HUMAN GENETICS

Heritability of intrinsic human life span is about 50% when confounding factors are addressed

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How heritable is human life span? If genetic heritability is high, longevity genes can reveal aging mechanisms and inform medicine and public health. However, current estimates of heritability are low—twin studies show heritability of only 20 to 25%, and recent large pedigree studies suggest it is as low as 6%. Here we show that these estimates are confounded by extrinsic mortality—deaths caused by extrinsic factors such as accidents or infections. We use mathematical modeling and analyses of twin cohorts raised together and apart to correct for this factor, revealing that heritability of human life span due to intrinsic mortality is above 50%. Such high heritability is similar to that of most other complex human traits and to life-span heritability in other species.

Understanding the heritability of human life span is fundamental to aging research. However, quantifying the genetic contribution to human life span remains challenging. Although specific life span–related alleles have been identified (*1*–*5*), environmental factors appear to exert a strong effect on life span (*6*). Clarifying the heritability of life span could direct research efforts on the genetic determinants of life span and their mechanisms of action.

Previous studies have estimated the heritability of life span in various populations with results ranging from 15 to 33% (*7*–*14*), with a typical range of 20 to 25%. Recently, studies on large pedigree datasets estimated it at 6 to 16% (*15*, *16*). These studies contributed to growing skepticism about the role of genetics in aging, casting doubt on the feasibility of identifying genetic determinants of longevity.

Current estimates for the heritability of human life span are thus lower than the heritability of life span in crossbred wild mice in laboratory conditions, estimated at 38 to 55% (*17*). They are also lower than the heritability of most other human physiological traits, which show a mean heritability of 49% (SD = 12%) (*18*). This discrepancy motivated us to explore possible biases and confounding factors that could underestimate heritability of human life span across studies.

Most life-span studies used cohorts born in the 18th and 19th centuries, with appreciable rates of extrinsic mortality (*19*). Extrinsic mortality refers to deaths caused by factors originating outside the body, such as accidents, homicides, infectious diseases, and environmental hazards (*20*, *21*). By contrast, intrinsic mortality stems from processes originating within the body, including genetic mutations, age-related diseases, and the decline of physiological function with age (*20*, *21*). Because current extrinsic mortality is nearly an order of magnitude lower than in historical cohorts, and cause-of-death data for historic twin cohorts are unavailable, inferring the heritability of life span due to intrinsic mortality (mortality from nonextrinsic causes) is of interest.

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Another factor that varies between studies is the minimum age at which individuals must be alive to be included, referred to as the cutoff age. To our knowledge, these two factors—extrinsic mortality and cutoff age—have not been systematically investigated for their effect on heritability estimates of life span.

Here, we explored the effects of extrinsic mortality and cutoff age on twin study estimates of heritability. We used model-independent mathematical analysis and simulations of two human mortality models to partition mortality into intrinsic and extrinsic components. We tested our conclusions on data from three different twin studies, including the SATSA (Swedish Adoption/Twin Study of Aging) study (*22*), containing data from twins raised apart that have not been previously analyzed for life-span heritability. To test generalizability to non-Scandinavian cohorts, we also analyzed siblings of US centenarians (*23*). We found that extrinsic mortality causes systematic underestimates of the heritability of life span and that cutoff age has a mild nonlinear effect on these estimates. When extrinsic mortality is accounted for, estimates of heritability of life span due to intrinsic mortality rise to about 55%, more than doubling previous estimates.

Results

Extrinsic mortality masks heritability

We mathematically investigated how extrinsic mortality influences heritability estimates derived from twin studies. Extrinsic mortality produces a plateau in mortality roughly from ages 20 to 40 and then rises exponentially at old ages with a slope shallower than that of intrinsic mortality (Fig. 1A and fig. S1, A and B). Crucially, extrinsic mortality declined sharply during the 19th and early 20th centuries (Fig. 1, A and B).

We found that an exponentially rising extrinsic mortality yields nearly identical results to treating extrinsic mortality as an age-independent constant m_{ex} for each cohort (see supplementary text). For the mathematical analysis, we therefore consider mortality as a sum of constant extrinsic mortality and an age-dependent intrinsic mortality: $m(t) = m_{ex} + f(t,\vec{\theta})$, where $\vec{\theta}$ are parameters that can vary genetically. For example, the Gompertz-Makeham model is included in this definition with an exponentially rising intrinsic mortality $f(t,\vec{\theta}) = ae^{bt}$, where the parameters are the Gompertz intercept and slope, $\vec{\theta} = (a,b)$. Our analysis does not assume a specific form for $h(t,\vec{\theta})$, and later we simulate two different models to validate the conclusions.

