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A Mathematical Model for Predicting Obesity Transmission With Both Genetic and Nongenetic Heredity

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Abstract

Objective—Obesity is transmissible across generations through both genetic and nongenetic routes, but distinguishing between these factors is challenging. We aimed to quantitatively study the contribution of these genetic and nongenetic effects to assess their influence on obesity prevalence.

Methods—We proposed a mathematical model that incorporated both genetic and nongenetic effects of obesity. Model parameters were estimated by using observational data. Model simulations were used to assess the sensitivity of model parameters. To strengthen our approach, we also performed the parameter estimation and simulation using data from the UK.

Results—Individuals homozygous for a 'hypothetical obesogenic gene' are suggested to be more susceptible to both social contagious risk and spontaneous weight gain risk. The model predicted that obesity prevalence reaches 41.03% (39.28, 44.31) and 26.77% (25.62, 28.06) at 2030 in the US and UK, respectively. The social contagious risk factor had a greater overall impact on the distribution of the population with obesity than did spontaneous weight gain risk or mother-to-child obesity transmission risk.

Conclusions—Although the proposed "first approximation" model captured the complex interactions between the genetic and nongenetic effects on obesity, this framework remains incomplete. Future work should incorporate other key features driving the obesity epidemic.

Keywords

mathematical model; heredity of obesity; social contagion

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INTRODUCTION

Obesity prevalence has increased steadily for the past few decades. Although obesity is considered to be a noncommunicable disease, evidence of the contagiousness of obesity has accumulated in the last 10 years. In 2007, Christakis and Fowler introduced a modeling framework that studied the impact of social influences on obesity, whereby individuals with more contact with other persons with obesity have a higher risk of becoming obese[1]. While the analytical methods have been debated[2], Christakis and Fowler reported that the association between weight gain risk and the connection with other persons with obesity remains even after the removal of other possible confounders, including common environmental factors. Thus, they concluded that obesity is contagious through social connections. The complete mechanism behind social contagion of obesity has not been fully elucidated, but scientific evidence for social contagion is accumulating. For example, it was recently found that adolescents tend to have more friends with similar physical activity levels and eating behaviors[3,4].

Obesity is also transmitted vertically from parents to offspring through or beyond genome sequences (intergenerational transmission)[5]. Heredity studies have found that a substantial proportion (60–80%) of the variance in BMI distribution can be explained by genetic variance[6,7]. Genome-wide association study has identified multiple genes and single-nucleotide polymorphisms that affect obesity[8,9]. Among them, the fat mass and obesity-associated gene (*FTO*) is strongly associated with increased BMI, although the detailed mechanism behind this association is not clear[10]. Interestingly, however, the *FTO* genotype is not associated with outcome after weight loss interventions[11]. Vertical transmission also results from the fetal environment imposed by parental, especially maternal, lifestyle[12]. Maternal obesity has an epigenetic impact on the expression of metabolic genes in children, a finding that has been experimentally documented in mice[13]. Furthermore, maternal obesity (and maternal diet during pregnancy and lactation) interrupts the construction of neural circuits in the hypothalamus, which regulate the offspring's appetite and which may influence a path toward obesity later in adulthood[14]. Also, maternal diet during pregnancy and lactation impacts children's growth[15]. Taken together, the data suggest that even after excluding genetic factors, children of mothers with obesity are at higher risk of obesity themselves.

Despite the evidence of intergenerational obesity transmission, quantification of the influence of intergenerational obesity transmission on obesity prevalence remains elusive. There are two significant challenges to quantifying this influence. First, estimating relative risk requires carefully designed, large-scale surveillance, which is difficult to conduct in a wide-reaching population. Qi et al. estimated the relative risk of the *FTO* gene using two large cohort studies (the Nurses' Health Study [NHS] and the Health Professionals Follow-Up Study [HPFS]), but their analysis was confined to specific populations and may not represent national population trends[16]. Second, the interdependency of the different sources of obesity risk is impossible to measure directly and separately. For example, the genetic correlation between direct genetic effect and maternal effect makes it hard to observe both effects separately. A mother carrying "obesity genes" may pass these genes to her offspring

(direct gene effect) and is susceptible to becoming obese herself, which increases her child's childhood obesity risk (phenotypic transmission).

