Lifetime reproductive success is an imprecise but largely unbiased predictor of long-term genetic contribution in historical humans

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ABSTRACT

We poorly understand the factors shaping variation in fitness among individuals, i.e. in their ability to make a contribution to the future gene pool. While short-term fitness proxies, e.g. lifetime reproductive success (LRS), are commonly used to measure fitness, how well do these proxies perform? Multigenerational human genealogical data allow the estimation of individual genetic contributions (IGC) – a fitness approximation closer to its theoretical definition – over many more years than is possible for other species. Here we use genealogical data from two local populations in Switzerland to estimate the IGC for 2,623 individuals on average 308 years after they were born. We find that the number of grandoffspring predicts IGC best explaining 28 percentage points more variation than LRS. Overall, LRS explains 29% of the variation in IGC, and 33% when accounting for offspring survival to adulthood. This suggests that offspring reproductive success is a key determinant of individual fitness. Nevertheless, we find that LRS only slightly underestimates the IGC of offspring as family sizes increase, and hence we find little evidence for an offspring quality–quantity trade-off. Together these findings suggest that, albeit relatively imprecise, LRS is a largely unbiased fitness proxy in this historic human population.

INTRODUCTION

Understanding the factors determining variation in fitness – generally understood to measure an individual's ability to contribute genes to the future population – is of fundamental importance in evolutionary biology (1–3). However, a detailed examination of the causes and consequences of variation in fitness is hampered by difficulties associated with estimating this key evolutionary parameter. Although most studies resort to short-term approximations of an individual's fitness (fitness proxies; e.g. survival, number of offspring), we have a poor understanding of the extent to which these predict the long-term genetic contribution of individuals.

Multi-generational pedigree information allows for the estimation of individual genetic contributions (IGC) – the proportional contribution of an individual to the gene pool at a specific point in time. If estimated over a sufficiently long period of time, IGC provides a measure of fitness that is as close to its theoretical definition as possible. Hence, we are able to quantify the performance of short-term fitness proxies by correlating them with long-term IGC. Thus far, this has been done for a number of bird species, using IGC estimated over a period of maximally 26 years, or 8 generations (4–6). These studies suggest that lifespan is a relatively poor predictor of IGC, followed by LRS (4), and that the number of grandoffspring is the best predictor of long-term IGC (5) (Supplementary Table 1).

As of yet, it remains unknown if these findings also apply to other species, including our own. Indeed, human genealogical data may span centuries rather than decades, as well as extend over more generations. This allows estimating IGC at many more time points (allowing for a much finer temporal resolution), and across more generations (bringing us closer to theoretical definition of fitness). Therefore, using human genealogies to estimate IGC can provide a better understanding of the determinants of variation in fitness in general, and the evolution of human life histories in particular.

To be informative, fitness proxies need to capture the key aspects of an individual's life history. First, to have the opportunity to reproduce or support the reproduction of relatives, individuals need to survive until reproductive age (7,8). Indeed, in humans, lifespan is associated with increased reproductive success (9). Furthermore, survival is an important determinant of within-generation changes in the gene pool and therefore an integral part of annual fitness proxies (e.g. (10)). Second, having survived, an individual must subsequently reproduce. As it directly captures the transfer of their genes to the next generation, the number of offspring an individual has over the course of its lifetime, commonly referred to as lifetime reproductive success (LRS (11)), is hence expected to be a better predictor of fitness than survival/lifespan. Third, an individual's contribution to future gene pools requires its offspring to survive to reproductive age and reproduce themselves. In humans in particular, offspring survival may be an important determinant of fitness: pre-demographic transition, birth rates were high, but so was infant mortality (12,13). Variation in offspring number, survival and reproduction is captured by an individual's number of grandoffspring. The latter encapsulates the key aspects of an individual's life history, and is therefore expected to be the most precise predictor of an individual's fitness. Although the number grandoffspring in expected to provide the most precise proxy for fitness (i.e. explain most variation), reliably counting the number of grandoffspring may not be feasible, for example if a significant proportion of the population disperses outside of the study site, or offspring cannot be linked to parents once they have reached independence. Furthermore, depending on the question at hand, the fact that the number of grandoffspring, or the number of offspring surviving to a certain age, conflates parental fecundity and offspring survival may be problematic (14–16). Although expected to be a less precise predictor of fitness, LRS does not suffer from these issues, and as a consequence is one of the most commonly used fitness proxies. However, we have a poor understanding of the relative importance of the various determinants of variation in the number of grandoffspring, and how much of the variation in the number of grandoffspring, and in IGC, is captured by LRS.