We begin with an intuitive demonstration. Consider a twin study composed of three genetic groups—A, B, and C—each characterized by distinct life-span parameters. Each monozygotic (MZ) twin pair shares identical genes and thus belongs to the same genetic group. Plotting the life span of one twin against the other yields a distribution of life spans within each group that is symmetric about the diagonal (Fig. 1C).

Heritability is computed from the correlations between the life spans of twins. The correlation between MZ twins can be expressed as $r_{MZ} = \mathrm{Var}(\mu)/(\mathrm{Var}(\mu) + \langle\sigma^2\rangle)$, where $\mathrm{Var}(\mu)$ is the variance of the means of groups, and $\langle\sigma^2\rangle$ is the average within-group variance (derivation in supplementary text). Correlation increases when groups are more distinct [larger $\mathrm{Var}(\mu)$] and tightly distributed [lower $\langle\sigma^2\rangle$]. Extrinsic mortality reduces $\mathrm{Var}(\mu)$ and, in the ranges observed in historical cohorts, raises $\langle\sigma^2\rangle$ by increasing tails where one twin dies early (Fig. 1D). Both effects of extrinsic mortality reduce the life-span correlations and heritability estimates.

The use of three groups is only for demonstration; in the supplementary text, we extended the analysis to an arbitrary number of groups. Simulations using Gompertz-Makeham distributions (each with its own slope parameter) showed similar effects when extrinsic mortality is added (Fig. 1, E and F). The conclusion also holds when analyzing dizygotic (DZ) twins (supplementary text).

We also tested a complementary case in which extrinsic mortality is held fixed while intrinsic mortality is reduced. This revealed a symmetric effect whereby either higher extrinsic mortality or lower intrinsic mortality reduces heritability (supplementary text and fig. S2).

