Epigenetic upregulation of FKBP5 by aging and stress contributes to NF-κB–driven inflammation and cardiovascular risk

Anthony S. Zannas a,b,c,d,1, Meiwen Jia a, Kathrin Hafner a, Jens Baumert b, Tobias Wiechmann a, Julius C. Pape e, Janine Arloth f, Maik Ködel b, Silvia Martinelli a, Maria Roitman a, Simone Röh a, Andreas Haehle a, Rebecca T. Emenh a, Stella Iurato a, Tania Carrillo-Roa a, Jari Lahti h, Katri Rääkkönen a, Johan G. Eriksson j,k, Amanda J. Drake m, Melanie Waldenberger a, Simone Wahl a, Sonja Kunze a, Susanne Lucae a, Bhek Bradley o,p, Christian Gieger a, Felix Hausch a, Alicia K. Smith o,q, Kerry J. Ressler o,q,r, Bertram Müller-Myhsok a,s,t, Karl-Heinz Ladwig o,t, Theo Rein a, Nils C. Gassen b,v, and Elisabeth B. Binder a,o,t

aDepartment of Translational Research in Psychiatry, Max Planck Institute of Psychiatry, 80804 Munich, Germany; bDepartment of Psychiatry, University of North Carolina at Chapel Hill, Chapel Hill, NC 27514; cDepartment of Genetics, University of North Carolina at Chapel Hill, Chapel Hill, NC 27514; dDepartment of Psychiatry and Behavioral Sciences, Duke University Medical Center, Durham, NC 27710; eInstitute of Epidemiology, Helmholtz Zentrum München – German Research Centre for Environmental Health, D–85764 Neuherberg, Germany; fInstitute of Computational Biology, Helmholtz Zentrum München, D-85764 Neuherberg, Germany; gDepartment of Chemistry, Institute of Organic Chemistry, Technische Universität Darmstadt, 64289 Darmstadt, Germany; hGelsei School of Medicine, Dartmouth College, Lebanon, NH 03755; iDepartment of Psychology and Logopedics, University of Helsinki, 00100 Helsinki, Finland; jTüRK Institute for Advanced Studies, University of Turku, 20500 Turku, Finland; kDepartment of General Practice and Primary Health Care, Helsinki University Hospital, University of Helsinki, 00100 Helsinki, Finland; lFolkhälsoan Research Center, 00290 Helsinki, Finland; mUniversity of British Heart Foundation Centre for Cardiovascular Science, The Queen’s Medical Research Institute, University of Edinburgh, Edinburgh EH16 4TJ, United Kingdom; nAtlanta Veterans Affairs Medical Center, Decatur, GA 30033; oDepartment of Psychiatry and Behavioral Sciences, Emory University Medical School, Atlanta, GA 30322; pDepartment of Gynecology and Obstetrics, Emory University Medical School, Atlanta, GA 30322; qDivision of Depression & Anxiety Disorders, McLean Hospital, Belmont, MA 02478; rDepartment of Psychiatry, Harvard Medical School, Boston, MA 02178; sMunich Cluster of Systems Biology, 85359 Munich, Germany; tInstitute of Translational Medicine, University of Liverpool, Liverpool L69 3GE, United Kingdom; uDepartment of Psychosomatic Medicine and Psychotherapy, Klinikum rechts der Isar, Technische Universität München, 80333 München, Germany; vDepartment of Psychiatry and Psychotherapy, University Hospital Bonn, 53105 Bonn, Germany

Edited by Huda Akil, University of Michigan, Ann Arbor, MI, and approved May 2, 2019 (received for review December 5, 2018)

Aging and psychosocial stress are associated with increased inflammation and disease risk, but the underlying molecular mechanisms are unclear. Because both aging and stress are also associated with lasting epigenetic changes, a plausible hypothesis is that stress along the lifespan could confer disease risk through epigenetic effects on molecules involved in inflammatory processes. Here, by combining large-scale analyses in human cohorts with experiments in cells, we report that FKBP5, a protein implicated in stress physiology, contributes to these relations. Across independent human cohorts (total n > 3,000), aging synergized with stress-related phenotypes, measured with childhood trauma and major depression questionnaires, to epigenetically up-regulate FKBP5 expression. These age/stress-related epigenetic effects were recapitulated in a cellular model of replicative senescence, whereby we exposed replicating human fibroblasts to stress (glucocorticoid) hormones. Unbiased models revealed that the clustered regulatory zones of FKBP5, which included NR1A1, an NF-κB regulatory kinase, whereas opposing FKBP5, either by genetic or pharmacological inhibition prevented the effects on NF-κB, thus suggesting an age-driven epigenetic signature enhanced FKBP5 response to NF-κB through a positive feedback loop and was present in individuals with a history of acute myocardial infarction, a disease state linked to peripheral inflammation. These findings suggest that aging/stress-driven FKBP5-NF-κB signaling mediates inflammation, potentially contributing to cardiovascular risk, and may thus point to novel biomarker and treatment possibilities.

Aging is the single most important risk factor for several disease phenotypes that are leading causes of morbidity and mortality (1). However, individuals of the same age exhibit substantial variability in their risk of developing aging-related disease (2). Among important factors influencing disease risk, studies show how psychosocial stressors, such as childhood trauma, as well as stress-related psychiatric disorders, including major depressive disorder (MDD), increase risk for aging-related diseases, most notably cardiovascular syndromes (3–7).

Significance

Diseases of the aging are the leading cause of morbidity and mortality. Elucidating the molecular mechanisms through which modifiable factors, such as psychosocial stress, confer risk for aging-related disease can have profound implications. By combining studies in humans with experiments in cells, we show that aging and stress synergize to epigenetically upregulate FKBP5, a protein implicated in stress physiology. Higher FKBP5 promotes inflammation by activating the master immune regulator NF-κB, whereas opposing FKBP5, either genetically or pharmacologically, prevents the effects on NF-κB. Further, the aging/stress-related epigenetic signature of FKBP5 is associated with history of myocardial infarction, a disease linked to inflammation. These findings provide molecular insights into stress-related disease, pointing to biomarker and treatment possibilities.


Conflict of interest statement: E.B.B. receives a research grant from Böhringer-Ingelheim to develop cellular and animal models of enhanced FKBP5 function. She is also coinventor on the following patent application: “FKBP5: a novel target for antidepressant therapy” (European Patent no. EP 1687443 B1).