LRS may not only be an imprecise predictor of fitness, it may also be inaccurate (i.e. biased). First, in species with parental care, such as humans, parents may provide less care to each additional individual offspring, giving rise to an offspring quality–quantity trade-off (17–19), resulting in individuals with higher LRS having lower quality offspring (i.e. more likely to die and/or reproduce less or not at all). Evidence for quality–quantity trade-offs has been found in a variety of species (20), but although humans display parental care and have a long period of offspring dependency (21–23), evidence in humans is mixed (24–26), with some studies suggesting it is only apparent in pre-industrial societies (27,28). Second, LRS could underestimate individual fitness, i.e. each additional offspring provides an increase in fitness that is greater than a per capita increase, for example through cooperative breeding or relatives helping raise offspring (29). Whether LRS is an unbiased estimate of fitness, and in what way, remains unresolved.

In birds, LRS provides a better predictor of IGC than lifespan, but it is worse than the number of grandoffspring (4,5). Also, the degree to which LRS predicts IGC depends on when offspring are counted. Specifically, although only counting offspring surviving to adulthood (i.e. recruits) may be problematic (see above; (14–16)), this strengthens the association with IGC (Supplementary Table 1;(4,6)). However, the ability of fitness proxies to predict an individual's fitness depends on the life history of the study species and hence is expected to show interspecific variation. Although patterns appear to be similar in humans (30), IGC have not been estimated beyond four generations, which is unlikely to be long enough for IGC to stabilise and become sufficiently representative of fitness (see methods for further details; (4,31,32)).

Here, we quantify how the key life history events determine human fitness using historical genealogical data containing the individual human life-histories from two parishes in the Canton of Glarus, Switzerland. This dataset spans 16 generations and contains individuals born from the 16th to the 20th century. We estimate IGC in both parishes, across at least 256 and on average 308 years, as our most comprehensive estimate of fitness. We use generalised linear mixed models (GLMMs) to examine how well four commonly used fitness proxies predict IGC: lifespan, lifetime reproductive success measured at birth (LRS) or counting only offspring surviving to adulthood (LRS_{SA}), and the number of grandoffspring. We predict the proportion of variance in IGC explained to increase from lifespan to LRS to LRS_{SA} to the number of grandoffspring, with each increasingly encapsulating more information on an individual's and their offspring's life history. By comparing the extent to which each proxy improves the prediction of IGC we elucidate the important factors in determining individual fitness, and quantify the value of LRS as a fitness proxy. In particular, by including LRS_{SA}, the relative importance of offspring survival vs mating and reproductive success can be quantified. Second, we examine the accuracy of LRS as a predictor of fitness by comparing the average IGC of offspring under different family sizes, providing a novel approach to testing for a role of a quality–quantity trade-off as an important driver of human life-history evolution.

METHODS

Dataset

We extracted life-history information, including an individual's year of birth, marriage and death, and the identity and date of birth of all of its children (if available), for 44,967 unique individuals born or married in two parishes in the Canton of Glarus, Switzerland: Linthal (46°55'N, 9°E) and Elm (46°55'N, 9°10'E) from a genealogical archive (33). This includes records for unmarried adults, children dying before reaching adulthood, and illegitimate children (though these are few, in line with expectations of historical European populations (34,35)). The data span over four centuries, containing individuals born from 1562 to 1996. These records were used to construct a pedigree containing

44,967 individuals, 35,882 maternities, 35,973 paternities, 89,904 full-sibling relationships, mean maternal and paternal sibship sizes of 4.01 and 4.42, respectively, 8,667 founders, and a maximum pedigree depth of 16 generations.

Population sizes of Linthal and Elm varied between 994-2,645 and 516-1,051, respectively, between the 18th-20th centuries (36,37). The household and family structure are thought to be representative of Central Europe as a whole (nuclear and patriarchal), with new households being formed after couples had accumulated enough wealth to get married (38). As such, the median age-at-first reproduction for females was 25, and for 95% of individuals occurred after 19 years of age. For individuals who reproduced, the median number of offspring was 4 (range = 1-24). Families were largely sustained through the farming of sheep and cattle, with additional earning through weaving and spinning becoming possible in the 18th century (39), particularly in Linthal. Over the course of the entire study period and across all individuals, the median lifespan was 49 years and 74% of individuals lived beyond age 5.