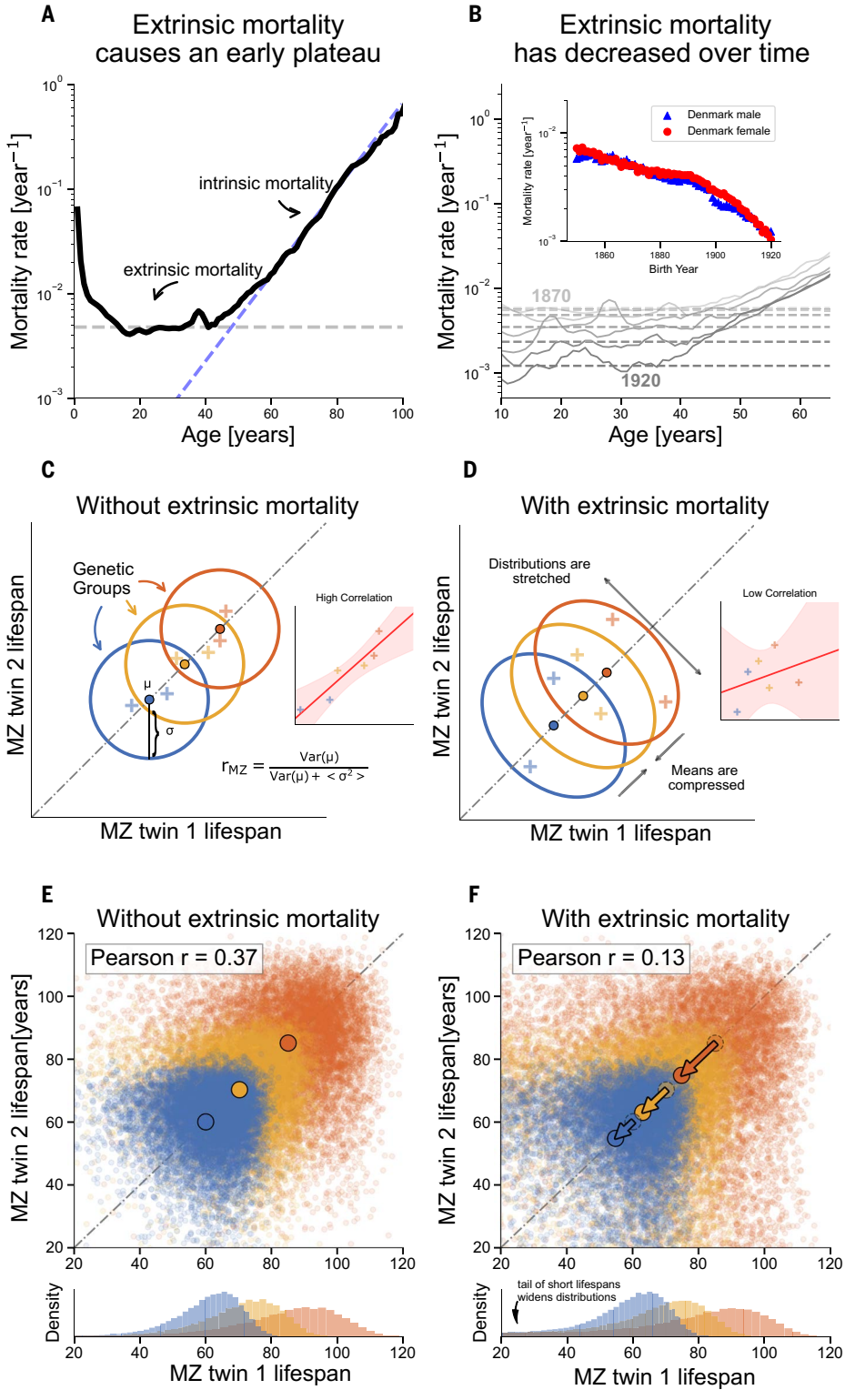

Fig. 1. Extrinsic mortality masks life-span correlations in twin cohorts. (**A**) Human mortality rates after age 15 show an early plateau driven by extrinsic mortality such as accidents or infections, followed by an exponential increase described by the Gompertz law, reflecting intrinsic, biologically driven aging. Data shown for Danish females born in 1880. (**B**) Historical mortality curves show a decline in extrinsic mortality over time (compare dashed lines). Inset shows estimated extrinsic mortality (m_{ex}) by birth year for Danish males and females. (**C**) Schematic: Life-span correlations between monozygotic (MZ) twins drawn from three hypothetical genetic groups with distinct means (μ) and low within-group variance (σ^2). High between-group variance leads to strong correlations (r_{MZ}) across twin pairs (inset). Colored dots show group means; crosses indicate sample twin-pair life spans. (**D**) Adding extrinsic mortality to (C) substantially reduces the observed correlations (inset) because it reduces between-group variance [Var(μ)] and increases within-group variation [$\langle\sigma^2\rangle$]. (**E**) Simulations of MZ twins from three genetic groups with distinct Gompertz slopes reproduce this effect. With no extrinsic mortality, correlation is high ($r = 0.37$). (**F**) Same as (E); with extrinsic mortality on the scale of historical levels ($m_{ex} = 0.003$ year^{-1}), correlation drops ($r = 0.13$). Colored dots show shifted group means; bottom: marginal life-span distributions. Gompertz simulation parameters $a = 5 \times 10^{-5}$ year^{-1}, $b = 0.08, 0.1, 0.12$ year^{-1}.

We conclude that extrinsic mortality lowers life-span correlations in twin studies, leading to an underestimation of the intrinsic genetic heritability of life span.

Correcting for extrinsic mortality raises estimates of heritability of twin life span to about 50%

Because historical cohort data lack sufficient cause-of-death information to correct for extrinsic mortality, we developed an approach to isolate the effects of extrinsic mortality and estimate the heritability of intrinsic life span. This required generating genetically distinct groups with their own life-span distributions.

We used two models to simulate life-span distributions: (i) the Makeham-Gamma-Gompertz (MGG) model, a flexible empirical fit to mortality data (*24*), and (ii) the saturating-removal (SR) model (*25*), a biologically motivated mechanistic model in which aging emerges from the interplay between rising damage production and a removal process that saturates at high damage (materials and methods). Both models contain several parameters, including an extrinsic mortality rate, m_{ex}. The two models provide similar results, and thus we present the SR model results in the main text and the MGG results in the supplementary text.

We analyzed males and females separately and found no significant difference in the estimated heritability of intrinsic life span, so we pooled them in all results. This agrees with previous studies (*8*, *9*).

We fitted each model to mortality curves of cohorts relevant to the twin studies from the Human Mortality Database, achieving excellent fits (coefficient of determination $R^2 > 0.977$, fig. S3; parameters in table S1). To incorporate genetic variation, we varied model parameters between individuals according to normal distributions, consistent with additive polygenic traits (*26*).

MZ twins, who share identical genomes, were simulated by giving both members of a pair identical parameter values. Parameter distribution widths were then calibrated to match the observed life-span correlations in each twin study (materials and methods). We then systematically decreased m_{ex} and recomputed life-span correlations, keeping all other parameters fixed. As extrinsic mortality was reduced, correlations increased, eventually plateauing at an asymptotic value around 50% when $m_{ex} = 0$—roughly double the correlation observed in historical twin studies (fig. S4).

This effect is illustrated in Fig. 2, A and B, calibrated to Danish cohorts born between 1870 and 1900. Simulated extrinsic deaths are shown in red; removing these deaths leads to more tightly correlated twin life spans (Fig. 2B).