Mathematical models can account for these interdependencies and allow investigators to hypothesize different scenarios by changing parameters. Because the dynamics of obesity resemble the dynamics of a contagious infectious disease, several investigators have proposed obesity prevalence models based on the Kermack-McKendrick infectious disease model[17]. Previous dynamic obesity prevalence models incorporated both social and nonsocial influences on obesity[18–21], and Hong et al. additionally incorporated genetic heredity[22]. Dawson et al. proposed a statistically based computational model that accounted for assortative mating and fertility rate differentiated by BMI that reflects the transient BMI distribution across generations[23].

Advancing previous approaches, here we construct a mathematical model in which we included both genetic and nongenetic effects. To demonstrate the usefulness of the model, we applied the model to address two key questions: (1) How much do genetic characteristics contribute to obesity prevalence? and (2) How do interventions that target social influences, nonsocial influences, and pregnancy-related influences on obesity risk impact trends in obesity prevalence?

METHODS

Models for the obesity epidemic

Following the approach derived from infectious disease modeling[24], we compartmentalized the population into two subgroups by phenotype: a class without obesity (underweight, normal, and overweight; BMI < 30 kg/m^2), termed S, and a class with obesity (BMI ≥ 30 kg/m^2), termed I. These classes were further divided into three subgroups by the genotype of a hypothetical obesogenic gene, AA, Aa, and aa. Thus, for example, S_{Aa} is the proportion of the population without obesity with the Aa genotype. We adopted Mendelian laws of genetic heredity. To present the simplest model that reflects reality, we did not consider continuous BMI values and other physiological and socioeconomic features. All time-dependent variables in the model and their descriptions are shown in Table 1. The proportion of the population determined by genotype (N_{ij}, where $i, j \in \{A, a\}$) is the sum of proportion of populations with and without obesity with the same genotype (i.e., $N_{ij} = S_{ij} + I_{ij}$). The allele frequencies for a and A, c_a and c_A, are described by N_{ij} as follows:

$C_a = N_{aa} + \frac{N_{Aa}}{2}, C_A = N_{AA} + \frac{N_{Aa}}{2}$, because the gamete from homozygous (AA or aa) individuals is A or a with a 100% chance, but the gamete from heterozygous (Aa) individuals is A with 50% chance or a with 50% chance. Here we describe the most important characteristics of the model; a comprehensive description is included in the online supporting information.

(1) Birth process—The natural birth rate is denoted by v. Newborn genotype is formulated by combining maternal and paternal genotype; the maternal (and paternal) gamete receives one of the paired alleles. Assuming random mating, the proportion of newborns with a specific genotype is determined by the allele frequencies: the proportions of

newborns with genotype *aa, AA*, and *Aa* are C_a^2, C_A^2, and $2c_A\ c_a$, respectively. The childhood obesity risk is differentiated by the maternal phenotype; the risk given the mother is nonobese is k_1; if the mother is obese, the risk is k_2. The maternal phenotype (obese or not) affects the phenotype of children regardless of maternal genotype. This is called "phenotypic (nongenetic) transmission".

(2) Obesity flow rates—All individuals without obesity are at risk of becoming obese after birth. We assumed progression to obesity with two terms: *social contagious weight gain risk* and *spontaneous weight gain risk*. To model potential social draws to obesity, we applied a first-order term that is linearly dependent on the proportion of the population with obesity. β_{ij} is the coefficient for the rate of transition from a class without obesity to a class with obesity due to social contagious weight gain risk and η_{ij} is the rate due to spontaneous weight gain risk for individuals with genotype *ij*, where the susceptibility to both rates is differed by individual genotype.

(3) Removal (death) process—The model includes a differential death rate dependent on phenotype (obese or nonobese). The parameter μ represents the natural death rate of the individuals without obesity (independent of genotype) and d_{ij} is the death rate of the individuals with obesity conditional on genotype *ij*. Combining the set of processes described yields the full model (Figure 1).