Estimation of individual genetic contributions

We estimated individual genetic contributions (IGC) following Hunter *et al.* (2019) (32), which uses pedigree information to estimate *expected* genetic contributions to future generations, under the *expectation* of random Mendelian segregation of alleles (e.g., each parent contributes 50% of an offspring's alleles). We used the complete pedigree available for individuals from Elm and Linthal to build a relationship matrix containing the relatedness coefficients between all pairs of individuals (e.g. for a parent and offspring, the shared relatedness coefficient would be 0.5) in R 4.1.1 (40) using the package *nadiv* 2.17.1 (41). These relatedness coefficients become expected genetic contributions when causality is considered (i.e. an individual *gives* its offspring 50% of their alleles and therefore the absolute expected genetic contribution an individual makes to its offspring is 0.5). We will henceforth refer to the individual making the expected genetic contributions as the *focal* individual and to the individual receiving the genetic contribution as the *descendant*.

IGC are equal to the expected genetic contributions proportional to the total genetic code present in a specific population at a specific time point. We used birth and marriage locations along with birth and death years to estimate when individuals were present in each population (Linthal and Elm were analysed separately) for all individuals with a recorded birth year (Linthal, N=20,028, 98%; Elm, N=16,811, 97%; Supplementary Material 1). We aimed to estimate the IGC for all individuals across all years of available data before carrying out data selection (see below). To do so, for each individual, and in each year, we subset the relationship matrix to include only the focal individual (row) and all individuals present in the specific population at that point (columns), starting at the focal individual's birth year (or arrival year if an immigrant, see Supplementary Material 1). The total expected genetic contributions for a focal individual in a given year is the sum of the total relatedness coefficients across all columns. This was then repeated for all the following years until 1990. Genetic contributions were converted into IGC by dividing them by the total number of individuals present in the population in that year. We did not include IGC through non-direct descent (e.g., kin genetic contributions) by temporarily removing parental IDs of the focal individuals from the pedigree before creating the relatedness matrix.

Data selection

Although initially IGC tend to fluctuate substantially over generations, they are expected to stabilise at an individual's reproductive value, which can be considered the ultimate measure of fitness

(31,42,43). Following previous work (4,6), we initially evaluated stabilisation of IGC by grouping individuals into 10-year birth cohorts and quantifying the Pearson correlation coefficient between IGC to each subsequent year and the final year considered (1990). When this remained above a 0.95 threshold for a period of 2 generations, IGC were considered to have stabilised. We defined a generation as the mean (± SE) parental age at offspring birth, which were 32.2 ± 0.04 and 32.1 ± 0.05 yr for Linthal and Elm, respectively.

According to these criteria, IGC stabilised for individuals born before 1717 in Linthal (around 7.5 generations) and before 1734 in Elm (around 8 generations; Supplementary Figure 1 and 2; the difference being likely due to the larger population size of Linthal). However, despite meeting the criteria for stabilisation of genetic contributions outlined above (4), visual inspection showed that although the fluctuations become minor, they had not yet plateaued (Supplementary Figure 3). Instead, we therefore selected only individuals whose IGC were estimated over a period of at least approximately 8 generations after they were born – a period spanning an equivalent number of generations as previous studies. In total, IGC to the year 1990 from 3,728 focal individuals (1,896 from Linthal and 1,832 from Elm) were used in the analyses. The length over which IGC were estimated was at least 257.68 and 257.08 yr, and on average 314.97 (±0.93) and 318.44 (±0.88) yr (for Linthal and Elm, respectively), with the birth years of focal individuals ranging between 1575-1735 (Supplementary Figure 4).

Fitness proxies

We considered the following fitness proxies: Lifespan (the difference between the death date and birth date), LRS (lifetime number of offspring produced), LRS_{SA} (lifetime number of offspring surviving to adulthood), and the number of grandoffspring (total number of offspring of an individual's offspring). Adulthood was defined as the sex-specific 5^{th} percentile of age-at-first reproduction for the whole dataset (females: 19.1 yr, males: 21.2 yr). We estimated lifespan, LRS, and LRS_{SA} for all individuals for which we had an estimated IGC and with known birth and death dates; N=2790), including individuals that died before adulthood. For the number of grandoffspring, we additionally required that the individual's offspring also had their complete life-history recorded (N=2790).

Statistical analyses

We used generalised linear mixed models (GLMMs) to examine the relationship between IGC and the four fitness proxies. We used a zero-inflated beta model in which the zero-inflated part of the model modelled the probability of an individual having no IGC to the present-day population (i.e. the probability of lineage extinction) using the logit-link function. The distribution of the non-zero proportional genetic contributions was modelled using a beta distribution.