This article is a PNAS Direct Submission.

This open access article is distributed under Creative Commons Attribution-NonCommercial-NoDerivatives License 4.0 (CC BY-NC-ND).

Data deposition: The data reported in this paper have been deposited in the Gene Expression Omnibus (GEO) database, https://www.ncbi.nlm.nih.gov/geo (accession nos. GSE128235, GSE81837, and GSE128237).

1To whom correspondence may be addressed. Email:aszannas@gmail.com or binder@psych.mpg.de.

This article contains supporting information online at www.pnas.org/lookup/suppl;doi:10.1073/pnas.1816847116/-/DCSupplemental.

Published online May 21, 2019.
Studies further suggest that aging and stress-related phenotypes may together confer disease risk by increasing peripheral inflammation (5, 8–11), but the underlying mechanisms are poorly understood.

Mechanistically, the effects of stress on inflammation and disease risk could be driven by stress-responsive molecules able to modulate immune function. A plausible such molecule to examine is the FK506-binding protein 51 (FKBP5) in T cells (12–19). Interestingly, FKBP5 up-regulation has been observed not only with stress exposure and glucocorticoid stimulation but also in the aging brain (20, 21) and in some disease phenotypes (15, 17, 20). However, it is unknown whether aging regulates FKBP5 in the immune system and how this effect, if present, could shape risk for cardiovascular disease. Both aging and stress can have lasting effects on the epigenome (22–25), and FKBP5 transcription can be regulated by epigenetic mechanisms (26–28); thus, a plausible hypothesis is that stress exposure along the lifespan could epigenetically deregulate FKBP5 in immune cells, potentially contributing to peripheral inflammation and disease risk.

Here we address these questions by combining genome-wide analyses in human cohorts with mechanistic investigations in cells. Convergent findings support a model whereby aging and stress-related phenotypes synergize to decrease DNA methylation at selected enhancer-related FKBP5 sites, epigenetically up-regulating FKBP5 in whole blood and in distinct immune cell subtypes. Higher FKBP5 in turn promotes NF-kB (nuclear factor kappa-light-chain-enhancer of activated B cells)-driven peripheral inflammation. Accordingly, the age/stress-related FKBP5 epigenetic signature is present in individuals with a history of acute myocardial infarction (MI), a disease state linked to peripheral inflammation. We further find that the cellular effects of stress on NF-kB are prevented by either CRISPR/Cas9 deletion of the FKBP5 gene or a selective FKBP5 antagonist, suggesting FKBP5–NF-kB signaling as a tractable treatment candidate. Together these findings provide molecular insights into mechanisms linking aging and stress with peripheral inflammation and cardiovascular risk, thereby pointing to biomarker and intervention possibilities.

Results
FKBP5 DNA Methylation Decreases Along the Lifespan at Selected Cytosine–Guanine Dinucleotides. DNA methylation at cytosine–guanine dinucleotides (CpGs) can change with age (24), an effect moderated in part by environmental factors (29), including psychosocial stress (23). These epigenetic changes can in turn contribute to disease risk by affecting the expression of molecules regulated by the age-related genomic sites, thus altering cell and tissue function (25, 30). Therefore, to gain insights into the mechanisms through which stress contributes to disease risk, it is relevant to examine the effects of stress on age-related CpGs.

To identify such age-related FKBP5 CpGs, we used Illumina HumanMethylation450 BeadChip (450K) data from three independent cohorts with broad age range and documented stress-related phenotypes: the Grady Trauma Project (GTP; n = 393, age range 18 to 77 y); the Cooperative Health Research in the Region of Augsburg F4 community study (KORA; n = 1,727, age range 32 to 81 y); and the Max Planck Institute of Psychiatry cohort (MPIP; n = 537, age range 18 to 87 y) (demographics in Dataset S1). These analyses included all available CpGs covered by the 450K within or in close proximity (10 kb upstream or downstream) to the FKBP5 locus (chromosome 6p21.31). After controlling for potential confounders, including age, sex, population stratification, and blood cell proportions in the GTP, KORA, and MPIP, as well as for smoking and other available cohort-specific covariates (see SI Appendix, Supplementary Methods for additional details), and after false discovery rate (FDR) correction for multiple comparisons, two CpGs (cg20813374 and cg00130530) showed consistent and robust age-related decrease in methylation across all cohorts (detailed statistics in Dataset S2). These two age-related sites lie in close proximity to each other proximally upstream of the FKBP5 transcription start site (TSS; −462 bp for cg20813374 and −484 bp for cg00130530; UCSC Genome Browser; Dataset S2) and show significant pairwise correlations in all cohorts (GTP: r = 0.83, P < 2.2 × 10⁻¹⁶; KORA: r = 0.61, P < 2.2 × 10⁻¹⁶; MPIP: r = 0.37, P < 2.2 × 10⁻¹⁶). The association of age with average methylation of the two CpGs is depicted in Fig. L4 and SI Appendix, Fig. S1A. To validate this finding with a non-hybridization-based DNA methylation method, we performed targeted bisulfite sequencing with the Illumina MiSeq in a smaller sample of female subjects, again observing robust pairwise correlation of the two CpGs (r = 0.62, P = 5.7 × 10⁻¹⁶) and significantly lower average methylation of the two sites with increasing age (n = 77, P = 1.9 × 10⁻⁸; SI Appendix, Fig. S2). Given the close proximity and consistent pairwise correlations between the two age-related FKBP5 CpGs, all subsequent analyses examined the average methylation level of these two sites.

Age-Related Decrease in FKBP5 Methylation Is Not Confounded by Blood Cell Type Heterogeneity and Occurs in Purified Immune Cell Subtypes. Peripheral blood cell counts change along the lifespan (31), raising the possibility that heterogeneity in blood cell type composition could be confounding our results (32), despite the consistent inverse relation we observed between aging and FKBP5 methylation after adjustment for calculated cell types in the regression models (Fig. L4 and Dataset S2). To rule out this possibility, we first performed a series of sensitivity analyses in our cohorts. The inverse relation between age and methylation of the two FKBP5 CpGs (cg20813374 and cg00130530) was consistent across the GTP, KORA, and MPIP cohorts (all P values <10⁻¹⁷; Fig. L4), and there was no consistent relation between calculated blood cell subtypes (the potential confounder) and either age or FKBP5 methylation levels (our variables of interest), suggesting that strong confounding by cell subtypes was not present (Dataset S3). This was further validated using an additional dataset of male and female subjects (n = 213) with both 450K data and differential complete blood counts; methylation of the age-related CpGs did not significantly correlate with any of the calculated types of blood cells (Dataset S3). This finding with a non-hybridization-based DNA methylation method, we performed targeted bisulfite sequencing with the Illumina MiSeq in a smaller sample of female subjects, again observing robust pairwise correlation of the two CpGs (r = 0.62, P = 5.7 × 10⁻¹⁶) and significantly lower average methylation of the two sites with increasing age (n = 77, P = 1.9 × 10⁻⁸; SI Appendix, Fig. S2). Given the close proximity and consistent pairwise correlations between the two age-related FKBP5 CpGs, all subsequent analyses examined the average methylation level of these two sites.