To estimate heritability, we extended the analysis to DZ twins, who share on average 50% of their segregating genes. For each pair, the first twin's parameter value was drawn from the distribution calibrated to MZ twins, and the second was assigned a correlated parameter value ($\rho = 0.5$) (materials and methods). This approach captured the empirical DZ correlations (fig. S4).

Heritability was then computed using Falconer's formula (*26*), $h^2 = 2(r_{MZ} - r_{DZ})$, which compares identical and nonidentical twins to isolate genetic effects. By reducing m_{ex}, we estimated the heritability attributable to intrinsic mortality, revealing that historical extrinsic mortality in Danish and Swedish cohorts masked genetic contributions to life span. As m_{ex} decreased, heritability rose and plateaued near ~50% as $m_{ex} \to 0$ (Fig. 2, C and D).

In addition, we assessed robustness to the choice of which parameter varies between individuals. In the main analysis, we varied the threshold parameter X_c in the SR model. We found that variations in most other model parameters can also replicate observed MZ twin correlations (fig. S5). By contrast, variation in extrinsic mortality alone cannot replicate observed MZ correlations, highlighting that genetic variation in intrinsic mortality is required.

This analysis assumed that extrinsic mortality is an age-independent constant m_{ex}. We also tested a model in which extrinsic mortality is the sum of a constant and an exponentially rising term with age, as found in modern US period mortality (*20*, *21*). The US data indicate that the exponential slope of extrinsic mortality is 80% of the slope of intrinsic mortality (fig. S1, A and B). The age-related rise of extrinsic mortality likely reflects growing frailty, such that stressors like infections and falls become increasingly fatal to older individuals.

For each individual, we modeled extrinsic mortality as a sum of a constant m_{ex} equal in all individuals and an exponential rise with a slope of 0.8 of that individual's intrinsic mortality (Gompertz) slope. This yielded heritability estimates identical to within 1% to the constant-extrinsic-mortality model (supplementary text and fig. S1C).

We found that a statistical, model-free framework that partitions deaths into intrinsic and extrinsic components according to their proportions in the general population provides even higher heritability estimates of >70% for Danish twins (supplementary text and fig. S6). Such a framework does not include the existence of distinct genetic groups for intrinsic mortality and is thus less accurate. The present model-based analysis is thus a conservative estimate.

We conclude that adjusting for extrinsic mortality raises the estimated heritability of life span to about 0.5—roughly twice that reported in twin studies.

The SATSA study of twins validates higher estimated heritability at lower extrinsic mortality

To test the prediction that lower extrinsic mortality increases estimated life-span heritability, we analyzed the SATSA twin cohort (*22*), restricting our analysis to twins born between 1900 and 1935, where both twins survived to age 61 (see materials and methods for rationale behind inclusion criteria). Life-span heritability has not been previously assessed in this dataset, which includes both twins raised together and apart.

We estimated uncorrected heritability (uncorrected for extrinsic mortality) (materials and methods) in three independent ways: (i) MZ twins reared apart ($n = 150$), (ii) DZ twins reared apart ($n = 371$), and (iii) MZ versus DZ twins reared together (196 MZ, 325 DZ). All three estimates agreed within one SE (fig. S7), supporting an additive genetic model of life span, with a combined variance-weighted estimate of 0.33 ± 0.06.

To obtain cohorts with different extrinsic mortality, we stratified the dataset into three birth cohorts (1900–1910, 1910–1920, 1920–1935). Extrinsic mortality dropped by a factor of 3 over this period (Fig. 3A). Uncorrected heritability rose by a factor of about 2, consistent with the declining extrinsic mortality (Fig. 3B). We conclude that lower extrinsic mortality raises heritability estimates of human life span.

Unlike previous twin datasets, SATSA includes cause-of-death records for cancer, cardiovascular disease (CVD), and dementia. We used this to explore whether heritability varies by cause of death (supplementary text). Using a probit liability-threshold framework, we estimated heritability to die from a given cause by ages 80, 90, and 100, conditional on survival to age 61.

Heritability of cancer death was age independent at about 0.3. CVD deaths showed higher heritability of about 0.5 at earlier ages and declined toward negligible values by age 100. Dementia deaths showed the highest heritability (≈0.7) by age 80 and stabilized around 0.4 to 0.5 by later ages (fig. S8). These results suggest that genetic contributions to life span vary by cause and age, with cancer showing a steady moderate heritability, whereas deaths from CVD and dementia are more strongly heritable by age 80 but their heritability declines at older ages.