We controlled for differences in IGC between birth parishes (Linthal or Elm) and the sexes (female or male) by including these as categorical fixed effects. An individual's 10-year parish-specific birth cohort was fitted as a random intercept to control for temporal variation in mean IGC. We controlled for offspring dispersal from their birth parish affecting IGC by including the proportion of offspring that did not marry outwith the parish they were born in as a fixed covariate. We further included a random slope for each of the fitness proxies to allow its relationship with IGC to vary among parish-specific birth cohorts. Initially all two-way interactions between sex, parish, and proportion of non-dispersing offspring were included, but they were removed if non-significant to aid the interpretation of first-order effects. Model structures were the same for the zero-inflated and beta parts of the model.

The sample size for these models was 2,623, which included only informative individuals for all effects.

To quantify how much variation in IGC each fitness proxies explained, we estimated the Bayesian R-squared for each of our models (44). The significance of the differences in Bayesian R-squared values were evaluated by examining if the 95% credible intervals overlapped (see Table 2).

We tested if a trade-off between offspring quantity (measured as LRS) and quality (measured as offspring IGC) causes LRS to provide a biased estimate of IGC by estimating the slope of a regression of the mean IGC of an individual's offspring against its own LRS. Here we used the same individuals as before, but excluding non-reproducing individuals, leaving 2,017 individuals. For this model, we performed a beta regression (with no zero-inflated distribution included) controlling for the same confounding fixed and random effects structures as above. Beta regressions require response variables to have values greater than zero and less than one and we therefore added 10^{-10} to all mean offspring genetic contributions. A negative relationship between LRS and mean offspring genetic contributions would indicate a quality–quantity trade-off; a positive relationship would indicate that LRS overestimates an individual's fitness at relatively small family sizes and underestimates fitness at large family sizes; no relationship would indicate LRS is an unbiased fitness proxy. We additionally examined if the lifespan of parents was an important covariate, as offspring whose parents died younger might receive less parental care, potentially impacting their IGC.

Both zero-inflated beta and beta models were implemented in the R package *brms* (2.16.1 (45)) using the Markov chain Monte Carlo (MCMC) sampler Rstan (2.21.2, (46)) using R 4.0.2 (40). For each model, we ran four runs of 6,000 iterations across four cores, sampling every 10 iterations, after a warm-up of 2000 iterations. We set the delta parameter to 0.99 to aid convergence. Default priors were used: flat for all fixed effects and a student's t distribution for random effects. Convergence of models was confirmed with R hat parameters equalling 1.00 and Monte Carlo standard error being approximately 0. The *pp_check* function was used to check that simulated data from the model matched the original data well. We used the probability of Direction (*pd*) (47) (the percentage of the posterior distribution that has the same sign as the median) to infer significance of effects. In line with Makowski *et al.* (47), we classified *pd* values as the following: 0.95-0.975 trend effects; 0.975-0.99 = significant; > 0.99 = highly significant. For random effects, *pd* is not applicable, and no significance criteria were used. Figures were created using the packages *brms*, *ggplot2* (3.3.5, (48)) and *ggpubr* (0.4.0 (49)).

RESULTS

Individual genetic contributions (IGC)

We estimated the IGC of 3,728 individuals (1,896 from Linthal and 1,832 from Elm), born between 1575-1735, to individuals present in the parishes of Linthal and Elm in 1990 (1,896 and 1,832 respectively). We found that the probability of an individual's lineage going extinct was high, with 72% of individuals having an IGC of zero to the 1990 population (Supplementary Figure 5a). This high probability of a lineage going extinct is partly due to 21% of all individuals not surviving to reproductive age, 41% having no offspring, 43% having no offspring surviving to adulthood, and 52% of all individuals having no grandoffspring (Supplementary Figure 5). Nevertheless, approximately 20% of the individual lineage extinctions occurred after individuals had at least one grandchild. Individuals whose lineages did not go extinct on average contributed 0.089% of the genetic material

present in the population in 1990 (Supplementary Figure 5a), although one male contributed 0.6% of the Linthal genetic material.

Lifespan, LRS, LRS_{SA}, and the number of grandoffspring were positively associated with IGC (Beta distribution, *pd* > 0.975, Table 1, Figure 1). We also found a negative effect of any of the fitness proxies on the probability of an individuals' lineage going extinct (zero-inflated distribution, *pd* > 0.975, Table 1).