To further understand how aging influences FKBP5 methylation in specific immune cell types, we analyzed publicly available DNA methylation data in whole blood, as well as FACSorted CD4 T cells and neutrophils, from male subjects with a broad age range (33). We again observed an inverse relation between age and methylation of the two FKBP5 CpGs in whole blood (n = 184, r = −0.30, P = 3.6 × 10⁻⁸). Importantly, the same effect size was present in purified CD4 T cells (n = 46, r = −0.32, P = 3.3 × 10⁻⁷), whereas this effect was in the same direction but nonsignificant in purified neutrophils (n = 48, r = −0.20, P = 1.7 × 10⁻¹; SI Appendix, Fig. S3). Together, these findings show that increasing age is associated with lower FKBP5 methylation in T cell (and likely other distinct immune cell) subtypes and that this effect is not solely the result of age-related changes in blood cell type composition.

Early Life Stress and Depressive Phenotypes Accelerate the Age-Related Decrease in FKBP5 Methylation. FKBP5 responds to stress and glucocorticoids and can undergo decrease in DNA methylation at distinct CpGs (26–28, 34, 35). Therefore, it is plausible that higher stress burden throughout life could induce lasting epigenetic changes, potentially accelerating decrease in methylation of the two age-related FKBP5 CpGs. To investigate this hypothesis, we examined the combined effects of age and stress-related phenotypes...
on average methylation of the two CpGs. As information on current depressive symptoms was available in all three cohorts, we first investigated this phenotype. After adjusting for all covariates (SI Appendix, Supplementary Methods), depressive phenotypes consistently accelerated the age-related decrease in FKBP5 methylation (total n = 2,249, meta-analysis interaction P = 2.6 × 10⁻²; Fig. 1B). This association remained significant after further adjusting for education, as a measure of socioeconomic status, in all cohorts (meta-analysis interaction P = 3.7 × 10⁻²). Because early life trauma is among the strongest risk factors for developing MDD (5), we further examined whether the effect of depression on age-related decrease in FKBP5 methylation is moderated by childhood trauma.

Fig. 1. Aging and stress are together associated with decreased DNA methylation at selected FKBP5 CpGs. (A) Methylation decreases at selected FKBP5 CpGs along the human lifespan (GTP: βage = −0.0045, SE = 0.0008, P = 8 × 10⁻⁶; KORA: βage = −0.0055, SE = 0.0005, P < 2 × 10⁻¹⁶; MPIP: βage = −0.0064, SE = 0.0012, P = 7 × 10⁻⁸; total n = 2,523). (B) Depressive phenotypes are associated with accelerated age-related decrease in FKBP5 methylation (total n = 2,249, meta-analysis interaction P = 2.6 × 10⁻², heterogeneity P = 2.7 × 10⁻³). Statistics per cohort: GTP: interaction P = 1.9 × 10⁻², βage for moderate/severe depression = −0.0075 (SE = 0.0014) vs. βage for non/mild depression = −0.0032 (SE = 0.0011); KORA: interaction P = 6.3 × 10⁻¹, βage for higher levels of depression = −0.0063 (SE = 0.0011) vs. βage for lower levels of depression = −0.0047 (SE = 0.0007); MPIP: interaction P = 1.9 × 10⁻¹, βage for depressed = −0.0077 (SE = 0.0015) vs. βage for nondepressed = −0.0044 (SE = 0.0019). (C) Early life separation is associated with lower methylation of the age-related FKBP5 CpGs in the HBCS (βseparation = −0.0932, SE = 0.0343, P = 7.4 × 10⁻⁴, mean DNA methylation difference 1.4%). The y axis in A, B, and C depicts the residuals of the average DNA methylation levels (M-values) of the two age-related FKBP5 CpGs (cg0813374 and cg01103530) and reported statistics are after adjustment for all covariates for each cohort (SI Appendix, Supplementary Methods); for a more intuitive visualization, selected panels are also depicted as percent DNA methylation (Beta-values) in SI Appendix, Fig. S1. (D) In vitro aging and exposure to the stress hormone (glucocorticoid) receptor agonist DEX additively decrease methylation at the age-related FKBP5 CpGs in the IMR-90 fibroblast model of replicative senescence (F1,45 = 6.3, interaction P = 4.6 × 10⁻², n = 4 replicates per group). Statistical comparisons were performed with two-way mixed-design ANOVA (per experimental design), using replicative age as the between-subject factor. Statistically significant effects were followed with Bonferroni-corrected pairwise comparisons, shown as follows: *P < 5 × 10⁻², statistically significant pairwise comparisons for young vs. old replicative age; *P < 5 × 10⁻², statistically significant pairwise comparison for vehicle vs. DEX-treated old cells. Error bars depict the SE around the group mean. The y axis in D depicts the average percent DNA methylation of the two FKBP5 CpGs.
severity as measured with the childhood trauma questionnaire (CTQ) in the GTP. This stratified analysis yielded a significant age-depression interaction in the higher-CTQ (interaction $P = 4.6 \times 10^{-5}$) but not the lower-CTQ group (interaction $P = 3.3 \times 10^{-3}$) and no main effect of childhood trauma severity ($P = 3.7 \times 10^{-2}$). Finally, to examine whether exposure to a severe and prolonged early childhood stressor itself is associated with lasting decrease in methylation of the age-related CpGs, we compared elderly individuals that had prolonged early life separation from their parents with sex- and age-matched nonseparated controls in a fourth cohort, the Helsinki Birth Cohort Study ($n = 160$, age range 58 to 69 y, demographics in Dataset S1). In this cohort, early life separation was associated with reduced methylation of the age-related CpGs ($P = 7.4 \times 10^{-3}$; Fig. 1C and SI Appendix, Fig. S1B).