Determining model parameters

The model was numerically simulated with input of baseline values and parameters. Because of the model's complexity, we simplified it so that we could better analyze it by using tools from calculus.

First we constrained the differential death rate, which translates mathematically to: $d_{aa} = d_{Aa} = d_{AA} = \mu$ (and this is justified by an epidemiological study[25]). We set the death rate equal to the birth rate, similar to a previous analysis[21]. The coefficients for the transition rate due to social contagious risk, β_{ij}, and the rate due to spontaneous weight gain risk, η_{ij}, are assumed to differ only in the homozygous *AA* subclasses (i.e., $\eta_{aa} = \eta_{Aa} \neq \eta_{AA}$, $\beta_{aa} = \beta_{Aa} \neq \beta_{AA}$). The phenotypic transmission from a mother without obesity is assumed to be zero for mathematical analysis ($k_1 = 0$).

The birth rate was obtained from publicly available records[26]. Other parameters were estimated by fitting our model to both the observed obesity prevalence data from the US National Health and Nutrition Examination Survey (NHANES)[27,28] and genotype distribution data (*aa*, *Aa*, and *AA*) from the Nurses' Health Study (NHS) (we used the *FTO* gene as a placeholder for any obesogenic gene)[16]. We used what is referred to as a shooting method to fit model parameters[29]. The shooting method is widely used to solve boundary value problems. In the estimation of model parameters, we moved the parameter values and computed the sum of squared deviations until the minimal value was realized by using the R package 'FME'. Obesity prevalence and genotype distribution in 1988 were used as initial values for simulation. We used the data from 1988 to 2007 for the parameter estimation, and the data from 2009 to 2014 were plotted to validate the model. The uncertainty of the

simulation was assessed by plotting the 95% confidence interval of the future obesity prevalence using the last 100 sets of parameters obtained during the MCMC process. To strengthen our approach, we examined whether our model could capture the observed convergence of obesity prevalence in Western countries since around 2000 using data from the United Kingdom. Obesity prevalence data are available from the Health Survey for England[30] (1993–2010 were used for estimation and 2011–2015 were used for model validation), and *FTO* genotype distribution was obtained from cohort surveillance[31] (The Avon Longitudinal Study of Parents and Children [ALSPAC], of which the participants were born in 1991–1992).

Assessment of different interventions to predict future obesity prevalence

We may be able to estimate the genetic and nongenetic effects on obesity development by conventional simulation methods in genetics, such as SIMLA, MERLIN, and PLINK[32]. However, the advantage of employing a mathematical model instead of conventional methods is that it enables us to project future obesity prevalence scenarios simply by changing parameters or initial conditions. Hereafter, after setting the estimated values of the parameters at baseline (Table 2), we investigated (1) how much the hypothetical obesogenic gene contributes to obesity prevalence and (2) how intervention programs influence future obesity prevalence. The obesity prevalence changes dynamically at first but reaches a specific value (which is determined by the set of parameters) as time goes by, and we observed this ‘converged prevalence’ or plateau to compare different scenarios. We used the best fit parameters as baseline.

(1) Genetic effect of a hypothetical obesogenic gene—In our model, the genetic effect is on the susceptibility to obesity due to social contagious risk, β, and that due to spontaneous weight gain risk, η, and both of the parameters differ by genotype. To investigate the population-level impact of those genetic effects, we observed simulations as the estimated values of β_{AA}, η_{AA} are moved toward the estimated values of $\beta_{Aa}(=\beta_{aa})$, $\eta_{Aa}(=\eta_{aa})$.

(2) Impact of obesity intervention programs—We created the above scenario to elucidate the genetic effect of a hypothetical obesogenic gene by varying parameters for individuals who possessed the hypothetical obesogenic gene. However, given that interventions to control weight usually target the whole population or are customized for individuals with specific phenotypes or demographics (obese, nonobese, pregnant, race/ethnicity, sex, etc) regardless of genotype, it may be more helpful to assess the impact of obesity intervention programs targeting the whole population or populations with a specific phenotype. In this study, we define “implementing intervention programs” as changing parameters. We assessed the impact of the following scenarios (a) impeding social contagion for whole population, (b) impeding spontaneous weight gain for whole population, and (c) managing gestational weight gain for pregnant women with obesity. (a) or (b) corresponds to reducing β or η of the whole population at the same time and (c) corresponds to reducing k_2. The above analysis for the assessment of intervention programs was carried out only for the case of the US. We used the statistical computing software R 3.3.1 and its library “deSolve” for simulation.

