.

To address these aims, we examined longitudinal data from middle-aged and older adults in couples who completed two study visits, two years apart. Given the scant prior data on the links among marital quality, health behaviors, and biological aging, we adopted a multi-method approach that capitalized on the thorough phenotyping of the sample and reflected the breadth of the underlying theories, with transparent reporting of all results. Given its widespread use and availability in research, self-rated marital satisfaction from the Couple Satisfaction Index (CSI) served as the primary measure of marital quality. Based on prior work demonstrating robust associations between marital behavior and health outcomes (Kiecolt-Glaser et al., 2015; Wilson et al., 2017), comprehensive sampling of marital behavior served as secondary measures, to replicate and deepen understanding of the behavioral patterns that characterize marital quality. These included snapshots of how partners treat each other during social support, positive event, and conflict discussions. The negative emotional discussions—conflict, wherein the couple seeks to solve a relationship problem, and support, wherein they aim to solve one partner's problem—can elicit a range of behaviors that share established associations with health outcomes (Wilson et al., 2017; Kiecolt-Glaser et al., 2005). These include both negative behavioral patterns (disgust, contempt, mocking, blaming, stonewalling) and positive ones (humor, listening, exploring a partner's concerns, offering support, accepting responsibility). In contrast, discussing positive events—or capitalization—represents a potentially positive emotional context, where partners have an opportunity to amplify or undermine one another's joy. Although very little prior work has linked capitalization support to health outcomes (Shrout et al., 2023), research has revealed that capitalization is a stronger predictor of relationship perceptions and successful responses to marital therapy compared to a spouse's support with personal problems (Hershenberg et al., 2016). Examining a range of marital behaviors enabled us to explore whether specific behavioral signatures drive associations with biological aging and couples' health behaviors.

Three focal immune-based measures captured biological aging: DNAm aging measured in peripheral blood mononuclear cells (PBMCs), T cell telomere length, and T cell $p16^{INK4a}$ expression. DNAm estimates biological age based on age- and health-related patterns in DNA methylation at CpG sites. The PCGrimAgeEAA, PCPhenoAgeEAA, and DunedinPACE DNAm algorithms were of particular interest in the current study due to their predictive validity for clinical outcomes in

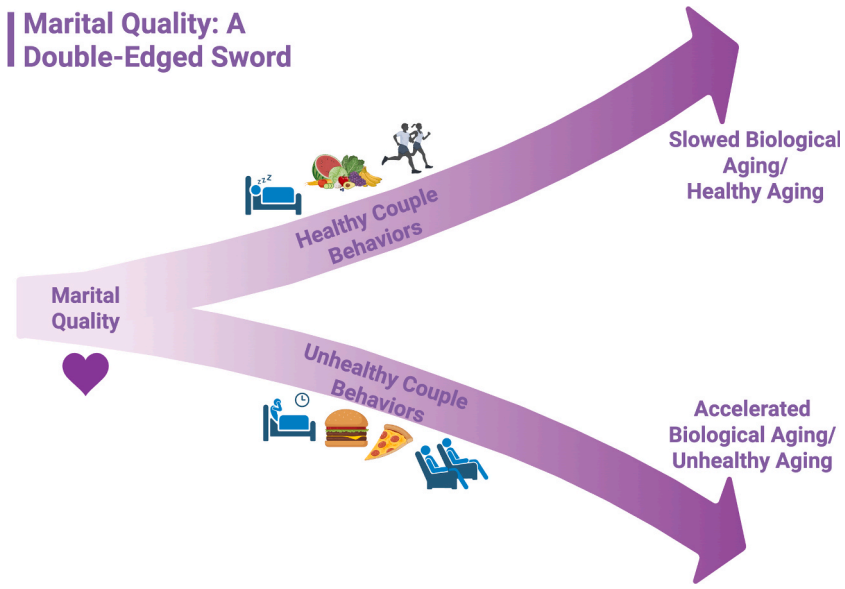

Fig. 1. Conceptual Model of Marital Quality, Couples' Health Behaviors, and Biological Aging. *Note.* Created in Biorender. Wilson, S. (2026) https://BioRender.com/yf7hrdd.

healthy populations (Levine et al., 2018; Lu et al., 2019; Belsky et al., 2022). Because the three were correlated and are all meant to index the rate of biological aging, we averaged the clocks to achieve a more precise signal and to reduce the number of statistical tests in the primary study (Fagundes et al., 2019), with individual clock data evaluated in secondary analyses. Telomeres are repetitive DNA elements at the ends of chromosomes that protect the coding genome from the end-attrition that occurs during each round of cell replication. Once telomeres are exhausted due to damage or attrition, cells experience genomic damage leading to cell cycle arrest, senescence, or apoptosis. Lastly, $p16^{INK4a}$ expression is an aging biomarker of interest because it serves as a key effector of cellular senescence and a cell cycle inhibitor that controls stem cell dynamics (Martin et al., 2014). All three aging biomarkers change with chronological age (Liu, 2009; Epel et al., 2008; Boks et al., 2015) and foreshadow clinically relevant aging outcomes (Marioni et al., 2018; Breitling et al., 2016). They capture distinct molecular functions (Marioni et al., 2018; Breitling et al., 2016) that span the major hallmarks of aging (López-Otín et al., 2013; Kennedy et al., 2014). They are also malleable—both susceptible to social and environmental stress. Inflammation is also considered a hallmark of aging (López-Otín et al., 2013) because it rises with age (i.e., *inflamm-aging*) and causes inadvertent tissue damage thought to advance aging (Franceschi et al., 2000; Franceschi and Campisi, 2014). However, because its functions and consequences are not specific to aging, we considered inflammatory markers as outcomes only in supplemental analyses.

Taken together, we hypothesized that higher marital quality (primarily, self-reported satisfaction and secondarily, observed behavior) would predict slowed biological aging in each biomarker—that is, decelerated DNAm aging, longer telomeres, and lower $p16^{INK4a}$ expression, as well as lower inflammation in supplemental analyses—both concurrently and over time. Grounded in both symptom-system fit theory and empirical evidence showing that a happy marriage can reinforce both healthy and unhealthy behaviors, we expected that marital quality's protective aging effects would hinge on couples' health behaviors: higher marital quality's salutary associations with slower biological aging would remain among couples with healthier behaviors. In contrast, higher marital quality would predict *faster* biological aging among those with *unhealthier* behaviors, consistent with symptom-system fit theory. In other words, we expected significant two-way interactions between marital quality and couples' health behaviors on biological aging, with the direction of the simple effect reversing (higher marital quality, faster aging) in the context of unhealthy couple behavior.

3. Methods

3.1. Participants

Middle-aged and older mixed-gender couples were recruited for a parent study on molecular aging. Interested couples in a marriage or marriage-like relationship completed online and in-person screens to determine eligibility. Couples were excluded if they were together and cohabiting fewer than three years, were younger than 40 years old, and had sensory or cognitive impairments that would interfere with study completion. To reduce bias in physiological data, couples were also excluded if either partner had a range of chronic health problems (e.g., cancer, autoimmune conditions, diabetes [Hba1c $>$ 6.5], chronic obstructive pulmonary disease, liver failure), smoked, abused substances, or took prescription medication that affected the immune system, e.g., steroids, methotrexate. A total of 412 interested individuals were excluded because they or their partner did not meet the stringent health criteria.

Power analyses for the parent study suggested that N $\approx$ 220 individuals nested within $\sim$ 110 couples would be sufficient to detect expected associations between marital quality and each of the three types of molecular aging biomarkers. The calculations used two-tailed tests, α=.05, and assumed a 10 % attrition rate. They also relied on sample size adjustment for a couple-level intraclass correlation coefficient (ICC) of 0.10, resulting in an effective sample size of N = 200—a conservative estimate given that in our prior studies, inflammatory cytokines had a negligible couple-level ICC (Kiecolt-Glaser et al., 2015). With these assumptions, the study was estimated to have 80 % power to detect small associations (r $\geq$ 0.21), as well as smaller effects with repeated measures.