These findings suggest that childhood trauma and depressive phenotypes together accelerate the age-related decrease in $FKBP5$ methylation in peripheral blood.

### The Effects of Both Aging and Stress on $FKBP5$ Methylation Are Recapitulated in Vitro.

The findings presented above identify two $FKBP5$ CpGs (cg20813374 and cg00130530) that show a consistent association of lower methylation levels with aging and stress-related phenotypes; however, these findings are inherently limited by the use of human subjects where experimental manipulation is not feasible. To experimentally support these associations, we used a cellular model of replicative senescence (IMR-90 fibroblasts) to test whether replicative aging and stress—which is commonly modeled in the dish with the stress (glucocorticoid) hormone receptor agonist dexamethasone (DEX) (26, 36)—influences $FKBP5$ methylation at these sites. Population doubling level (PDL) was calculated as previously (37), and $FKBP5$ methylation was measured with targeted bisulfite pyrosequencing and compared between cells of young (PDL = 22) and old (PDL = 42) replicative age treated for 7 d with either vehicle (DMSO) or 100 nM DEX. In accordance with our in vivo findings, in vitro aging and DEX additively decreased DNA methylation at the two $FKBP5$ CpGs (interaction $P = 4.6 \times 10^{-5}$, DNA methylation decrease in old vs. young cells = 10.1%, and additional methylation decrease in old cells treated with DEX vs. vehicle = 3.4%; Fig. 1D). Together with our observations in human cohorts (Fig. 1A–C), these convergent findings show that aging and stress may influence $FKBP5$ methylation across different cohorts, distinct cell types, and contexts.

### Decreased Methylation at the Age/Stress-Related $FKBP5$ CpGs Is Associated with $FKBP5$ Up-Regulation in Peripheral Blood.

DNA methylation patterns can shape gene expression, thereby contributing to cellular function and phenotypic expression (38, 39). The age/stress-related $FKBP5$ CpGs identified above lie proximally (<500 bp) upstream of the TSS for all highly expressed isoforms of $FKBP5$ and are intronic only for the minimally expressed variant 2 of the gene (UCSC Genome Browser, UCSC Genes Track; GTEx portal). Integrative analysis of chromatin states using ChromHMM (40) showed that the two CpGs colocalize with signatures that are consistent with either enhancers or flanking active TSS in a large number of cell types (Dataset S4). In immune cells, the CpGs are commonly mapped to either an enhancer or flanking active TSS (SI Appendix, Fig. S4). Further, in most cell types the two sites show intermediate levels of methylation and colocalize with H3K4me1 and H3K27me3 signatures (Roadmap Epigenome Browser; shown for immune cell proxy in SI Appendix, Fig. S5). This landscape is most consistent with a poised enhancer (41) that upon transcription factor binding could interact and regulate the downstream $FKBP5$ TSS.

To examine whether DNA methylation of these CpGs influences gene transcription, we used $FKBP5$ mRNA data measured in the GTP cohort with Illumina HumanHT-12 Expression BeadChip arrays ($n = 355$). DNA methylation levels of the age/stress-related sites were inversely associated with $FKBP5$ mRNA levels ($P = 1.6 \times 10^{-5}$; Fig. 2A). We found similar negative correlations in publicly available data from breast tissue samples of control female subjects ($n = 84$, $r = -0.26$, $P = 1.6 \times 10^{-7}$; SI Appendix, Fig. S6) (42). Since $FKBP5$ transcription is robustly induced by glucocorticoids (28, 43) and given that the CpGs are located in predicted poised enhancers (SI Appendix, Fig. S5), we speculated that methylation at the age/stress-related $FKBP5$ CpGs could moderate the effect of cortisol on $FKBP5$ levels. After confirming a robust positive correlation between cortisol and $FKBP5$ mRNA ($r = 0.41$, $P = 1 \times 10^{-12}$), we found that the cortisol–$FKBP5$ relationship was significantly stronger in individuals with below- compared with above-median methylation levels in the GTP (interaction $P = 1.4 \times 10^{-3}$; Fig. 2B). In addition, the phenotypes associated with lower methylation levels moderated the relationship between cortisol and $FKBP5$ mRNA; specifically, this relationship was significantly stronger in older subjects as defined with a median split of age (interaction $P = 2.4 \times 10^{-3}$; Fig. 2C) and in individuals with higher severity of depression and childhood trauma (interaction $P = 7.5 \times 10^{-5}$; Fig. 2D). These findings are in line with previous observations that stressors can induce lasting epigenetic effects on other sites of the $FKBP5$ locus (26–28) and suggest that the effects of aging and stress converge at distinct CpGs to epigenetically up-regulate $FKBP5$ in human blood.