RESULTS

Interpretation of the numerical predictions

Before formalizing and quantifying model results, we emphasize that the model represents a 'first approximation' that incorporated several key components which are considered to be potentially important drivers of the obesity epidemic. Because we may be missing other components and drivers of the obesity epidemic we cautions that the predictions be interpreted with the model assumptions which we revisit in the discussion section.

Estimated parameters and predicted obesity prevalence

The best-fit parameters are shown in Table 2. The coefficient for the transition rate due to social contagious risk (β) and the transition rate due to spontaneous weight gain risk (η) for a homozygote of the hypothetical obesogenic gene AA was estimated to be higher than for the other genotypes (aa and Aa), which means that homozygotes for the hypothetical obesogenic gene are more susceptible to obesity. The childhood obesity risk given that the mother is obese, k_2, was estimated as 0.19 and 0.26 for the US and UK, respectively.

The obesity prevalence trajectory is shown in Figure 2A and 3A. At first, obesity prevalence continuously increases and reaches 41.03% (95% CI: [39.28, 44.31]) and 26.77% (95% CI: [25.62, 28.06]) at 2030 in the US and UK. As time evolves further obesity prevalence gradually reaches a stable state at 52.77% (95% CI: [48.69, 58.30]) and 26.84% (95% CI: [22.22, 32.62]) in the US and UK, respectively.. We can observe that the model tracks the obesity prevalence after the period used for estimation (open circles in Figure 2A and 3A). Interestingly, the prevalence converges earlier in the UK than in the US. Figure 2B and 3B show the genotype distribution trajectory, which appears nearly stable during the time period of simulation. Repeated numerical simulations confirmed that the initial obesity prevalence does not alter the converged obesity prevalence; the initial genotype distribution, however, substantially alters it.

Figure S4 (in the online supporting information) shows the percentage of new cases (or incidence) of obesity due to the social contagious risk factor among people who become obese at time t, $p(t)$ in the US. The number of individuals who become obese at time t is $\beta_{AA}I(t) + \eta_{AA})S_{AA} + (\beta_{Aa}I(t) + \eta_{Aa})S_{Aa} + (\beta_{aa}I(t) + \eta_{aa})S_{aa}$ and that because of the contagious risk is $\beta_{AA}I(t)S_{AA} + \beta_{Aa}I(t)S_{Aa} + \beta_{aa}I(t)S_{aa}$, which leads to $p(t) = \frac{\beta_{AA}I(t)S_{AA} + \beta_{Aa}I(t)S_{Aa} + \beta_{aa}I(t)S_{aa}}{(\beta_{AA}I(t) + \eta_{AA})S_{AA} + (\beta_{Aa}I(t) + \eta_{Aa})S_{Aa} + \beta_{aa}I(t) + \eta_{aa})S_{aa}}$. $p(t)$ increases as the contagious risk, in other words, the population with obesity, increases. During the course of the epidemic, about 75% of the population become obese due to the contagious risk.

Genetic effect

To see the population-level impact of the hypothetical obesogenic gene, we simulated the model varying β_{AA} from 0.184 (baseline) to 0.012, which is equal to the estimated value of $\beta_{Aa}(\beta_{aa})$ (Figure 4A). When β_{AA} was reduced to 0.012, the converged prevalence fell to 40.35%. Similarly, we varied η_{AA} from the baseline (0.0046) to the level of η_{Aa} (0.0027) and observed the converged obesity prevalence (Figure 4B). In this case, the prevalence

slightly decreased, but the impact was quite small compared with social contagious risk. The converged obesity prevalence reached 52.71% as η_{AA} reached the level of η_{Aa}.