3.2. Procedure and marital interactions

Study procedures were approved by the Ohio State University Institutional Review Board; participants provided written informed consent before completing study activities. When participants arrived at the hospital research unit, both partners were fit with a venous catheter. Following a brief relaxation period, participants provided baseline blood

samples, from which all assays were performed. Couples ate a standardized breakfast and then completed three interactions together in the following order: a positive event discussion, a support seeking discussion, and a conflict discussion, with 15–20 min rest between each. The research team remained out of sight during videorecording.

Positive Event Discussion. In accordance with previous studies (Gable et al., 2006), couples completed a 10-minute positive event (i.e., capitalization) discussion where each partner shared 1–2 events that evoked positive emotions from their personal, individual life rather than an experience involving both partners. Before the discussions, each partner identified their events. The other partner was instructed to listen and respond as they normally would as if they were at home, and to stay focused on their partner's topic. Partner order was randomized, and they reversed roles after 5 min.

Social Support Discussion. Couples engaged in a 10-min social support discussion in which each partner either solicited or offered support (Pasch and Bradbury, 1998). Before the discussion, partners identified something they would like to change about themselves. The topic could be any personal difficulty or goal (e.g., striving for a job promotion, maintaining a healthier diet), but could not be a source of marital tension. Couples were asked to converse about the topic as they normally would, as if they were at home. Partner order was randomized, and they reversed roles after 5 min.

Conflict Discussion. Couples engaged in a marital problem discussion to resolve one or more of their marital issues. To initiate the discussion, an experimenter conducted a 10–15-min interview to identify the most contentious topics for both partners (Kiecolt-Glaser et al., 2005). These topics were selected from an inventory each spouse completed about their relationship problems (e.g., money, communication, or in-laws) (Kiecolt-Glaser et al., 2005). Couples were given 20 min to discuss the chosen topics.

3.3. Marital quality measures

Marital Satisfaction. The 32-item Couples Satisfaction Index (CSI-32), developed using item response theory, assessed each individual's self-reported marital satisfaction (Funk and Rogge, 2007). Items from the CSI were summed to create a composite score ranging from 0 to 161. Higher scores reflect greater relationship satisfaction. Scores below 104.5 indicate a clinical level of relationship distress. On average, individuals were highly satisfied in their relationship ($Mean_{CSI} = 128.3$, $SD = 26.5$), though marital satisfaction scores spanned a wide range (36–160), with 15.9 % of the sample meeting criteria for clinically significant relationship distress (<104.5). The CSI distinguishes between (Funk and Rogge, 2007) distressed and nondistressed partners with greater precision than other marital satisfaction scales. Internal reliability was high ($\alpha = 0.98$).

Coded Capitalization Behavior. Each partner's behavior in the responder role was coded from the discussion about their partner's positive event. In line with prior research (Gable et al., 2006), coders received extensive training across two separate variables, responsiveness and active-constructive behavior. Each interaction was coded by at least 6 coders. The three components of responsiveness—understanding, validation, and caring—were coded separately and then averaged to create a composite index of partner responsiveness (intraclass correlation coefficient, ICC = 0.88). The composite index scores of partner responsiveness ranged from 1 to 7, with higher scores indicating greater responsiveness. The two dimensions of capitalization support—active and constructive behavior—were coded and then averaged to create an index of partners' active-constructive behavior (ICC = 0.84). Index scores of partners' active-constructive behavior ranged from 3 to 21, with higher scores indicating greater active-constructive behavior. Responsiveness and active-constructive behavior were each correlated between partners (r = 0.32–.39), and in turn, couples' responsiveness and active-constructive scores were strongly correlated (r = 0.90). Thus, to capture the interdependence of behavior in dyadic interaction, the two scores were averaged to create a composite couple-level capitalization score, with higher scores indicating greater capitalization support.

Coded Positive and Negative Behavior during Social Support and Conflict. The Rapid Marital Interaction Coding System, 2nd Generation (RMICS2) (Heyman, et al., 2017) was used to index positive and negative behaviors across the social support and conflict discussions. RMICS2 is designed to code dyadic behavior and interaction patterns, and thus both partners' behaviors are coded simultaneously to create individual- and couple-level ratings. Consistent with prior research and the dyadic, interdependent nature of the conversational turns in the laboratory-based interactions (Kiecolt-Glaser et al., 2015), this study focused on couple-level ratings.

Couples' negative behavior summed two RMICS2 codes: high-intensity hostility (e.g., intense negative affect and profoundly negative statements that indicate contempt, belligerence, or character assassination, such as "Of course you always think about yourself. That's just what you do.") and low-intensity hostility (e.g., mild to medium intensity negative affect and mildly to moderately negative verbal statements that indicate blame, criticism, or demands, such as "I'm bothered by you not fixing anything around the house."). Couples' negative behavior ratings were computed for conflict conversations and support conversations, with higher scores indicating more negative behaviors during the discussion.

Couples' positive behaviors summed two RMICS2 codes: high-intensity positivity (e.g., intense positive affect, and statements that focus on deep connection and character, such as high-intensity self-disclosure and humor; examples include "I love you" and "You're the funniest person I know.") and low-intensity positivity (e.g., positive affect and verbal statements that facilitate low-level bonding within the couple, such as "I appreciate that you cleaned the house the other day without me asking you to."). Couples' positive behavior ratings were computed for conflict conversations and support conversations, with higher scores indicating more positive behaviors during the discussion.

Positive behaviors were averaged between conflict and support conversations (r = 0.28), as were negative behaviors (r = 0.34). Inter-rater agreement was high, with a Holley and Guilford's *G* value of 0.98 for negative behaviors and 0.84 for positive behaviors.

3.4. Health behavior measures

Physical Activity. Physical activity was measured with the International Physical Activity Questionnaire (IPAQ), developed by an International Consensus Group and validated against accelerometer measurements. Respondents reported how much time (in minutes) they spent in vigorous activity, moderate activity, and walking over the past 7 days. A total score was calculated by summing the total time spent in these activities and expressed as metabolic equivalent (MET) minutes. The IPAQ has comparable or better measurement properties relative to other established self-reports for adults (Craig et al., 2003).

Sleep Quality. The Pittsburgh Sleep Quality Index (Buysse et al., 1989) assessed sleep quality and disturbances over a one-month interval, with high diagnostic sensitivity and specificity in distinguishing good and poor sleepers. The scale yields a total score ranging 0–21 which includes subjective sleep quality, sleep latency, sleep duration, habitual sleep efficiency, sleep disturbances, use of sleeping medications, and daytime dysfunction. Higher scores reflect more sleep problems. To align with the interpretation of the other health behaviors in this study, we reverse-scored this scale so that higher scores reflected better sleep quality.

Diet Quality. The gold-standard United States Department of Agriculture (USDA) Multiple-Pass Approach was used to assess typical dietary behavior, with three 24-hr dietary recall interviews before and after each visit (Blanton et al., 2006). Recalls were completed on two weekdays and one weekend day averaged together to provide reliable data for normal dietary intake. The data were entered into the Nutrition

Data System for Research (NDSR) nutrient database system (Minneapolis, MN). Then, the Alternate Mediterranean Diet (aMED) scoring system was used to assess diet quality. This system, an adaptation of the original Mediterranean diet score, is the most widely used Mediterranean diet scoring method in epidemiological studies in the U.S. (Fung et al., 2005). It evaluates adherence to the Mediterranean diet by assessing nine components: vegetables, fruits, nuts, whole grains, legumes, fish, the ratio of monounsaturated to saturated fats, red and processed meat, and alcohol intake. Each component is scored dichotomously (0 or 1 point) based on median splits for the study population. The scores for all nine components were summed on a continuous scale, ranging 0–9, with higher scores indicating greater diet quality. Higher aMED scores have been reliably associated with lower inflammation and endothelial dysfunction (Fung et al., 2005) as well as longer telomeres (Crous-Bou et al., 2014) and delayed mortality (Harmon et al., 2015).