### $FKBP5$ Up-Regulation Promotes NF-κB–Related Peripheral Inflammation and Chemotaxis. To examine potential functional effects of $FKBP5$ up-regulation in an unbiased manner, we used genome-wide gene expression data from peripheral blood in the GTP cohort ($n = 355$) to identify genes that are coregulated with $FKBP5$. After FDR correction for multiple comparisons (FDR-adjusted $P < 0.05$), $FKBP5$ correlated significantly with a total of 3,275 genes (Dataset S5). Using these transcripts as input and the unique array genes expressed above background in blood (except $FKBP5$) as reference (9,538 genes), we performed pathway and disease association analysis in WebGestalt. The strongest enrichment was observed for inflammation and was conferred by a total of 123 inflammation-related genes (FDR-adjusted $P = 8.1 \times 10^{-6}$; Fig. 3A and Dataset S6). Notably, $FKBP5$ showed robust positive correlation with a host of proinflammatory genes, such as interleukin and toll-like receptors (Dataset S7). Furthermore, $FKBP5$ levels were positively associated with the granulocyte proportion ($r = 0.22$, $P = 5.8 \times 10^{-5}$) and the granulocyte-to-lymphocyte ratio ($r = 0.31$, $P = 7.4 \times 10^{-4}$, SI Appendix, Fig. S7), an inflammation marker that is associated with increased cardiovascular risk and mortality (44, 45), but not with the proportions of CD4 T cells ($r = -0.05$, $P = 3.6 \times 10^{-1}$). These associations suggest that $FKBP5$-related inflammation could be driven by enhanced chemotaxis of granulocytes and other proinflammatory cells. As plausible mediator of this effect, we focused on interleukin-8 (IL-8), a major chemokine that recruits and activates granulocytes and other proinflammatory cells (46). Although $FKBP5$ down-regulation has been found to suppress IL-8 production in melanoma cells (19), no studies have examined whether $FKBP5$ down-regulation influences IL-8 secretion by immune cells. To address this possibility, we overexpressed $FKBP5$ in Jurkat cells, a human T cell line that allowed efficient and reproducible transfection with $FKBP5$ expression vectors (~32-fold induction; Fig. 3B), and measured their potential to secrete IL-8. $FKBP5$ overexpression nearly doubled IL-8 secretion upon immune stimulation ($P = 4.4 \times 10^{-7}$; Fig. 3C), supporting that increased $FKBP5$ in T cells could drive chemotaxis of proinflammatory cells. To further examine whether the effects of $FKBP5$ on the immune system may be driven by distinct transcription factors, we performed transcription factor target analysis in the GTP cohort using the same input and reference gene sets (3,275,9,538). The strongest enrichment was observed for NF-κB (FDR-adjusted
Figs. S10 and Dataset S8), a master immune regulator that has been linked to FKBP5 (13, 17), and this was driven by a total of 75 NF-xB gene targets (Figs. S4 and Dataset S9). To experimentally confirm that FKBP5 up-regulation promotes NF-xB signaling in immune cells, we performed dual-luciferase reporter assays comparing NF-xB activity between Jurkat cells over-expressing FKBP5 and cells transfected with control vector. FKBP5 overexpression led to increased NF-xB activity in response to immune stimulation (P = 5.5 x 10^{-3}; Fig. 3D). Together these findings support that FKBP5 up-regulation in immune cells promotes NF-xB-dependent peripheral inflammation accompanied by the release of proinflammatory cytokines, such as IL-8. Therefore, our subsequent analyses sought to better characterize the mechanisms through which FKBP5 impacts the NF-xB pathway.

Changes in FKBP5 Levels Are Associated with Extensive Alterations in the NF-xB Coexpression Network. To determine the network-level effects of FKBP5 deregulation on NF-xB signaling, we used the gene expression data in the GTP cohort (n = 355) to calculate the pairwise correlations between genes encoding molecules that directly interact within the NF-xB pathway, as defined in the KEGG Pathway Database. These pairwise correlations were adjusted for the expression levels of all other genes in the pathway and compared between subjects above vs. below the median split for FKBP5 expression levels. As shown diagrammatically in Dataset S10 and schematically in Fig. 3E, several partial pairwise correlations within the NF-xB pathway differed between the two groups, but the strongest and only significant effect after multiple test correction was noted for the MAP3K14-CHUK pair (r_{lower FKBP5} = 0.13 vs. r_{higher FKBP5} = -0.28; FDR-adjusted P = 1.1 x 10^{-2}, permutation P = 2.6 x 10^{-3}). This effect remained robust after controlling for sex, age, cortisol, and Houseman-corrected blood cell proportions (FDR-adjusted P = 1.3 x 10^{-4}, permutation P = 7.1 x 10^{-3}), indicating that the effects of FKBP5 on NF-xB signaling are not confounded by cortisol levels or blood cell composition.

FKBP5 Up-Regulation Promotes NF-xB Signaling by Strengthening the Interaction of Key Regulatory Kinases. Since FKBP5 is involved in scaffolding of regulatory protein complexes, it could enhance NF-xB signaling by influencing protein–protein interactions between regulators of the NF-xB pathway. Intriguingly, MAP3K14 and CHUK, the transcript pair most influenced by FKBP5 levels (Fig. 3E), respectively encode the NF-kappa-B-inducing kinase (NIK) and the antagonist of nuclear factor kappa-B kinase subunit alpha (IKKα), two key regulatory kinases of the alternative NF-xB pathway. NIK interacts with and phosphorylates IKKα at serine 176 (pIKKα; Fig. S8), thereby activating IKKα and facilitating NF-xB signaling (47, 48).

To examine whether FKBP5 modulates the NIK–IKKα protein complex, we performed a series of protein–protein binding experiments in human Jurkat cells and peripheral blood mononuclear cells (PBMC). These experiments showed binding of FKBP5 with both NIK and IKKα and binding between NIK and IKKα (Fig. 4A). We then examined whether glucocorticoid treatment and FKBP5 up-regulation can influence the FKBP5–NIK–IKKα complex. Both cell types were stimulated with DEX that robustly induces FKBP5 expression (28, 43). After confirming the DEX-induced up-regulation of FKBP5 (~2.2-fold), we found that DEX treatment significantly increased the binding between FKBP5, NIK, and IKKα in both Jurkat cells and PBMC; this increase was abolished by concomitant treatment with the selective FKBP5 antagonist SAFit1 (49) in both cell types (Fig. 4A and B). Accordingly, these effects on protein binding were accompanied by an increase in pIKKαS176, whereas pIKKαS176 induction was abolished by treatment with SAFit1 (Fig. 4C). This effect on pIKKαS176 was recapitulated by FKBP5 overexpression and again blocked by concomitant treatment with SAFit1 in Jurkat cells (Fig. 4D). Additionally, in this cell line deletion of the FKBP5 gene with CRISPR/Cas9 abolished the effect of DEX on pIKKαS176 levels but did not influence vehicle-treated cells (SI Appendix, Fig. S8), thus mimicking the effects of SAFit1. In line with these functional effects on the NIK–IKKα complex, FKBP5 overexpression nearly doubled NF-xB activity in Jurkat cells, whereas this effect was again prevented by concomitant treatment with SAFit1 (Fig. 4E). As schematically summarized in Fig. 4F, these convergent findings show that FKBP5 up-regulation strengthens NIK–IKKα binding, increases pIKKαS176, and in effect promotes NF-xB signaling.