IGC (distribution and extinction probability) were dependent upon several other factors. First, individuals born in the Linthal parish had lower IGC, perhaps reflecting the greater population size in that parish (all models, beta distribution, *pd* > 0.975, Table 1). They also had a greater probability of lineage extinction in the LRS-model (zero-inflated distribution, *pd* > 0.975, Table 1), but this was not found across other models. Males were also found to have higher IGC than females (beta distribution, *pd* > 0.975, Table 1), but only had a lower probability of lineage extinction in the lifespan model (zero-inflated distribution, *pd* > 0.975, Table 1). These effects remained independent of whether the individual was born in Linthal and Elm (*pd* < 0.975, Supplementary Table 2). Further, individuals with a higher proportion of non-dispersing offspring were found to have higher IGC (beta distribution, *pd* > 0.975, Table 1). This was also found to be positively related to lineage extinction in the lifespan and the number of grandoffspring models (zero-inflated distribution, *pd* > 0.975, Table 1), negatively related in the LRS_{SA}-model and there was no association in the LRS-model. These effects remained the same regardless of individual sex and birth parish (*pd* < 0.975, Supplementary Table 2). Finally, we found that IGC of individuals varied among birth cohorts (both in their extinction probability and values; see random effects, Table 1). There was also variation among birth cohorts in the slope of the relationship between each fitness proxy and IGC, but this variation was small except in the slope of the relationship between probability of lineage extinction and LRS, LRS_{SA} and the number of grandoffspring.

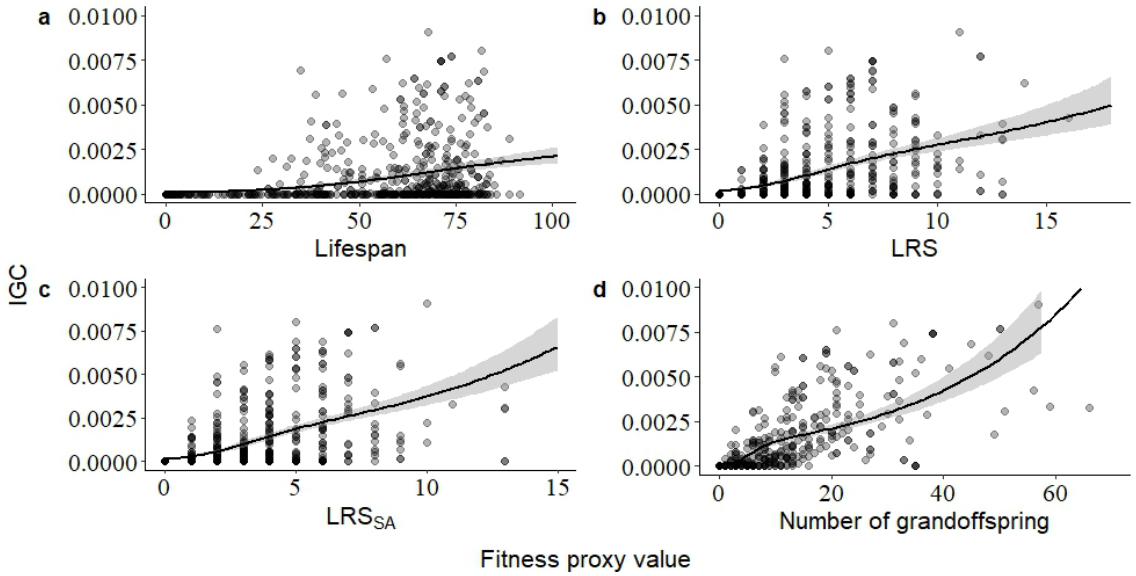

Figure 1: The relationship between IGC and four fitness proxies: (a) lifespan, (b) LRS, (c) LRS_{SA}, and (d) the number of grandoffspring. The plots were produced using the *conditional_effects()* function from the R package *brms* to standardise points across values for covariates. Shaded areas indicate 95% credible intervals. Data points too far away from the values conditioned upon were removed from the plot. Symbols are partially transparent to aid visualisation.

Table 1: Output from four beta zero-inflated models of IGC with different fitness proxies included: Lifespan, LRS, LRS_{SA}, and the number of grandoffspring. Showing the fixed and random effect estimates (posterior distribution median [95% credible intervals]). The output from both the zero-inflated and beta distributions are shown. Significant effects (probability of Direction > 0.975) are shown in bold. Non-significant two-way interactions were removed from the models. Model results with non-significant interactions included are shown in Supplementary Table 2.