Couple Health Behavior Scores. Given the study's aim to examine the links between marital quality and biological aging as a function of the couple's health behaviors, partners' health behaviors were averaged together into a continuous couple-level score to compare couples with healthier behaviors to those with less healthy behaviors. Sleep quality ($r = 0.23$, $p = 0.001$), diet quality ($r = 0.43$, $p < 0.0001$), and physical activity ($r = 0.18$, $p = 0.009$) significantly tracked together within couples.

3.5. Assays

T cell Isolation. Human T cells were isolated from density gradient derived PBMCs using the EasySep Human T Cell Enrichment kit (StemCell Technologies, Vancouver, Canada). The DNA and RNA was extracted from the T-cells using a Quick DNA/RNA Miniprep Plus kit (Zymo Research, Irvine, CA). The concentration and purity of the DNA/RNA was assessed using a NanoDrop One (Fisher Scientific, Pittsburgh, PA).

DNA methylation. DNA from PBMCs was aliquoted and sent to TruDiagnostic (Lexington, KY) where DNA methylation was assayed. Using a custom EPICv2 array via the Illumina Infinium EPIC2 BeadChips, TruDiagnostic analyzed DNA methylation by quantifying the methylation status of more than 930,596 sites across the genome and processing the resultant data with the minfi pipeline, removing low-quality samples with the qcfilter function in the ENmix package (Xu et al., 2021). The minfi ssnoob method normalized the data to minimize sample variation (Fortin et al., 2017).

Established DNAm clock algorithms were applied to generate DNAm aging measures. Biological aging was estimated from PBMC DNA methylation using PCGrimAge (Lu et al., 2019); PCPhenoAge (Levine et al., 2018) and the third-generation DunedinPACE measure (Belsky et al., 2022). Principal component (PC)-based versions of GrimAge and PhenoAge were computed using custom R scripts from the Morgan Levine Lab PC-Clocks repository (https://github.com/MorganLevineLab/PC-Clocks) (Higgins-Chen, 2022). DunedinPACE was computed using the PACEProjector function from the DunedinPACE R package (https://github.com/danbelsky/DunedinPACE). For PCGrimAge and PCPhenoAge, epigenetic age acceleration (EAA) was derived by regressing the DNAm-based age estimate on chronological age and extracting the model residuals. Positive residuals indicate accelerated biological aging relative to chronological age, whereas negative residuals indicate decelerated aging. Because EAA is an age-adjusted, within-cohort deviation measure, it can be interpreted without a separate external control group and enables comparisons on a participant-relative scale. DunedinPACE estimates reflect the pace of aging anchored at a value of 1, which reflects one year of biological aging for every chronological year.

PCGrimAgeEAA, PCPhenoAgeEAA, and DunedinPACE were analyzed in the current study due to their predictive validity for clinically relevant aging outcomes. Acceleration in GrimAge, PhenoAge, and DunedinPACE has predicted earlier chronic disease onset and mortality across samples, including the VA Normative Aging Study and Framingham Offspring Study; effect sizes for these clocks were larger than for other clocks in these healthy adult samples (e.g., Hannum, Horvath) (Levine et al., 2018; Belsky et al., 2022). Given the correlations among the DNAm clocks ($r = 0.40$–0.57), the values were z-scored and averaged to reduce the number of statistical tests and to increase the precision of estimates.

Telomere Length. Telomere length was measured in DNA from PBMC-derived T cells with quantitative polymerase chain reaction (qPCR) and expressed as the ratio of the abundance of telomeres vs. the abundance of a single copy gene (human beta-globin) (T/S), the average between two runs. The assay's details have been described elsewhere (Kiecolt-Glaser et al., 2013; Lin et al., 2020; Lin et al., 2010; Cawthon et al., 2002). The inter-assay coefficient of variation was 2.1 ± 1.5 % for this study. Intra-class correlation (ICC) of duplicate DNA extraction from 29 samples was 0.976 (CI: 0.948–0.988).

***p16^{INK4a}* Expression.** A Nanostring nCounter Custom Gene Expression Codeset (OSU_Senescence) was used for mRNA analysis (Burd, 2020). The integrity and concentration of all RNA samples run on the OSU_Senescence platform was confirmed using an Illumina Tapestation. Post-run analysis included automated quality control procedures to ensure measurement linearity and quality. Samples not meeting quality controls were examined for irregularities and removed from further analyses if it was deemed that RNA clean-up and/or re-analysis could not correct for these issues. Values reflect transcript abundance normalized to internal control RNAs.

Serum Cytokines. Serum IL-6 was measured by colorimetric enzyme-linked immunosorbent assay (ELISA) using R&D Systems high sensitivity kits while TNF-α was measured using an electrochemilluminescence method with Meso Scale Discovery kits and read using the Meso Scale Discovery Sector Imager 2400, following kit instructions (Meso Scale Discovery, Rockville, MD). Each subject's samples were assayed for all cytokine markers in one run, thus using the same controls for all time points (Kiecolt-Glaser et al., 2015). Sensitivity for the IL-6 serum cytokines was 0.031 pg/mL. The intra-assay coefficient of variation for IL-6 was 4.1 %, and the inter-assay coefficient of variation was 6.5 %; corresponding values for TNF-α were 2.97 and 3.27 %, respectively, with a sensitivity of 0.69 pg/mL.

Stimulated Cytokines. PBMCs were treated with 1.0 μg/ml lipopolysaccharide (LPS) for 24 h to measure the production of IL-6, TNF-α, and IL-1β (Calder et al., 2001). After 24 h, the cells were pelleted by centrifugation (2000 rpm for 5 min) and the supernatant removed, aliquoted and frozen at −80C until assayed using Meso Scale Discovery Tissue culture proinflammatory multiplex plate kits. All samples, including each person's control cell cultures incubated in media alone, were run at the same time for each subject. The intra-assay coefficient of variation for IL-6 was 4.29 %, and the inter-assay coefficient of variation was 11.57 %; corresponding values were 4.06 % and 11.12 % for TNF-α, and 2.32 % and 10.06 % for IL-1β. Apart from serum cytokines, LPS-stimulated inflammation sheds unique light on the reactivity of the immune system to an external stimulus; this reactivity changes with age (Bruunsgaard et al., 2001), contributes to inflammaging (Franceschi et al., 2000), and also responds to marital stress (Wilson et al., 2017).

3.6. Analytic plan

Data Preparation. To facilitate comparisons across marital quality measures, negative behavior was reverse-scored, and all four measures were z-scored. Couple health behaviors were also z-scored. PCGrimAgeEAA, PCPhenoAgeEAA, and DunedinPACE were z-scored and averaged to create a DNAm composite in order to improve precision, similar to prior research (Fagundes et al., 2019). Telomere length and *p16^{INK4a}* expression were log-transformed to correct the skew of their residuals but were left unstandardized to provide more information about effect magnitudes; standardized estimates that enable comparisons across outcomes are reported in Tables S2-3. Whereas DNAm age acceleration

data indexed the acceleration or pace of biological aging, log-transformed telomere length and $p16^{INK4a}$ did not.

Primary Analyses. Linear mixed models were fit using SAS v9.4 PROC MIXED with biological aging markers as individual-level outcomes. Models used Kenward-Roger degrees of freedom adjustment (Kenward and Roger, 1997). All models proceeded in a stepwise fashion, first examining the main effect of marital quality, then the moderating role of each dyadic health behavior. Regions of significance probed statistically significant ($p < 0.05$) interactions using the Johnson-Neyman technique (Johnson and Neyman, 1936). This method empirically derives the values of the moderator, i.e., the regions at which the predictor-outcome association is statistically significant. In the Results, B_{region} represents the boundary, or the first statistically significant simple effect in the region; this is reported along with the corresponding value of the moderator and the range of the significant region. Details on implementation in SAS 9.4 are given in Supplemental Material.