NF-xB Signaling Promotes FKBP5 Expression via an NF-xB Response Element Containing the Age/Stress-Related CpGs. Notably, the above-identified age/stress-related FKBP5 CpGs flank an NF-xB response element (SI Appendix, Fig. S9), raising the possibility that NF-xB signaling could itself modulate FKBP5 expression in immune cells via this site. To address this possibility, we performed...
Fig. 3. FKBP5 up-regulation promotes NF-κB-driven peripheral inflammation. (A) FKBP5-related genes in peripheral blood show enrichment for inflammation-related genes and NF-κB gene targets. The number of genes for each analysis is shown in parentheses. Statistical details are provided in Datasets S5–S9. (B) Western blotting confirming FKBP5 overexpression in Jurkat T cells transfected with FKBP5-FLAG vs. cells transfected with the control vector. (C) FKBP5 overexpression nearly doubles IL-8 secretion by Jurkat T cells stimulated overnight with 25 ng/mL of phorbol-12-myristate-13-acetate and 375 ng/mL of ionomycin (PMA/I). The bar graph depicts IL-8 secretion in stimulated cell supernatants measured with ELISA from two independent experiments (t = 8.8, P = 4.4 x 10^{-7}, n = 8 per condition). For each experiment, fold ratios of IL-8 secretion were calculated relative to stimulated cells expressing the control vector. IL-8 was not detectable in nonstimulated cells. (D) FKBP5 overexpression increases NF-κB activity in stimulated Jurkat T cells. The bar graph depicts NF-κB reporter activity in stimulated cells measured with dual-luciferase reporter assays from three independent experiments (t = 3.2, P = 5.5 x 10^{-3}, n = 9 per condition). For each experiment, fold ratios of NF-κB activity were calculated relative to nonstimulated cells expressing the control vector. (E) FKBP5 expression changes are associated with extensive alterations in the NF-κB coexpression network in peripheral blood. The circles depict genes encoding molecular partners of the NF-κB pathway. Continuous lines (edges) represent positive and dotted lines negative pairwise correlations corrected for expression levels of all other genes in the pathway (details in SI Appendix, Supplementary Methods). Edge widths are proportional to the absolute value of the respective correlation coefficient. The gene pair with the most robust difference in correlation between the two groups (CHUK-MAP3K14) is highlighted in orange. Statistical details for all gene pairs are provided in Dataset S10. Error bars depict the SE around the group mean. **P < 10^{-2}; ***P < 10^{-3}.

dual-luciferase reporter gene assays using a CpG-free vector (50). We inserted into this vector the FKBP5 sequence that surrounds the NF-κB response element and includes the two CpG sites of interest but completely lacks any other CpGs (SI Appendix, Fig. S9). Immune stimulation induced expression of this reporter construct in monocyte-derived human cell lines (THP-1) (Fig. S4), thus supporting functionality of this response element in immune cells. Furthermore, in vitro DNA methylation of the age/stress-related FKBP5 CpGs within this reporter construct resulted in statistically significant reduction (~40%) of baseline expression levels and nearly abolished the induction seen with immune stimulation (Fig. S4). To further examine whether these functional effects are mediated by alterations in NF-κB binding, we used a biotinylated oligonucleotide-mediated chromatin immunoprecipitation (ChIP) method (51) (Fig. S5 and SI Appendix, Fig. S9). After confirming immune stimulation-driven NF-κB binding in THP-1 cells to the enhancer, in vitro DNA methylation essentially abolished NF-κB binding to the age/stress-related enhancer site (Fig. 5 C and D). Together, these findings demonstrate that NF-κB signaling—which, as we showed above, is promoted by FKBP5 (Figs. 3 and 4)—can in turn trigger FKBP5 expression in immune cells, thereby forming a positive feedback loop that can potentiate FKBP5–NF-κB signaling.
This positive feedback can thus be accentuated by decreased methylation of the NF-κB-responsive FKBP5 enhancer, which can occur as a consequence of aging and stress.

**Age/Stress-Related Decrease in FKBP5 Methylation Is Associated with a History of Acute MI.** Proinflammatory states confer risk for cardiovascular disease, most notably acute cardiovascular syndromes (52). Thus, the convergent findings presented above, indicating that lower methylation of the age/stress-related FKBP5 CpGs up-regulates FKBP5, which in effect promotes peripheral inflammation, prompted us to examine whether this lower methylation signature is also associated with higher risk for acute coronary events. To address this possibility, we used data on self-reported history of MI that were available in both the KORA (1,648 subjects without vs. 62 subjects with history of MI) and the MPIP (310 controls vs. 8 cases) cohorts. Given the small number of subjects with MI as compared without MI in our cohorts, we used a statistical approach that resolves case–control imbalances by calculating and controlling for propensity scores for the MI assignment (53). After adjustment for all covariates (SI Appendix, Supplementary Methods), methylation of the age-related sites was significantly lower in individuals with history of MI in both cohorts (KORA: \( \beta = -0.0535, P = 7.9 \times 10^{-3} \); MPIP: \( \beta = -0.1992, P = 1.2 \times 10^{-3} \); Fig. 6A). This association remained significant after further controlling for education in both the KORA (\( P = 4.7 \times 10^{-3} \)) and MPIP (\( P = 2.6 \times 10^{-7} \)).

**Discussion**

Aging and stress-related phenotypes are associated with heightened inflammation and cardiovascular risk (5, 8–11), but the underlying molecular mechanisms remain elusive. Here we uncover a role for FKBP5 in these relations. As schematically summarized in Fig. 6B, our findings suggest that aging and stress synergistically decrease DNA methylation at selected regulatory FKBP5 CpGs that moderate the efficiency of an NF-κB–responsive enhancer. Reduced methylation at this site enhances...
FKBP5 responses in immune cells, an effect that promotes NF-κB-driven peripheral inflammation, in part through protein–protein interactions between FKBP5 and key regulatory kinases of the NF-κB pathway. NF-κB binding to the FKBP5 enhancer can in turn stimulate FKBP5 expression, thereby forming a positive feedback loop of FKBP5–NF-κB signaling that potentially contributes to proinflammatory states and heightened cardiovascular risk. Finally, we find that both CRISPR/Cas9 deletion of FKBP5 and treatment with a selective FKBP5 antagonist can prevent the cellular effects of stress and FKBP5 up-regulation on NF-κB signaling.