Cutoff age has a mild nonlinear effect on heritability

Different twin studies use different minimum ages of inclusion, known as the cutoff age. We therefore examined how cutoff age influences heritability estimates under varying levels of extrinsic mortality. We found that the effect of cutoff age depends in a nonlinear way on

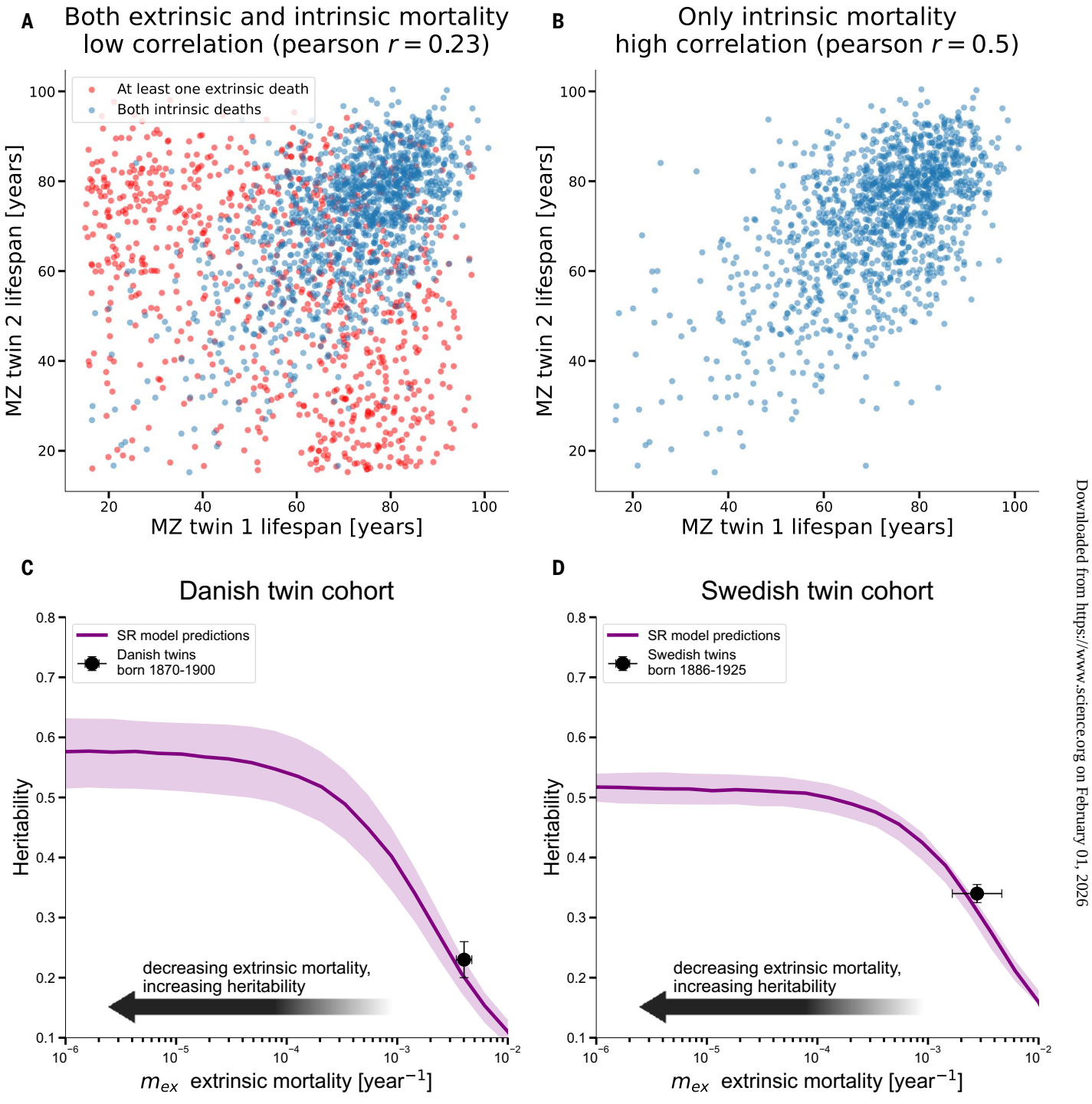

Fig. 2. Life-span heritability increases when accounting for extrinsic mortality. (**A**) Simulation of $n = 5000$ MZ twin pairs from the Danish twin cohort using the SR model. Twin pairs with at least one extrinsic death are in red. Life-span correlation is about 0.23. (**B**) Same as (A) but without extrinsic deaths. Removing extrinsic deaths increases correlation to 0.5. (**C**) Heritability estimate $2(r_{MZ} - r_{DZ})$ as a function of extrinsic mortality (m_{ex}) for the Danish twin cohort born between 1870 and 1900 (*8*). (**D**) Same as (C) for Swedish twins born between 1886 and 1923 (*9*). Model parameter fits are given in table S1.

extrinsic mortality. When extrinsic mortality is high, raising cutoff age increases heritability estimates by excluding early deaths that are mostly extrinsic. Conversely, at low extrinsic mortality, raising cutoff age lowers heritability estimates, by excluding information from intrinsic early deaths. The transition between these two regimes occurs near $m_{ex} = 0.001$ year^{-1} (Fig. 3C and fig. S9). In fig. S10, we plot the heritability of life span as a function of cutoff age at $m_{ex} = 0$.