To maximize the available data, concurrent models examined biological aging markers as outcomes at both visits as a function of same-visit marital quality and health behaviors. Models with telomere length and $p16^{INK4a}$ as outcomes controlled for the fixed effects of visit, age, gender, comorbidities, education, and BMI. Models with DNAm aging as the outcome replicated this approach, except for excluding age as a covariate because estimates were previously residualized on this variable. Random person-level intercepts accounted for within-person correlations across the two visits, and couple-level intercepts accounted for couple-level correlation. However, in some of the models, random intercepts could not be estimated for all levels simultaneously due to a lack of sufficient variability. The random structure of each model was determined empirically; we constrained to zero any random model parameters that did not successfully converge on a non-zero estimate. In Supplemental Material, we provide equations for the final models.

To assess the temporal precedence of marital quality and health behavior on later biological aging, prospective-change models examined the roles of marital quality and dyadic health behavior at Visit 1 as predictors of prospective change in biological aging markers from Visit 1 to Visit 2, controlling for biological aging at Visit 1 (i.e., auto-correlation in the outcome) (Cronbach and Furby, 1970; Kessler and Greenberg, 1981). Change scores were treated as outcomes, rather than raw Visit 2 values, to gauge whether aging biomarkers had changed in expected ways; these two model variants are equivalent when controlling for baseline levels of biological aging (Allison et al., 1990; Werts and Linn, 1970).

Given its prominence and widespread use in the literature, individuals' marital satisfaction served as the primary indicator of marital quality, whereas couples' marital behavior provided secondary measures of marital quality, adding depth to the sample's phenotyping of marital quality. For this reason, results from models including marital satisfaction were confirmed by correction for multiple testing, while marital behavior models were considered exploratory. Specifically, false discovery rate (FDR) correction (Benjamini and Hochberg, 1995) was applied to two confirmatory families of tests: 1) concurrent associations with marital satisfaction (including health behavior moderation) and 2) prospective associations with marital satisfaction and health behavior moderation. In accordance with prior recommendations to consider thresholds of up to 20 % when the area of scientific inquiry is nascent (Glickman et al., 2014; McDonald et al., 2014), we selected an *a priori* FDR threshold of 15 %, opting for a somewhat stricter criterion within the acceptable range to strengthen confidence in identified results while preserving sensitivity to potentially meaningful effects. At this threshold, the expected proportion of false positives among results deemed significant is no more than 15 %. Reported in Table S2, FDR-adjusted q-values—which represent the minimum false discovery rate at which a result would be considered significant—allow readers to evaluate effects at alternative FDR thresholds.

Supplemental Analyses. Supplemental analyses further probed the results of primary and secondary analyses. These included examining individual DNAm clocks as outcomes, including other covariates (alcohol intake, relationship length), examining the robustness of findings while accounting for within-couple discordance in health and marital behaviors, and exploring inflammation as an outcome. The latter was assessed by examining two composite scores, similar to prior research (Fagundes et al., 2019): a serum cytokine composite (log-transformed IL-6 and TNF-α, z-scored and averaged) and an LPS-stimulated cytokine composite (IL-6, TNF-α, and IL-1β, z-scored and averaged).

4. Results

4.1. Sample description

The sample (n = 214 individuals in 107 couples, Table 1) consisted of mostly non-Hispanic white participants (92.1 %) with a bachelor's degree or graduate education (86.9 %) who had never smoked (77.1 %) and had no chronic conditions (79.3 %). They ranged 40 to 87 years old. Of the 107 couples who completed the baseline visit, most returned two years later for the second visit (n = 92, 86.0 %). Four couples (3.7 %) agreed to complete surveys at the second visit without blood samples,

Table 1
Baseline descriptives of the study sample.

	M (SD) or n (%)
Age	56.81 (11.29)
Gender (Female)	107 (50.00 %)
BMI	27.58 (4.89)
Education (College degree or greater)	186 (86.92 %)
Comorbidities (1 or more)	44 (20.66 %)
Race-ethnicity	
Non-Hispanic White	197 (92.06 %)
Non-Hispanic Black	8 (3.74 %)
Asian	6 (2.80 %)
Native American or Alaskan Native	1 (0.47 %)
Mixed Race	1 (0.47 %)
Past smoker	49 (22.90 %)
Weekly alcohol intake	3.33 (4.13)
Length of relationship	28.62 (14.06)
CSI	128.35 (26.50)
Couple negative behavior (reverse-scored)	−0.03 (1.01)
Couple positive behavior	−0.01 (0.80)
Couple capitalization behavior	0.00 (0.97)
Couple sleep problems	0.00 (1.00)
Couple physical activity	0.00 (1.00)
Couple Mediterranean diet quality	0.00 (1.00)
Telomere length	1.24 (0.31)
$p16^{INK4a}$ expression	12.36 (15.56)
DNAm	0.00 (0.82)
PhenoAgeEAA	0.21 (4.83)
GrimAgeEAA	0.08 (2.32)
DunedinPACE	0.82 (0.09)
Serum cytokines	0.00 (0.81)
Stimulated cytokines	0.00 (0.85)

CSI = couples satisfaction index; PSQI = Pittsburgh Sleep Quality Index; IPAQ = International Physical Activity Questionnaire; DNAm = DNA methylation, average of 3 epigenetic aging clocks. All Ns and %s are quantified at the individual level, out of the total N = 214 adults, i.e., all available baseline data. All aggregated measures (couple marital behaviors, couple health behaviors, DNAm composite, and serum and stimulated cytokine composites) were z-scored and, thus, reflect standard deviation units. Age was measured in chronological years. BMI reflects kg/m^2. Weekly alcohol intake reflects the number of standard drinks consumed in a week. Length of relationship is reported in years. CSI scores ranged from 0 to 160, with higher scores indicating greater relationship satisfaction. Telomere length reflects the T/S ratio, and $p16^{INK4a}$ expression reflects normalized transcript abundance. PhenoAgeEAA and GrimAgeEAA report residuals from models regressing DNA-based age estimates on chronological age. Positive residuals indicate accelerated epigenetic aging. DunedinPACE estimates represent pace of biological aging for every chronological year, anchored at 1. Estimates greater than 1 indicate accelerated pace of biological aging.

and 11 couples (10.3 %) were lost to follow-up. There were very few differences between couples who returned and provided blood samples at follow-up and those who did not, with similar demographics, relationship, and health dimensions (i.e., age, education, comorbidities, smoking history, alcohol intake, years together as a couple, and marital satisfaction). In non-significant trends, non-Hispanic white individuals were more likely to return (87.3 %) than persons of color (70.6 %, $X^2(1) = 3.63$, $p = 0.057$), and completers had higher BMI compared to non-completers ($t(211) = -1.83$, $p = 0.069$; $M_{completers} = 27.82$, $M_{non\text{-}completers} = 26.07$).

Univariate descriptives of all raw measures appear in Supplemental Material. Descriptive zero-order correlations among study variables are depicted in Table S1. In brief, as expected, older participants had shorter telomeres and higher $p16^{INK4a}$ at both visits. The correlation with DNAm age acceleration was non-significant at Visit 1 but small and positive at Visit 2, with older adults showing greater accelerations in DNAm aging. Telomere length was inversely associated with DNAm aging at both visits, but neither correlated with $p16^{INK4a}$. Marital satisfaction and negative marital behavior shared moderate correlations at both visits; otherwise, correlations among marital quality measures were small, reflecting their distinct value. Likewise, couples' health behaviors—diet, sleep, and physical activity—were largely uncorrelated.

4.2. Concurrent associations with self-rated marital satisfaction (primary models)

Main Effects. Concurrently, more satisfied individuals had lower T cell $p16^{INK4a}$ expression, on average (Table S2, $B = -0.131$, $SE = 0.060$, $p = 0.030$, 95 % CI [−0.249, −0.013]). With every 1-SD increase in marital satisfaction, there was an accompanying 12.29 % decrease in T cell $p16^{INK4a}$ expression. However, this association did not survive FDR correction (Table S2). Associations with DNAm aging and telomere length were not significant.