By interrogating all 450K-covered FKBP5 CpGs for age-related changes in DNA methylation, a biological process thought to contribute to disease states (25), we identified two closely juxtaposed sites at which CpG methylation decreases through an interplay of aging, early life stress, and depressive symptoms. These findings were replicated in both individuals of European descent and African Americans collectively from seven independent human cohorts (total n > 3,000) with whole-blood DNA methylation data. Further analyses in purified blood cells showed that age-related decrease in FKBP5 methylation occurs in CD4 T cells but not in neutrophils, suggesting that aging may affect FKBP5 methylation differentially across immune cell types. Notably, depressive phenotypes had consistent effects on FKBP5 methylation in all analyses, whereas the impact of early life stress differed across cohorts, directly influencing methylation in the HBCS but only moderating the epigenetic effects of depression in the GTP. This difference may reflect the more homogeneous stressor as well as the older and narrower age composition in the HBCS. Despite this difference, the impact of both early life stress and depression consistently occurred in the same direction, decreasing FKBP5 methylation in older ages. Together with previous work (22–24, 26–29), these findings suggest that the epigenetic influence of environmental

Fig. 5. NF-κB signaling drives FKBP5 expression via a response element gated by the age/stress-related CpGs. (A) Data from dual-luciferase reporter gene assays using a CpG-free luciferase reporter construct, which includes the FKBP5 sequence surrounding the NF-κB response element and the age/stress-related CpGs (insert sequence shown in SI Appendix, Fig. S9) but completely lacks other CpGs. This reporter construct was in vitro-methylated and transfected into monocye-derived human cell lines (THP-1). Cells were then stimulated overnight with 25 ng/mL phorbol-12-myristate-13-acetate and 375 ng/mL ionomycin (PMA/I), a combination that robustly induces NF-κB signaling. Data are derived from two independent experiments (n = 12 replicates per condition). Comparison was performed using two-way ANOVA with methylation and treatment as factors (F4,44 = 59.5, interaction P < 10−3), and statistically significant effects were followed with Bonferroni-corrected pairwise comparisons. (B–D) The effect of in vitro DNA methylation on PMA/I-induced NF-κB binding to the NF-κB response element was examined using biotinylated oligonucleotide-mediated ChIP in THP-1 cells (oligonucleotide sequence shown in SI Appendix, Fig. S9). Schematic summary of the experimental setup is shown in B. After ChIP, NF-κB/p65 binding was quantified by Western blotting using antibodies specific for NF-κB (C: example blots; D: quantifications). CTRL (control) 1: magnetic beads lacking conjugated streptavidin; CTRL 2: cells transfected with nonbiotinylated oligonucleotide. Bar graph shows data derived from four independent experiments (n = 2.5, P = 4.4 × 10−2, n = 4 per condition). Statistical t test compared cells carrying the unmethylated probe treated overnight with vehicle or PMA/I. Binding was not quantifiable for cells carrying the methylated probe. Data are always shown as fold changes compared with the vehicle-unmethylated cells. Error bars depict the SE around the mean with P values for pairwise comparison as shown are follows: ***P < 10−4, statistically significant pairwise comparisons for methylated vs. unmethylated. *P < 5 × 10−2, **P < 10−2, statistically significant pairwise comparisons for vehicle vs. drug treatment.

Fig. 6. Association of age/stress-related FKBP5 decrease in DNA methylation with a history of MI and overall scheme summarizing study findings. (A) Age/stress-related decrease in FKBP5 methylation is associated with a history of MI in two independent cohorts: KORA, n = 1,648 subjects without vs. 62 with history of MI, β = −0.0535, SE = 0.0201, P = 7.9 × 10−4, mean DNA methylation difference = 1.8% and MPB, n = 310 subjects without vs. 8 with history of MI, β = −0.1992, SE = 0.0611, P = 1.2 × 10−3, mean DNA methylation difference = 5.3%. The y axis depicts average DNA methylation levels of the two age/stress-related FKBP5 CpGs (cg20813374 and cg00130530), after adjusting for all covariates (SI Appendix, Supplementary Methods). Error bars depict the SE around the mean. (B) Schematic summary of study’s findings showing how aging, childhood trauma, and depressive symptoms interact to decrease FKBP5 methylation at selected CpGs (cg00130530 and cg20813374) located proximally upstream of the TSS. These epigenetic changes enhance FKBP5 responses in immune cells, an effect that in turn promotes NF-κB signaling, whereas this is prevented when cells are concomitantly treated with selective FKBP5 antagonists. Notably, NF-κB signaling is not only activated by FKBP5 but it can also trigger FKBP5 transcription through an NF-κB response element that is flanked and moderated by the age/stress-related CpGs. This forms a positive feedback loop of FKBP5-NF-κB signaling that may be enhanced in individuals with lower methylation at this site. Enhanced FKBP5 responses and NF-κB activity may in turn promote chemotaxis of proinflammatory cells and peripheral inflammation, potentially contributing to cardiovascular risk.
exposures and life stress may become more evident as life advances. Using an in vitro model of replicative senescence, we further show that replicative aging and stress hormone (glucocorticoid) exposure additively decrease methylation at the same age/stress-related CpGs. Although cellular senescence and glucocorticoid exposure in a dish have limitations as models of in vivo processes, our convergent findings in humans and cells suggest that aging and stress synergistically influence selected FKBP5 CpGs across different cohorts, distinct cell types, and contexts.

Epigenetic effects involving FKBP5 have been previously reported to occur in intronic glucocorticoid response elements, possibly as a result of glucocorticoid receptor binding to the DNA (26, 28, 54); here we identified lower methylation levels at two CpGs that include a functional NF-xB response element site and colocalize with a poised enhancer within 500 bp upstream of the FKBP5 TSS in most immune cells, including CD4 T cells, the cell type that shows age-related decrease in FKBP5 methylation. This functional annotation and our human cohort and in vitro data together suggest a model whereby age/stress-related decrease in FKBP5 methylation can enhance transcription factor binding and consequent FKBP5 responses in distinct immune cell types. The cross-sectional nature of our cohort data precludes firm conclusions about causal directions, but we speculate that decreased methylation at the age/stress-related FKBP5 sites may additively result from the combined effects of cellular aging, repeated activation of the enhancer, and stress-induced FKBP5 transcription along the human lifespan. Although the overall effect size of these DNA methylation changes is modest, small effect sizes in a complex tissue, such as whole blood, likely reflect the mean of variable effects across distinct cell types. This is suggested by the larger age-related decrease in FKBP5 methylation in T cells than neutrophils in the FACS-sorted dataset (SI Appendix, Fig. S3). Another limitation of the 480K array is its sparse coverage of CpGs present in the human genome. Future studies may uncover additional FKBP5 sites of interest by employing methods that allow more comprehensive coverage, such as targeted bisulfite sequencing (55).