We conclude that in modern cohorts with extrinsic mortality below 0.001 year^{-1}, lower cutoff ages are preferable, as they retain early deaths that are informative about genetic contributions to life span.

Siblings of US centenarians give similar heritability estimates

To test whether our findings extend beyond Scandinavian twins, we analyzed US siblings of centenarians born between 1873 and 1910 (mean

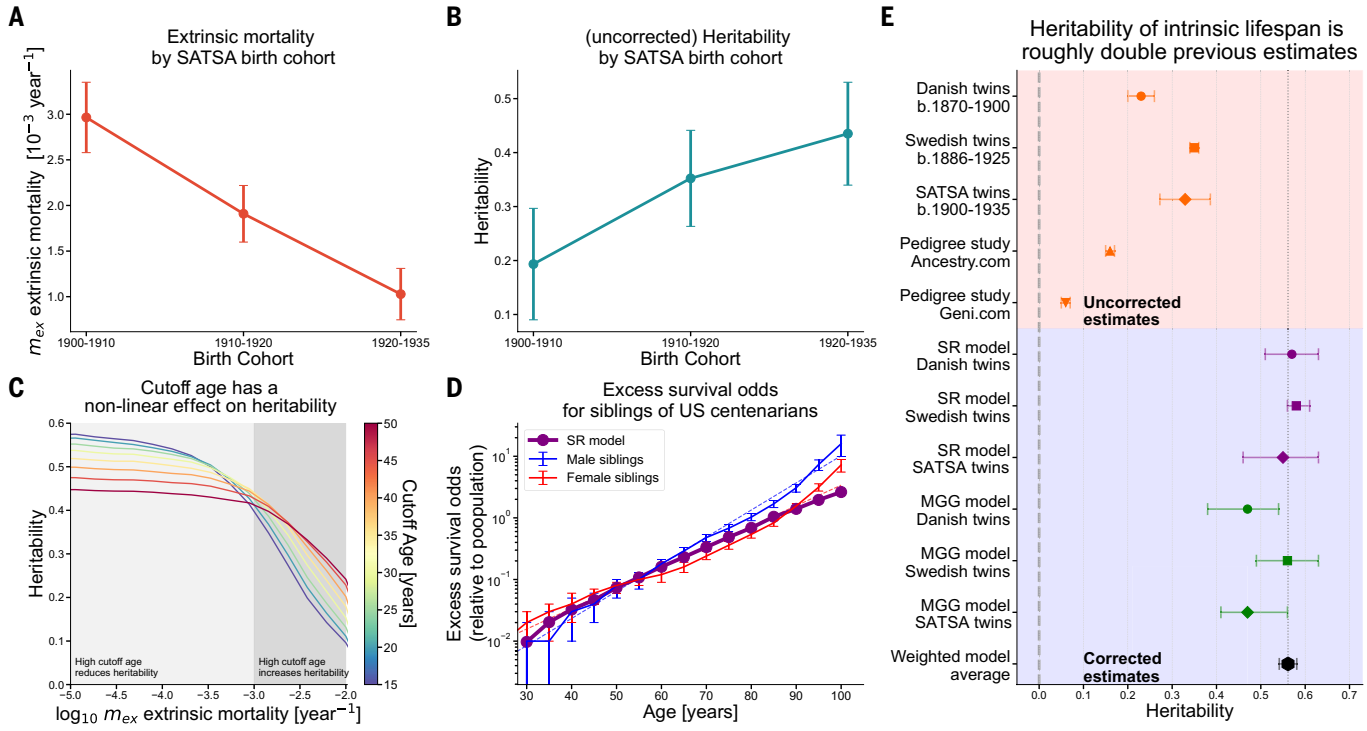

Fig. 3. Heritability of intrinsic life span: Data and model comparisons. (**A**) Extrinsic mortality m_{ex} by birth cohort from SATSA (*22*). (**B**) Weighted heritability estimates from SATSA twin pairs reared together and apart (uncorrected for extrinsic mortality) show an increase across birth cohorts as extrinsic mortality declines. (**C**) Heritability as a function of extrinsic mortality (*x* axis, logarithmic scale) and cutoff age (color scale). High cutoff ages increase heritability at high extrinsic mortality (dark gray) but reduce heritability when extrinsic mortality is low (light gray). Results are from the SR model calibrated to Danish cohort parameters. (**D**) Excess survival odds for siblings of US centenarians [data from (*23*)], with males (blue) and females (red). Dotted lines show exponential fits. SR model predictions (purple), calibrated to US cohorts, are shown for comparison. (**E**) Heritability estimates from Danish twins (*8*), Swedish twins (*9*), SATSA study (*22*), and two pedigree studies (*15*,*16*) compared to corrected estimates of heritability of intrinsic life span from SR (purple) and MGG (green) models at $m_{ex} = 0$ and cutoff age = 15. Error bars denote SE. Model parameters in table S1.