Health Behavior Moderation. When dyadic health behaviors were considered, physical activity moderated the link between marital satisfaction and $p16^{INK4a}$ expression (Fig. 2, $B_{interaction} = -0.117$, $SE = 0.050$, $p = 0.020$, 95 % CI [−0.216, −0.018]): higher marital satisfaction predicted lower $p16^{INK4a}$, specifically among couples at the mean of physical activity and above ($B_{region} = -0.122$, $SE = 0.059$, $p < 0.05$, 95 % CI [−0.239, −0.00513]). Namely, among these couples, for every 1-SD increase in marital satisfaction, $p16^{INK4a}$ expression decreased by 11.48 %. However, this moderating effect was not significant following FDR correction (Table S2). Neither sleep nor diet served as moderators; links to DNAm aging and telomere length were not significant.

4.3. Concurrent associations with marital behavior (exploratory models)

Main Effects. Paralleling concurrent associations with self-rated marital satisfaction, in exploratory replication models, more positive marital behavior was associated with slower biological aging. Namely, couples who provided more capitalization support while discussing positive events had longer telomeres (Table S3, Supplemental Results). Associations with DNAm aging, $p16^{INK4a}$, and those involving negative and positive marital behaviors during conflict and social support were not significant.

Health Behavior Moderation. Like patterns seen in self-rated satisfaction, some dimensions of observed marital behavior were concurrently associated with more favorable biological aging, but only among couples with better health behaviors. That is, the association between capitalization and $p16^{INK4a}$ varied by couples' sleep quality (Fig. 3A, Table S3), wherein only couples with better sleep quality showed associations between higher-quality capitalization behavior and lower $p16^{INK4a}$ expression. The same was true for fewer negative behaviors predicting slower epigenetic aging, specifically among couples with better diets (Fig. 3B, Table S3). Details of these results appear in Supplemental Material.

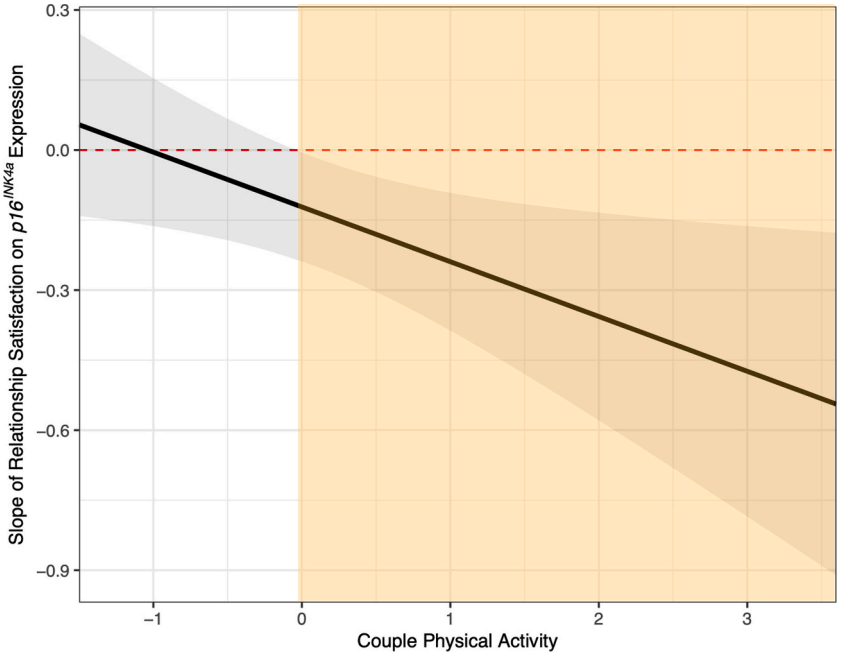

Fig. 2. Marital Satisfaction Relates to Lower $p16^{ink4a}$ Expression Only Among Physically Active Couples ***Note.*** Depicted are the regions of significance for the moderating effect of couple physical activity on the association between marital satisfaction and $p16^{ink4a}$ expression. Notably, this association did not survive multiple-testing correction but is depicted so that readers may assess patterns across measures, with appropriate caution. The regression slope of this association appears on the y-axis, with the range of couple physical activity on the x-axis. The red dashed line depicts a null association, and the bands represent 95 % confidence intervals. The black solid line itself represents the model-based unstandardized slope of the predictor on the outcome at varying levels of the z-scored moderator, controlling for sex, age, visit, BMI, comorbidities, and education. The association is statistically significant in areas of the plot where both the upper and lower confidence intervals are on one side of the red line (highlighted in yellow). In this case, slopes are statistically significant at and above 0 (i.e., the mean of couple physical activity). The significant region included 144 data points (from individuals across both visits).

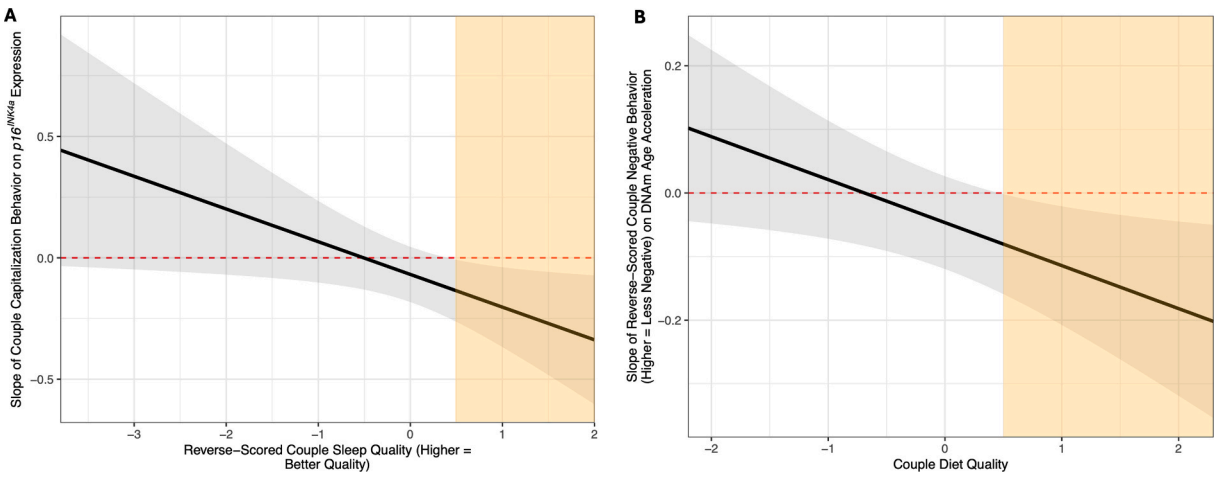

Fig. 3. Couple Health Behaviors Moderate Marital Behaviors' Concurrent Associations with Biological Aging Markers. ***Note.*** The regression slope of each association appears on the y-axis, with the range of couple health behavior on the x-axis. The red dashed line depicts a null association, and the bands represent 95 % confidence intervals. The black solid line itself represents the model-based slope of the predictor on the outcome at varying levels of the z-scored moderator, controlling for sex, visit, BMI, comorbidities, and education. Age was also controlled in models with $p16^{INK4a}$ expression as outcome. Slopes in plot 3A are unstandardized, whereas slopes in plot 3B are effectively standardized given that the predictor, outcome, and moderator in this model were all z-scored. The association is statistically significant in areas of the plot where both the upper and lower confidence intervals are on one side of the red line (highlighted in yellow). For these models, the thresholds are: (A) 0.5 SDs above the mean and higher (with 127 data points in the significant region), and (B) 0.5 SDs above the mean and higher (with 138 data points in the significant region).