	Lifespan		**LRS**		**LRS_{SA}**		**Number of grandoffspring**	
	Zero inflated	Beta	Zero inflated	Beta	Zero inflated	Beta	Zero inflated	Beta
Fixed effects								
Intercept	**2.048 [1.405 – 2.689]**	**-7.098 [-7.499 – -6.683]**	**3.202 [2.435 – 4.009]**	**-7.752 [-8.164 – -7.358]**	**3.202 [2.435 – 4.009]**	**-7.752 [-8.164 – -7.358]**	**1.304 [0.558 – 2.074]**	**-7.307 [-7.656 – 6.985]**
[Fitness proxy]	**-0.053 [-0.058 – -0.047]**	**0.005 [0 – 0.008]**	**-0.841 [-0.976 – -0.711]**	**0.113 [0.093 – 0.134]**	**-0.841 [-0.976 – -0.711]**	**0.113 [0.093 – 0.134]**	**-0.567 [-0.675 – -0.468]**	**0.035 [0.031 – 0.04]**
Birth Parish (Linthal)	0.051 [-0.241 – 0.364]	**-0.378 [-0.521 – -0.231]**	0.321 [-0.036 – 0.686]	**-0.485 [-0.612 – -0.358]**	0.321 [-0.036 – 0.686]	**-0.485 [-0.612 – -0.358]**	0.384 [-0.112 – 0.894]	**-0.560 [-0.699 – 0.43]**
Sex (Male)	**-0.209 [-0.393 – -0.025]**	**0.321 [0.219 – 0.422]**	0.204 [-0.03 – 0.423]	**0.302 [0.208 – 0.398]**	0.204 [-0.03 – 0.423]	**0.302 [0.208 – 0.398]**	0.081 [-0.262 – 0.405]	**0.338 [0.247 – 0.427]**
Proportion of non-dispersing offspring	**1.218 [0.664 – 1.784]**	**0.634 [0.287 – 0.991]**	**-1.113 [-1.903 – -0.352]**	**1.097 [0.725 – 1.48]**	**-1.113 [-1.903 – -0.352]**	**1.097 [0.725 – 1.48]**	**1.784 [1.044 – 2.536]**	**0.467 [0.125 – 0.811]**
Random effects								
Parish-specific birth cohort (random intercept)	0.138 [0.005 – 0.471]	0.213 [0.009 – 0.609]	0.296 [0.023 – 0.672]	0.086 [0.005 – 0.208]	0.296 [0.023 – 0.672]	0.086 [0.005 – 0.208]	0.370 [0.02 – 0.824]	0.074 [0.004 – 0.196]
Parish-specific birth cohort × fitness proxy (random slope)	0.003 [0 – 0.008]	0.006 [0.001 – 0.014]	0.317 [0.211 – 0.459]	0.011 [0 – 0.031]	0.317 [0.211 – 0.459]	0.011 [0 – 0.031]	0.251 [0.166 – 0.381]	0.007 [0.003 – 0.012]

How well do fitness proxies predict IGC?

Although all fitness proxies predicted IGC, we found that they significantly varied in their predictive power. As expected, the number of grandoffspring explained most variation in IGC (R^2=56.7%, Table 2), explaining 43.7 percentage points more variation than lifespan, 27.8 percentage points more than LRS and 23.3 percentage points more than LRS_{SA} (Table 2). Contrary to expectations, the difference in predictability between LRS and LRS_{SA} was very small (ΔR^2=4.4%, Δ95% Credible Intervals (CrI)=0.6% – 8.3%, Table 2). A null model containing no fitness proxy but all other first-order fixed effects explained only 2.3% (95% CrI= 1.4% – 3.4%) of the variation in IGC.

Table 2: On the diagonal, Bayesian R^2 values (R^2 and 95% credible intervals) by each fitness proxy (lifespan, LRS, LRS_{SA}, and the number of grandoffspring) and other significant covariates retained in the model. Pairwise Pearson correlation coefficients (ρ) between fitness proxies are shown above the diagonal (also see Supplementary Figure 6) and the difference in Bayesian R^2 values are shown below the diagonal (ΔR^2 and Δ95% credible intervals). Δ95% credible intervals that do not overlap with zero are in bold.

	Lifespan	LRS	LRS_{SA}	The number of grandoffspring
Lifespan	13.1% [10.6 - 15.7]	r = 0.52	r = 0.50	r = 0.41
LRS	**ΔR^2 = 15.9% [12.1 – 19.8]**	R^2 = 29.0% [25.2 – 32.8]	r = 0.94	r = 0.71
LRS_{SA}	**ΔR^2 = 20.3% [16.5 – 24.2]**	**ΔR^2 = 4.4% [0.6 – 8.3]**	R^2 = 33.4% [29.6 – 37.2]	r = 0.75
Number of grandoffspring	**ΔR^2 = 43.7% [40 – 47.1]**	**ΔR^2 = 27.8% [24.1 – 31.2]**	**ΔR^2 = 23.3% [19.6 – 26.7]**	R^2 = 56.7 [53.0 – 60.1]

Is LRS an unbiased estimate of IGC?