1898) (*23*). Siblings share roughly half their genomes and thus are modeled in the same way as DZ twins. Life-span correlations in this dataset were unavailable; instead, the study reported excess survival odds—the excess odds of reaching age T given a centenarian sibling, relative to the general population (materials and methods).

To model this sibling dataset, we calibrated our model parameters to US 1900 mortality data. We found that a distribution width of 23% for X_c provides a good fit to the excess survival ratios (Fig. 3D and fig. S11, C and D; parameters in table S1), similar to the distribution width inferred in the twin studies. Excess survival odds to reach age T rises exponentially with a slope similar to the Gompertz slope. At very old ages (>90), the US sibling data show higher odds than predicted, for reasons that remain unclear. We used the calibrated model to calculate life-span heritability at $m_{ex} = 0$, again obtaining ~50% (Table 1).

To test the robustness of this approach, we analyzed the excess survival odds in the same Danish twin cohort used for the life-span correlation analysis (*8*). We found an exponential rise similar to the US siblings, which is well fit by our model using the same parameters that describe the twin life-span correlations (fig S11, A and B). We conclude that 50% heritability of life span is not specific to Scandinavian twin cohorts, as similar estimates are obtained from US centenarian sibling data.

Definition of intrinsic heritability of life span and its estimated value (~55%)

Our approach allows adjustment of both extrinsic mortality and cutoff age, enabling a standardized estimation of the genetic contribution to life span. We propose defining the heritability of intrinsic life span (HIL) as the heritability estimate obtained under zero extrinsic mortality and a cutoff age of 15, the typical age at which all-cause mortality is minimal. Thus, HIL estimates the genetic contribution to life span due to intrinsic biological deterioration, conditional on reaching sexual maturity.

Using this definition, we found that predicted HIL is consistent across the three twin datasets, the centenarian sibling dataset, and the two modeling frameworks (SR and MGG), yielding an estimate of HIL = 0.55 ± 0.01 (SE) (Fig. 3E and Table 1).

We also tested whether compression of mortality affects the HIL. Over the past century, survival curves have generally become more rectangular, reflecting greater life span equality as life expectancy rose (*27*, *28*). To model this compression, we slightly shifted our model's threshold parameter X_c to fit modern survival curves (Denmark period mortality 1980–2020, fig. S12A) that are more rectangular than those of the historical twin cohorts (supplementary text), while preserving the same width of the parameter distribution. We found that heritability estimates at $m_{ex} = 0$ declined by about ~2%, comparable to the SE of our estimates (fig. S12B), HIL = 0.55 ± 0.01. We conclude that mortality compression alone does not substantially affect life-span heritability.

Discussion

We introduced a method to adjust life-span heritability estimates for extrinsic mortality and cutoff age, in the absence of cause-of-death data. Our approach modeled genetic variation by introducing heterogeneity into two mortality frameworks—the MGG model and the SR model, calibrated to historical twin cohort data from Denmark, Sweden,

Table 1. Twin life-span heritability estimates (h^2) and asymptotic heritability at zero extrinsic mortality. Life-span heritability estimates [Falconer $h^2 = 2(r_{MZ} - r_{DZ})$] from three twin studies (Danish twins, Swedish twins, SATSA twins) are shown with their respective birth cohorts, cut-off ages for inclusion, extrinsic mortality levels, and sample sizes. Predictions from two mortality models [Saturating-Removal (SR), Makeham Gamma-Gompertz (MGG)] at zero extrinsic mortality are shown for the study's original cutoff age and at cutoff age of 15. Model predictions based on US siblings of centenarians are also shown. Parentheses indicate 67% confidence interval. Model parameters are listed in table S1.