4.4. Prospective associations with self-rated marital satisfaction (primary models)

Main Effects. Mirroring cross-sectional associations, those with higher self-reported marital satisfaction at baseline experienced smaller increases in $p16^{INK4a}$ two years later (Table S2, B = −0.182, SE = 0.069, p = 0.009, 95 % CI [–0.318, −0.046]). With each 1-SD increase in marital satisfaction, there was a 16.64 % decrease in $p16^{INK4a}$ expression. This association survived FDR correction. Other main-effect associations were non-significant (ps > 0.055).

Health Behavior Moderation. Couples' health behaviors modified longitudinal patterns. In accordance with symptom-system fit theory, higher self-reported marital satisfaction predicted telomere shortening over two years among couples with lower-than-average sleep quality (Fig. 4A, $B_{interaction}$ = 0.084, SE = 0.039, p = 0.035, 95 % CI [0.006, 0.162]; B_{region} = –0.050, SE = 0.024, p < 0.05, 95 % CI [–0.097, −0.003]). Among these couples, with each 1-SD increase in marital satisfaction, telomeres shortened by 4.89 %. This effect remained significant with FDR correction. The same was true for those with poorer-than-average diets (Fig. 4B, $B_{interaction}$ = 0.057, SE = 0.023, p = 0.016, 95 % CI [0.011, 0.104]; B_{region} = –0.046, SE = 0.023, p < 0.05, 95 % CI [–0.091, −0.0002]). Among these couples, for every 1-SD increase in marital satisfaction, telomeres shortened by 4.47 %. This moderating effect, too, remained significant following FDR correction. In sum, the symptom-system fit pattern emerged between higher marital satisfaction and telomere shortening as a function of poor sleep and diet; low physical activity did not play a role. The effect of marital satisfaction on $p16^{INK4a}$ expression was not moderated by couples' health behaviors, nor did moderating associations arise in relation to DNAm aging.

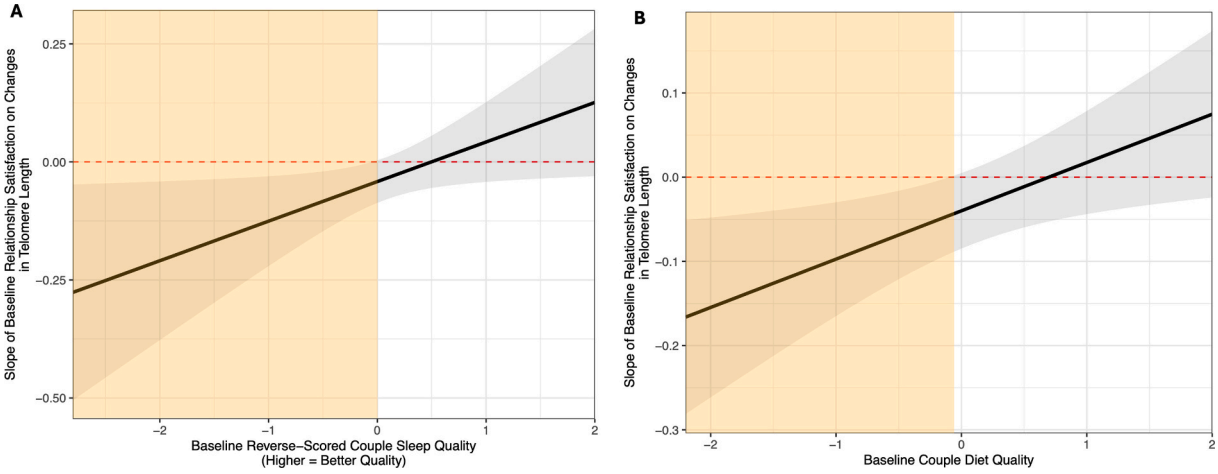

Fig. 4. Marital Satisfaction's Prospective Effect on Telomere Length Moderated by Couples' Health Behaviors ***Note.*** The regression slope of each association appears on the y-axis, with the range of couple health behavior on the x-axis. The red dashed line depicts a null association, and the bands represent 95 % confidence intervals. The black solid line itself represents the unstandardized model-based slope of the predictor on the log-transformed outcome at varying levels of the z-scored moderator, controlling for sex, age, visit, BMI, comorbidities, and education. The association is statistically significant in areas of the plot where both the upper and lower confidence intervals are on one side of the red line (highlighted in yellow). For these models, the significant regions are: (A) the mean and below (n = 48), and (B) −0.1 SD below the mean and lower (n = 66).

4.5. Prospective associations with marital behavior (exploratory models)

Main Effects. In exploratory replication models, longitudinal associations with marital behavior reflected those with self-reports. Couples who treated each other with greater positivity at baseline had greater telomere *shortening* two years later (Table S3, Supplemental Results).

Health Behavior Moderation. Couples' health behaviors moderated these longitudinal associations, and differed across biological aging markers. Consistent with symptom-system fit theory, couples who treated each other with greater positivity at baseline had accelerated DNAm aging two years later, but only when they had poorer-quality diets (Fig. 5, Supplemental Results).

4.6. Supplemental analyses (exploratory)

Individual DNAm Clocks. In supplemental analyses, concurrent and prospective findings with DNAm aging replicated across individual DNAm clocks, although more consistently with PCGrimAgeEAA than with PCPhenoAgeEAA or DunedinPACE (See Supplemental Material, Tables S4-5).

Alcohol Intake. Findings were robust to the role of alcohol intake (Table S8).

Relationship Length. Controlling for relationship length did not alter results (Table S9). Notably, relationship length and age shared a strong correlation (r = 0.73), as is common in age-diverse couple samples (Wilson and Kiecolt-Glaser, 2022; Wilson et al., 2020).

Within-couple Health Behavior Differences. Controlling for within-couple differences in health behaviors did not attenuate any of the significant findings (Table S11).

Within-couple Marital Behavior Differences. When controlling for within-couple differences in marital behavior, all significant findings remained the same except two (Table S10): though the concurrent association between positive behavior discordance and $p16^{INK4a}$ expression was not significant (p = 0.523, 95 % CI [−0.003, 0.005], its inclusion attenuated the concurrent moderating effect of couples' sleep on the association between positive couple behavior and $p16^{INK4a}$ expression ($B_{interaction}$ = −0.133, SE = 0.071, p = 0.063, 95 % CI [−0.272, 0.007]). Similarly, although the difference between partners' positive behavior did not significantly predict changes in DNAm aging (p = 0.886, 95 % CI [−0.017, 0.021], controlling for this difference weakened the moderating effect of couples' diet on the link between couples' positive marital behavior and prospective changes in DNAm aging ($B_{interaction}$ = −0.092, SE = 0.051, p = 0.076, 95 % CI [−0.193, 0.010]).

Inflammation. Concurrently, no significant associations arose in relation to marital satisfaction (Table S6). However, those with more positive behavior also had lower LPS-stimulated inflammatory cytokines (Table S7). Couple physical activity moderated the concurrent association between couple negative behavior and LPS-stimulated cytokine levels, such that less negative behavior was associated with *higher* stimulated inflammation among couples with lower-than-average physical activity, consistent with the symptom-system fit pattern (Fig. S1A, Supplemental Results). A similar moderating effect arose with more positive behavior was linked to higher stimulated inflammation levels among less active couples (Fig. S1B, Supplemental Results). Consistent with the healthy-behavior hypothesis, among couples with healthier diets, those showing higher-quality capitalization behavior also had lower serum inflammation (Fig. S1C, Supplemental Results).

In prospective analyses, marital satisfaction and its moderation by health behaviors on inflammation were not significant (Table S6). However, couple sleep moderated links between couples' baseline positive behavior and subsequent changes in stimulated cytokines in ways that evidenced both healthy-behavior and symptom-system-fit patterns (Fig. S2, Supplemental Results).