The per-capita IGC of an individual's offspring increased with increased LRS, but the slope of this relationship was very shallow (*pd* > 0.975, posterior mode=0.068, 95% CrI=0.042 – 0.091, Figure 2). Thus we find no evidence for an offspring quality–quantity trade-off which would manifest itself as a negative relationship, and instead this finding suggests that LRS slightly underestimates IGC in larger family sizes and overestimates IGC in lower family sizes. Furthermore, individuals who lived longer had offspring with higher IGC (*pd* > 0.975, posterior mode=0.013, 95% CrI=0.010 – 0.017). Mean IGC was also lower for the offspring of males, and for individuals born in Linthal (*pd* > 0.975, posterior mode=-0.293, 95% CrI=-0.420 – -0.161). We also found a positive and significant interaction between parish and sex (*pd* > 0.975, posterior mode=0.281, 95% CrI=0.094 – 0.456), such that the differences between males and females in Linthal was very small. Further, similar to the previous models, we found that the proportion of an individual's offspring that did not disperse increased the mean IGC of those offspring (*pd* > 0.975, posterior mode=0.507, 95% CrI=0.285 - 0.724), but this relationship did not vary according to parish and sex (*pd* > 0.975, Supplementary Table 3). Finally, we found that variance in the mean IGC of offspring was explained by their parents' birth cohort (posterior mode=0.468, 95% CrI=0.330 - 0.649). The parent's birth cohort also affected the slope of relationship between LRS and mean offspring IGC but this variation was relatively small (posterior mode=0.049, 95% CrI=0.030 - 0.073).

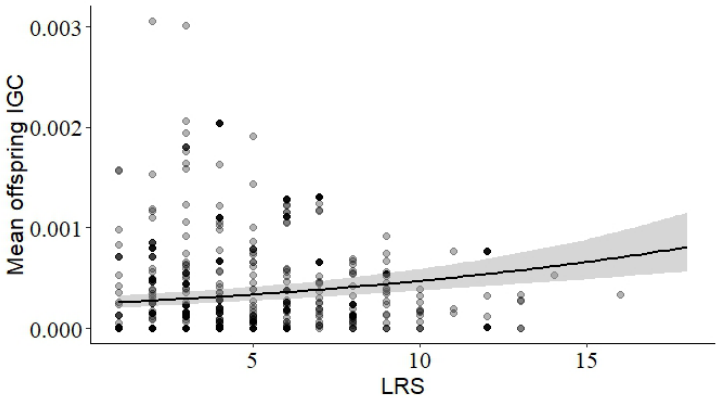

Figure 2: The relationship between mean offspring IGC and LRS. The plots were produced using the *conditional_effects()* function from the R package *brms* to standardise points across values for covariates. Shaded areas indicate 95% credible intervals. Data points too far away from the values specified were removed from the plot and data points included are partially transparent to aid visualisation.

DISCUSSION

We quantified the role of the most important life-history events in determining variation in human fitness. We approximated fitness by estimating IGC after, on average, 308 years, using historical genealogical data for two populations from the Swiss Canton of Glarus. We found that the number of grandoffspring was a significantly more precise predictor of IGC than LRS, LRS_{SA}, or lifespan. However, despite it explaining less variation in IGC, LRS was found to be a largely unbiased (i.e. accurate) predictor of IGC.

The model containing the number of grandoffspring explained 57% of variation in IGC, whereas the next best fitness proxy (LRS_{SA}) explained only 33%, followed by LRS (29%) and lifespan (13%). This is broadly in line with results based on genetic contributions estimated over 4 generations in 19th century Sweden (30). The fact that the number of grandoffspring comes out on top is not unexpected, as the number of grandoffspring incorporates the most information about the life-history of an individual and its offspring. However, together with our finding that LRS_{SA} barely outperformed LRS (explaining only 4% more variation in IGC) and that lifespan explains only 13% of the variation in ICG, this suggests that offspring mating and reproduction is a much greater determinant of human fitness than offspring survival, despite childhood mortality in pre-industrialised populations being high. This suggests that in human studies where the number of offspring has been measured at birth, researchers gain little from recording whether these individuals survived to adulthood or not.

The weak relationship between lifespan/survival and IGC has implications for how selection acts in post-demographic transition societies: although infant mortality has declined and lifespan continues to increase, (50), these changes may not impact IGC. Instead, these results suggest that the opportunity for selection in humans is greatest for traits associated with reproduction. In line with this, humans show high variation in mating and reproductive success (51), and mating success is a key determinant of human reproductive success (52). The relative importance of mating and reproductive success in determining IGC and how much these results vary across human populations – and according to what conditions – would be worthy of future study.