					Heritability of life span				
						Model predictions at $m_{ex} = 0$		Heritability of intrinsic life span ($m_{ex} = 0$, cutoff age = 15)	
Study	**Birth cohorts**	**Number of pairs**	**Extrinsic mortality (across-year interval) m_{ex} (10^{-3} year^{-1})**	**Cutoff age (years)**	**Study estimate**	**SR**	**MGG**	**SR**	**MGG**
Danish twin registry (*8*, *38*)	1870–1900	$n_{mz} = 1033$ $n_{dz} = 1839$	4 (3.4–4.7)	15	0.23 (0.2, 0.26)	0.57 (0.51, 0.63)	0.47 (0.38, 0.54)	0.57 (0.51, 0.63)	0.47 (0.38, 0.54)
Swedish twin registry (*9*)	1886–1925	$n_{mz} = 3477$ $n_{dz} = 6403$	2.78 (1.66–4.65)	37	0.35 (0.34, 0.36)	0.51 (0.5, 0.53)	0.46 (0.4, 0.51)	0.56 (0.55, 0.59)	0.56 (0.49, 0.63)
SATSA cohort (*22*)	1900–1935	$n_{mz} = 196$ $n_{dz} = 325$ $n_{mz,apart} = 150$ $n_{dz,apart} = 371$	1.53 (0.86–2.74)	61	0.33* (0.27, 0.39)	0.44 (0.35, 0.5)	0.33 (0.29, 0.38)	0.53 (0.42, 0.62)	0.47 (0.41, 0.56)
US siblings of centenarians† (*23*)	1873–1910	$n_{siblings} = 2092$	3.5	20	–	0.61	0.43	0.62	0.45

*Estimate based on three independent methods, including twins reared together and apart (see materials and methods).
†Extrinsic mortality for this cohort was compared to the 1900 US cohort, following (*23*). Model predictions are from the best-fit to excess survival odds.

and SATSA, as well as US siblings of centenarians. Accounting for extrinsic mortality doubles the estimated heritability of intrinsic life span—from the commonly cited 20 to 25% to ~55%.

The key insight is that extrinsic mortality systematically masked the genetic contribution to life span in traditional analyses. When SATSA cohorts are stratified by birth year, declining extrinsic mortality is associated with rising heritability estimates. A 55% life-span heritability is in line with the heritability of life span in mice (*17*) and with the heritability of most other physiological traits, which average around 50% (*18*).

Heritability is a statistic that applies to a particular population in a particular environment at a particular time (*26*, *29*)—it is not a fixed quantity like the gravitational constant. It is therefore expected that studies examining different cohorts, time spans, and environments have reported different life-span heritability estimates. Recent large pedigree analyses (*15*, *16*) that reported low estimates (~10%) relied on self-reported data spanning ~300 years, encompassing historical cohorts with high extrinsic mortality, inconsistent age cutoffs, and complex assortative mating patterns. The inclusion of individuals from diverse regions and time periods introduced substantial environmental heterogeneity, which lowered the estimated proportion of genetic variance. By contrast, after correcting for cutoff age and extrinsic mortality, we focus on Scandinavian twin cohorts, providing estimates of the genetic contribution to intrinsic life span under more homogeneous environmental conditions.

Even with our corrected estimates, roughly half of life-span variation remains unexplained by additive genetics. This remaining variance likely stems from environmental influences (lifestyle, socioeconomic factors, health care access) (*6*, *30*–*32*), intrinsic biological stochasticity (*33*–*35*), nonadditive genetic effects, and epigenetic modifications (*32*, *36*, *37*).

Limitations of this study include reliance on assumptions of the twin design, such as the equal environment assumption. Nonetheless, heritability estimates from SATSA twins reared apart agree within one SE with those from standard twin designs, supporting the robustness of twin-based estimates. Access to detailed cause-of-death data would provide an important test of our conclusions. Finally, our adjustment method depends on the structure of the SR and MGG mortality models, though their agreement is reassuring.

In summary, correcting for extrinsic mortality raises the estimate for the heritability of human life span in twin and sibling studies to ~55%, more than twice previous estimates and in line with heritability of most human traits. Identifying the genetic variants underlying this heritability would help us to understand the fundamental mechanisms of human aging.

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SUPPLEMENTARY MATERIALS

science.org/doi/10.1126/science.adz1187
Materials and Methods; Supplementary Text; Figs. S1 to S14; Tables S1 and S2; References (*40–45*); MDAR Reproducibility Checklist

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Heritability of intrinsic human life span is about 50% when confounding factors are addressed

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Editor's summary

Many researchers have tried to understand longevity in humans and what could be done to improve it. However, this is a difficult topic to study because it takes a long time to collect data on human life spans, and many different factors can contribute to mortality. One key distinction is between extrinsic mortality (violence, accidents, infections, etc.) and intrinsic mortality due to genetic mutations and/or aging-related diseases. Shenhar *et al*. analyzed more than a century's worth of data from three different Scandinavian twin cohorts and concluded that the current estimates of longevity heritability are much too low (see the Perspective by Bakula and Scheibye-Knudsen). In the late 1800s and early 1900s, when these study cohorts were born, extrinsic causes played a large role in mortality, but once those are excluded, longevity appears to be about 50% heritable, similar to many other traits. —Yevgeniya Nusinovich