5. Discussion

Among middle-aged and older couples, those with higher marital quality, measured via both self-report and observed marital behavior, showed evidence of slowed biological aging. However, these associations largely emerged in couples with healthier behaviors—better sleep, more physical activity, and healthier diets. After accounting for these

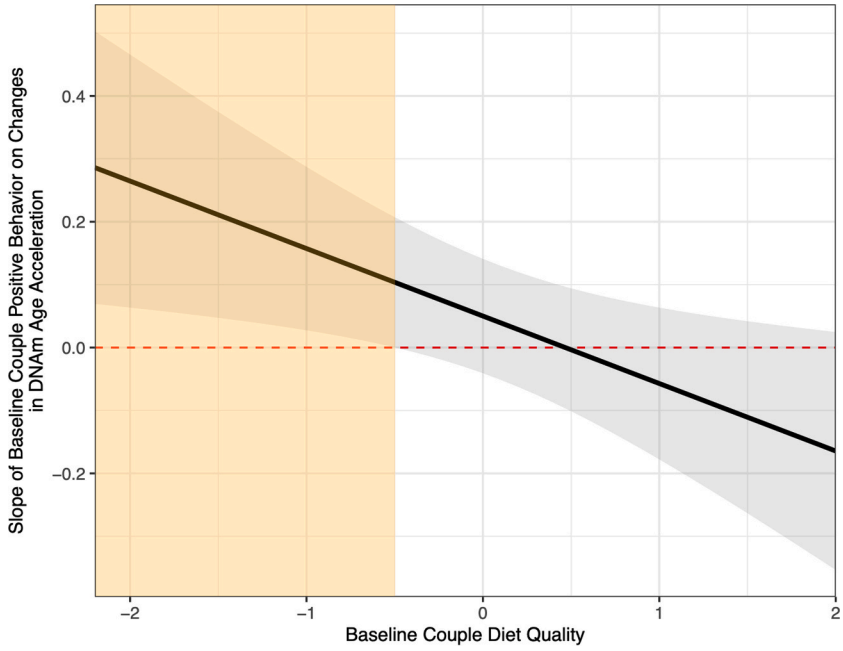

Fig. 5. Marital Behaviors' Prospective Effect on Biological Aging Markers Moderated by Couples' Health Behaviors ***Note.*** The regression slope of each association appears on the y-axis, with the range of couple health behavior on the x-axis. The red dashed line depicts a null association, and the bands represent 95 % confidence intervals. The black solid line itself represents the model-based slope of the predictor on the outcome at varying levels of the moderator, controlling for sex, visit, BMI, comorbidities, and education. The association is statistically significant in areas of the plot where both the upper and lower confidence intervals are on one side of the red line (highlighted in yellow). For this model, the threshold is −0.5 SD below the mean and lower (n = 43).

favorable cross-sectional associations by controlling for baseline levels of biological aging, better baseline marital quality was associated with shortening telomeres and accelerated DNAm aging over the two-year study period—but only among couples with poorer sleep and diet quality. In confirmatory models focusing on marital satisfaction, the primary measure of marital quality, multiple-test correction attenuated the healthy cross-sectional pattern observed with couples' physical activity and $p16^{INK4a}$ expression. However, prospective associations between higher marital satisfaction and shortening telomeres under poor health behaviors, i.e., predicted by symptom-system fit theory, persisted in the face of multiple-test correction. Comparisons across all models echo these insights: standardized slopes were larger in prospective analyses than in concurrent analyses, highlighting that associations may grow in both magnitude and health relevance over time. Standardized slope comparisons also revealed that links with telomeres exceeded those with $p16^{INK4a}$ expression, which in turn eclipsed effect magnitudes of DNAm aging, a preliminary observation that must be replicated in future multi-measure research. Among the patterns that emerged across the range of marital quality measures, diet and sleep quality seemed to play a stronger role with telomere length and DNAm aging, whereas sleep and physical activity modulated $p16^{INK4a}$ expression more consistently. In supplemental analyses, theory-predicted patterns replicated with both serum and LPS-stimulated inflammatory cytokines: better marital quality predicted lower inflammation among couples with higher diet and sleep quality, but it predicted *higher* inflammation among less active couples and those with poorer sleep. Building on symptom-system fit theory and existing evidence on dyadic health behavior, this study unearths a key discovery: that a happy marriage's consequences for aging may depend on the health routines it reinforces.

Among the concurrent findings, marital satisfaction was linked to $p16^{INK4a}$ expression in peripheral blood T lymphocytes, with those in more satisfying relationships exhibiting lower levels and those in more *dis*satisfying relationships showing higher levels. This finding did not hold with multiple-test correction; however, the prospective association between marital satisfaction and $p16^{INK4a}$ expression did survive multiple-test correction. Indeed, the pattern extends results from one other study reporting that, among a sample of 73 young and middle-aged adults in 40 couples, a history of arguing with the spouse was linked to higher $p16^{INK4a}$ expression, paralleling its connections to general dimensions of daily and chronic stress (Rentscher et al., 2019). Together, these findings join research in mice that has documented the exacerbating effects of psychosocial stress on the accumulation of $p16^{INK4a}$-positive senescent cells (Lyons et al., 2024).

In addition, concurrent results build on prior associations linking marital quality to telomere length. According to cross-sectional studies utilizing self-report data, individuals who reported stronger attachment security with their partner (Murdock et al., 2018), who considered their spouse a source of support (Barger and Cribbet, 2016), and who reported greater sexual intimacy (Cabeza de Baca et al., 2017), also had longer telomeres. The current study's data show that associations also manifest in how partners treat each other, as rated by trained coders. Namely, couples who took a more active role in rejoicing in their partner's positive event, and who were more responsive in those discussions, had longer telomeres. While capitalization is known to boost mood, intimacy, and physiological linkage between partners (Shrout et al., 2023; Peters et al., 2018), this study is the first to document connections to markers of biological aging, which foreshadow the long-term course of health in adulthood (Kennedy et al., 2014). Indeed, while self-rated marital satisfaction was treated as a primary indicator of marital quality given its widespread use in research, findings showed that a range of marital behaviors in varied emotional contexts may underlie the predictive power of marital satisfaction. Moreover, these behavioral signatures uncovered other associations with DNAm aging and diet that were not seen with satisfaction—consistent with prior observations that marital behavior may detect health associations with greater sensitivity than self-report measures (Kiecolt-Glaser et al., 2015; Wilson et al., 2017).

An important qualifier of the cross-sectional results, marital quality was associated with biological aging primarily among couples with healthier diet and sleep quality; similar patterns arose between marital satisfaction and physical activity that did not survive multiple-test correction. To illustrate the association, couples with high-quality diets and low levels of negative behavior had aged ~2 to 6.5 months more slowly according to GrimAgeEAA compared to couples with poor diets, or those with good diets and more negative behavior. Indeed, couples' health behaviors help to explain the marked variation in the ties between marital quality and health identified by Robles and colleagues' seminal meta-analysis (Robles et al., 2014). The authors suspected that health behaviors played an important role but could not evaluate this hypothesis due to the small number of studies that measured and accounted for them. Moreover, the effect sizes linking marital quality to health outcomes were comparable to the health consequences of health behaviors themselves, such that both were small in magnitude. This study underscores that, despite their equivalent effect sizes on health outcomes, a happy marriage cannot compensate for poor sleep, little exercise, or unhealthy diet; both relationships and health routines must be fostered to promote healthy biological aging, perhaps through a positive feedback loop that forms over time. Notably, the finding that more favorable biological aging occurs in the context of healthy couple behaviors and marital quality aligns with prior research citing better treatment outcomes and adherence among those in closer, more satisfying romantic relationships (Trief et al., 2004; Knoll et al., 2012). Prior evidence points to positive social control as a possible mechanism, wherein praise for engaging in healthy behaviors, encouragement, practical support, and modeling have a greater positive impact in the context of a satisfying relationship (Knoll et al., 2012; de Montigny et al., 2017).