Through a combination of unbiased network analyses in human cohorts and mechanistic investigations in immune cells, we characterized a multilevel positive regulatory feedback between the stress-responsive cochaperone FKBP5 and the NF-xB signaling cascade. More specifically, FKBP5 was found to exert pronounced effects on NF-xB–related gene networks and to promote NF-xB signaling by strengthening the interactions between NIK and IKKα, two key regulatory kinases of the NF-xB pathway. These findings are congruent with previous observations that FKBP5 down-regulation can inhibit NF-xB signaling (13, 15, 17–19) and show that FKBP5 interacts with NIK and mediates the glucocorticoid-driven modulation of the NIK–IKKα regulatory complex in immune cells. Intriguingly, NF-xB can in turn trigger FKBP5 transcription through an NF-xB response element that is flanked and moderated by the age/stress-related CpGs, thereby forming a positive feedback loop that can potentiate FKBP5–NF-xB signaling, especially in individuals with lower methylation at these FKBP5 CpGs. Both CRISPR/Cas9 deletion of the FKBP5 gene and treatment with the selective FKBP5 antagonist SAF11 prevent the cellular effects of stress, as modeled in vitro by stress hormone treatment, and FKBP5 overexpression on NF-xB signaling. In contrast, as shown both here and in a previous study (49), SAF11 does not influence immune function under baseline conditions, suggesting that FKBP5 antagonism may represent a pharmacological intervention that—if targeted at individuals with up-regulated FKBP5—could prevent some of the unwarranted age/stress-related alterations in immune function. However, the potential in vivo relevance of the pharmaceutical modulation of FKBP5–NF-xB signaling will need to be tested in future studies.

We also find convergent evidence that FKBP5 promotes inflammation, a biological process tightly linked with NF-xB signaling. This effect may in part result from the enhanced chemotaxis and recruitment of proinflammatory cells, a possibility supported by the positive association of FKBP5 mRNA levels with the granulocyte-to-lymphocyte ratio and the ability of FKBP5 to augment immune cell secretion of the major chemokine, and NF-xB target, IL-8 by Jurkat cells, which is a T cell line. The latter finding extends a previous study showing that FKBP5 down-regulation suppresses NF-xB–mediated production of IL-8 in melanoma cells (19). Both IL-8 levels and the granulocyte-to-lymphocyte ratio are inflammatory markers associated with heightened cardiovascular risk and mortality (45, 56, 57). Together these findings suggest that older individuals with higher stress burden, who show exaggerated FKBP5 responses, are also more prone to developing heightened inflammation and acute cardiovascular risk upon stress exposure. This hypothesis is supported by our observation, in two independent cohorts, that history of MI is associated with decreased methylation at the age/stress-related FKBP5 CpGs. FKBP5 up-regulation could thus represent one molecular link for the known association of depression and early life adversity with heightened inflammation and cardiovascular risk (3, 4, 6, 58, 59). Nevertheless, the association of MI with decreased FKBP5 methylation should be interpreted with caution until further validation in larger, independent studies with more balanced case–control assignment. Furthermore, mechanistic dissection of the potential role of FKBP5 in cardiovascular risk will require longitudinal studies examining the convergent effects of stress and aging in purified immune cell types.

In conclusion, our findings suggest that aging and stress decrease DNA methylation at selected enhancer-related FKBP5 sites, contributing to epigenetic up-regulation of FKBP5 in immune cells, increased NF-xB–driven peripheral inflammation, and heightened cardiovascular risk. While disease risk is undoubtedly shaped by multiple molecular effectors and mechanisms, the present study offers insights by uncovering a mechanism through which aging and stress confer disease risk at the molecular level. Such molecular insights may help identify biomarkers and novel treatment candidates for stress-related disease and will require orchestrated translational research efforts. Despite these intriguing possibilities, social policies should always strive to ameliorate or, when possible, prevent excessive psychosocial stress in the first place.

Materials and Methods

Given space constraints in the main text, selected methods are provided here and further details can be found in SI Appendix, Supplementary Methods. The effects of aging and stress-related phenotypes on FKBP5 DNA methylation were examined in the GTP, KORA, MIPF, and HBCS cohorts (60, 61). CpG methylation across the FKBP5 locus was measured with the Infinium HumanMethylation450 BeadChip, and identified CpGs were further validated with targeted bisulfite sequencing. CpG annotation was performed with the UCSC Genome Browser and the Roadmap Epigenome Browser. Genome-wide gene expression data were measured in the GTP using the HumanMRT-112 v4 and v4 Expression BeadChips (62). Enrichment analysis for disease-associated genes and for gene targets of transcription factors was performed using WebGestalt. For NF-xB coexpression network analyses, pathway data were derived from the KEGG Pathway Database, and gene pair correlation coefficients were adjusted using the R package GeneNet. Cell culture experiments were performed in PBMC from healthy donors, as well as Jurkat, THP-1, or IMR-90 cell lines. FKBP5 knockout Jurkat cells were generated using CRISPR/Cas9 plasmids containing gRNA that targets human FKBP5 and a GFP reporter. The functional effect of DNA methylation at the age/stress-related FKBP5 site was analyzed with dual-luciferase assays using a Cpg-free luciferase reporter construct (50). Statistical analyses were performed with Sigma Plot version 13.0 (for experimental data) or R version 3.1.0 (for all other data).
ACKNOWLEDGMENTS. This work was supported by a Marie-Sklodowska Curie fellowship (Grant 653240) to A.S.Z., a grant from the National Institute of Mental Health (MH071538) to K.J.R., a European Research Council starting grant within the FP7 Framework to E.B.B. (Grant 281383, GxE molmec), a grant from the National Institute of Mental Health (U19 MH096956), a grant by the German Federal Ministry of Education and Research (BMBF) through the Integrated Network IntergrAment (Inter-genetic understanding of Causes and Mechanisms in Mental Disorders) under the auspices of the eMed Programme (Grant 01ZX13143) to E.B.B., and by the Academy of Finland (Grants 284859, 2848591, and 312670). Part of this work has been included and presented in the PhD dissertation of A.S.Z. (2013).

18. S. Romano et al., FKBP51 employs both scaffold and isomerase functions to promote NF-κB activation in melanoma. Nucleic Acids Res. 43, 6983–6993 (2015).