LRS explained 29% of the variation in IGC, 28 percentage points less than the number of grandoffspring. However, we found only a slight positive relationship between LRS and the mean IGC of an individual's offspring (Figure 2). The difference in the relative abilities of the fitness proxies to

predict IGC is therefore mostly due to the greater precision that counting the number of grandoffspring provides, and not due to systematic bias in LRS. LRS was also a significantly better predictor of IGC than lifespan (by 16%) showing that reproductive success is a larger determinant of human fitness than age-at-death. Furthermore, because the number of grandoffspring confounds the fitness of multiple individuals, which can be problematic when estimating the strength of phenotypic selection (14–16), we suggest that LRS provides an evolutionary relevant and relatively unbiased fitness proxy when it comes to the study of selection in humans, assuming our findings are representative for other populations and time periods.

When we compare our results to those from other species, a clear general pattern appears: the more information on an individual's and their offspring's life-histories are captured by a fitness proxy, the more variation in IGC that a fitness proxy predicts (4–6). The main difference between the results from this human study and the three previous bird studies was that when we measured LRS at a later point in the offspring's life (i.e. LRS_{SA}) the ability of LRS to predict IGC did not increase greatly. This is in contrast to (5), which found offspring survival is a key determinant of reproductive success. Our results therefore suggest that offspring survival to adulthood is a less important determinant of fitness in humans than it is in the bird species studied so far, and that mate selection and reproduction are much more important sources of variation in fitness. Further, although at first sight high, our finding that 70% of individual lineages went extinct over the study period is similar to previous bird studies, which reported extinction probabilities of 61-71% (Supplementary Table 1), and feasible given levels of lineage extinction in humans after four generations (53). In summary, there is evidence for differences between humans and birds species in which life-history events determine IGC, but the small number of species and the lack of different human populations (across cultures) studied limit broader extrapolation.

There were several other factors that were important in determining both the variation and extinction probability in IGC. First, males had higher IGC, indicating sex is an important factor in the study of human fitness. This is perhaps due to cultural sex-biases in inheritance, as well as biological factors such as the absence of menopause in males. In our study population, individuals with the highest reproductive success were males who's first wives died around the age of menopause, allowing the widowers to remarry a younger female and achieve a lifetime reproductive success far greater than males who did not remarry. Second, individuals born in Linthal also tended to have lower IGC than individuals born in Elm. This is probably due to higher population sizes in Linthal meaning lower IGC as IGC are measured as a proportion. However, variation in the levels of immigration and emigration in each population could also be a factor. Migration is likely an important driver of the variation in IGC – as shown by the proportion of an individual's offspring who dispersed affecting their IGC – and a methodological challenge for their estimation where populations are not closed (32). Finally, the birth cohort of individuals explained variation in IGC reaffirming the importance of the early-life environment in the study of human life history (54,55). However, it should be noted that together, these factors were relatively minor determinants of variation in IGC, given that a model containing no fitness proxy but all other effects explained only 2% of the variance in IGC.

The positive relationship between an individual's LRS and the mean IGC of offspring strongly argues against the presence of a quality–quantity trade-off in humans. This result is not due to variance in the lifespans of parents, as the lifespan of parents was controlled for in models. Instead it is suggestive of differences in resource acquisition between individuals dominating the relationship and potentially masking the trade-off (56). The positive relationship is perhaps due to individuals who have larger LRS values having a lower chance of lineage extinction. One possible explanation for quality–quantity trade-offs not manifesting themselves in humans, despite theoretical expectations, is due to cooperative breeding. Having older siblings can improve survival to adulthood (29), and therefore – although these sibling effects are complex (29,57) – it is possible that sibling helpers can reduce the costs of producing more offspring in humans. The absence of an offspring quality–quantity trade-off

disagrees with the results from studies using survival (58–60) or reproduction of offspring (26,28) as the measure of quality but is consistent with the results from one study using IGC (30).

Although still in its infancy, the use of pedigree data to estimate long-term genetic contributions opens a range of exciting avenues. Building on our work using human genealogical data, and the work on non-human animals by others (4–6), future work would benefit from a further exploration of the similarities and differences among the different methodologies at our disposal. In particular, the comparison between gene dropping methods (4,5) and expected genetic contributions (e.g. this study) and examining the relative role of drift versus natural selection in shaping variation in IGC (61). Furthermore, while our study has highlighted the ability of human genealogical data to provide insight into human evolution (62,63), and the measurement of fitness more broadly, applying these methods to similar data for an array of human populations (see (64), for a review) will allow us to quantify the degree to which these findings vary across cultures, environments and time.

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