After accounting for baseline levels of biological aging, more positive marital behavior at baseline predicted telomere *shortening* over time. This pattern may reflect statistical suppression: adjusting for the beneficial associations between baseline marital quality and biological aging revealed a second, distinct process—the other side of the double-edged sword. In line with symptom-system fit theory, couples' unhealthy behaviors—their poorer sleep and diet quality—drove the unfavorable associations between better marital quality and faster biological aging over time. To illustrate, couples with poorer diets who treated each other with greater positivity at baseline aged 7.6 to 12.5 months faster over the next two years in GrimAgeEAA compared to their counterparts with better diets, or with low-quality diets and less positive behavior. Confirmatory models involving marital satisfaction survived multiple-test correction, which further attests to the findings' robustness. An extension of prior cross-sectional work showing that happy couples with unhealthy behaviors have higher BMI (Skoyen et al., 2018), the current study is the first to chart the long-term health implications of this toxic pairing.

In supplemental analyses with inflammation as the outcome, both hypothesized patterns emerged, with marital quality predicting lower inflammation among those with good health behaviors and higher inflammation in couples with unhealthy routines. Notably, the latter symptom-system fit pattern emerged in cross-sectional and prospective analyses alike, which further strengthens the findings. Moreover, results emerged in relation to both serum and stimulated cytokines. These reflect two respective dimensions of inflammation—resting levels and reactivity to an external stimulus—both of which change with age, engage in a vicious cycle with the senescence associated secretory phenotype (SASP), and are triggered by marital stress (Wilson et al., 2017; Franceschi et al., 2000; Bruunsgaard et al., 2001; Polsky et al., 2022). Their associations with marital quality and couples' health behaviors underscore the central role of the immune system in the aging cascade. Beyond the intrinsic ties between inflammation and aging, terminally differentiated T cells are thought to be the primary source of short telomeres (Weng, 1995). Moreover, $p16^{INK4a}$ promotes exhaustion

and apoptosis in CD8+ T cells (Zhang, 2024) and is most abundant in the CD28+ CD57+ T cell population, which is associated with senescence (Onyema, 2015).

Although the statistically significant findings in this study aligned with our theory-based predictions, hypothesized effects were not significant in all models. With one exception, results tended to show either the healthy pattern—i.e., higher marital quality predicting slower biological aging among couples with healthy routines—*or* the unhealthy, symptom-system fit pattern. The healthy pattern predominated in concurrent analyses, whereas the unhealthy pattern emerged primarily in prospective models. Beyond statistical suppression, this may be due to the relatively healthy and highly educated nature of our sample. A different sample, perhaps larger and more diverse in socioeconomic resources and health behaviors, may have shown both patterns at once or featured the symptom-system-fit pattern more prominently. Moreover, associations were larger and more consistent in telomere length and $p16^{INK4a}$ expression than DNAm aging. The latter consisted of three DNAm clock metrics, which themselves were constructed from multiple CpG sites according to algorithms trained on relevant factors like chronological age, morbidity, and mortality. In this way, DNAm age acceleration may be particularly tuned to standard health-relevant covariates (e.g., comorbidities, BMI) that relationship quality and health behaviors can also jointly shape. Compared to telomere length and $p16^{INK4a}$ expression, DNAm aging metrics are likely to be more stable and show less dynamic range. In addition, even though psychosocial stress shares associations with all three types of aging biomarkers, they reflect distinct molecular processes and are influenced by unique physiologic stressors, outside of psychosocial stress (López-Otín et al., 2013; Serrano et al., 1997; Fagagna et al., 2003).

Although partners can reinforce and encourage one another's health behaviors toward healthy ends, as seen in the current study's favorable concurrent associations, this virtuous cycle may be fragile, reflected in their attenuation with multiple-test correction. Despite that prior work has postulated healthy behaviors as a mechanism of marital quality's health benefits, e.g., (Robles et al., 2014), correlations between better marital quality and healthy couple behaviors were small and sporadic. Indeed, though stress can induce unhealthy food choices and disrupt sleep and exercise (Ng and Jeffery, 2003; Stults-Kolehmainen and Sinha, 2014), the reverse is not always true: marital satisfaction can reinforce either healthy or unhealthy habits. Further, healthy behaviors—a diet full of whole foods and free from processed, sugary foods; daytime activities that involve exercise and minimize sedentary behavior; nighttime rituals that ensure restful sleep—are notoriously difficult to maintain (Wood and Neal, 2016). Given that processed foods are designed to be appetitive (Lemos et al., 2022), that exercise is inherently more effortful than sedentariness, and that screens and busy schedules encroach on bedtime routines, even couples who strive for healthy behaviors may succumb to the rewarding, unhealthy cycle explained by symptom-system fit theory. Moreover, it cannot be assumed that couples share healthy goals: a partner who has not committed to positive health behavior change may actively undermine the other's health-promoting efforts (Novak et al., 2020). These social processes likely contribute to the variable success of lifestyle-change interventions.

Among the study's limitations were to its generalizability: couples in this sample were predominantly White, highly educated, and healthier than their peers in the broader population. For this reason, future work must assess our hypotheses in more racially and socioeconomically diverse samples as well as in clinical populations. In addition, with a multi-method approach that capitalized on the thorough phenotyping of the sample and reflected the breadth of the underlying theories, came the accompanying drawback of multiple tests. To address Type I error concerns, we treated self-reported marital satisfaction as a single primary marital quality measure given its well-established psychometric properties and wide use, and thus applied multiple-test correction to these models; the behavioral samples, including understudied dimensions of relationship-enhancing patterns like positive behavior and active-constructive capitalization support, served to replicate and deepen our understanding of the general appraisals. Further, in terms of our interpretive approach, we sought to synthesize the larger patterns of findings rather than give undue weight to one-off results. For this reason, we caution against overemphasizing or overinterpreting singular results and instead offer these up as fodder for follow-up in future studies. Replication of this study in subsequent work is critical, as it will provide definitive answers regarding the robustness of effects. In addition, with a two-wave design, we were able to examine how baseline marital quality and health behaviors predicted subsequent changes in biological aging, which offered the advantage of establishing temporal precedence. Future research using three-wave designs should further extend this work by investigating whether *changes* in marital quality and health behaviors predict subsequent changes in biological aging. Finally, even as this study builds on the insights of relationship science—that positive marital processes can reinforce both healthy and unhealthy routines—marriage-health theories leave open key questions that future work must address: how do *toxic* marital patterns interplay with couple health behaviors, and with what consequences for healthy aging? Both laboratory and daily-life studies that tease apart the temporal sequence of negative and positive marital patterns as well as couples' health behaviors will help to deepen our understanding of these critical dynamics.

Taken together, health-promoting behaviors are challenging to sustain, and a romantic partner, arguably the most important and proximal social influence for partnered individuals, can reinforce healthy and unhealthy behaviors alike. The current study documented the implications of these dual processes in relation to markers of biological aging. In the presence of healthy couple behaviors, higher marital quality was associated with slowed biological aging, whereas when paired with unhealthy couple behaviors, marital satisfaction served as an aging accelerant. The findings underscore the critical role of health behaviors and the nuanced connections of the marital relationship to healthy aging.

CRediT authorship contribution statement

Stephanie J. Wilson: Writing – review & editing, Writing – original draft, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Annelise A. Madison:** Writing – original draft, Visualization. **M. Rosie Shrout:** Writing – review & editing, Writing – original draft, Project administration. **Lisa M. Christian:** Writing – original draft. **Elissa S. Epel:** Writing – review & editing, Resources, Methodology. **Christin E. Burd:** Writing – review & editing, Resources, Methodology. **Jue Lin:** Writing – review & editing, Resources, Methodology. **Samuel H. Molli:** Writing – original draft, Visualization. **Rebecca Andridge:** Writing – review & editing, Visualization, Formal analysis. **Harry T. Reis:** Writing – review & editing, Resources, Methodology. **Janice K. Kiecolt-Glaser:** Writing – review & editing, Supervision, Project administration, Methodology, Investigation, Funding acquisition, Conceptualization.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplemental Material

Supplemental information on the study's methods and results can be found online at https://doi.org/10.1016/j.bbi.2026.106869.

Data availability

The code is provided among the attachments, and the data will be made available upon request.

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