Impact of obesity intervention programs

To see the impact of different obesity intervention programs, we compared the converged obesity prevalence by relatively changing the parameters: the coefficient for the transition rate due to the social contagious weight gain risk (β), the transition rate due to the spontaneous weight gain risk (η), and phenotypic transmission risk (k_2) in the US. Figure 5 shows the obesity prevalence when we magnified (or reduced) each obesity risk for all genotypes simultaneously, where 1 (relative change) corresponds to the estimated level of each risk. We found that the relative change in the social contagious weight gain risk modifies the converged obesity prevalence more than changing the other risk. For example, if we reduce the transition rate due to socially contagious weight gain risk to the 50% level of the baseline value, the prevalence reaches 39.60% as time goes to infinity. Meanwhile, even if the transition rate due to spontaneous weight gain risk, η, is reduced to the 50% level of the baseline, it can reach 48.00%. The effect of the intervention against the phenotypic transmission risk, k_2, is also quite limited (48.94%).

DISCUSSION

Our model describes the time evolution of obesity prevalence and the prevalence of a hypothetical obesogenic gene accounting for phenotypic and genetic heredity. When we combined empirical data with our proposed model, we found a difference in social contagious weight gain risk and spontaneous weight gain risk between homozygotes and others, which suggests that individuals with the homozygous genotype of the hypothetical obesogenic gene are more susceptible to obesity. The simulation suggested that the genetic factor is important because it modifies susceptibility to socially contagious weight gain risk. Furthermore, we found that reducing the social contagious risk factor had the biggest impact on obesity prevalence.

Although some of our results are readily applied we again emphasize that given both the reasonable and controversial (meaning we cannot judge reasonability at this stage) assumptions used to simplify the model as listed in Table S1, the results should not be interpreted without considering those assumptions. We have to be especially careful in interpreting the effect of “intervention” programs. While the model can be used to provide insight into hypothetical questions regarding, for example, the impact of policy decisions, these conclusions should be balanced against the model assumptions. Relaxing or changing these assumptions may lead to different conclusions.

Our model contains several strong assumptions. For example, we didn’t consider paternal effect. Despite this, maternal obesity may have a stronger influence on infant obesity[33] for both biological and sociological reasons: the prenatal (intrauterine) environment is a risk factor for chronic disease including obesity, and the mother-child relationship in nutrition intake is stronger than between father and child[34]. Another assumption we did not consider is other social factors or age-dependency that can affect spontaneous weight gain risk. Moreover, all of the parameters were fixed over time. We made these stronger yet reasonable

assumptions to keep the model simple and tractable, given the trade-off between complexity and tractability of mathematical models. However, incorporating these additional factors into the mathematical model is a future aim of our work.

We are not the first to model the genetic effect of obesity. Hong et al. incorporated the role of genetic effects in a mathematical model and investigated these effects on obesity prevalence[22]. This study assumed that the mortality rate of obese individuals was higher than that of normal-weight individuals and that the obesity risk is the social contagious risk only, which led them to conclude that the population with the hypothetical obesogenic gene variant (*AA* or *Aa*) would continue to decrease in the long run (1000 years later) and that "the effect of environmental factors on the dynamics of obesity are negligible." Hence, this is a good demonstration that results can differ depending on the model assumptions and study purpose.

There remains a plausibility problem regarding modeling assumptions; however, the strength of our model is that we can correct the model based on different assumptions. For example, phenotypic transmission is not uniformly supported by all recent large-scale cohort studies[35–37]. Thus, readers using the model who do not think the assumption of phenotypic transmission is acceptable can realize this in the model by simply assuming $k_2 = 0$. Also, if the assumption that spontaneous weight gain risk is time constant is not acceptable (we fixed the parameter over time because we don't know how it changes in the future), the reader can use a time-dependent function for spontaneous weight gain risk. Furthermore, it is still not well known how the *FTO* gene works on social behavior. This is the reason we set different parameters for the social contagious risk of different genotypes ($\beta_{aa} = \beta_{Aa} \neq \beta_{AA}$). If readers do not agree with this assumption, they can realize their assumption simply by setting $\beta_{aa} = \beta_{Aa} = \beta_{AA}$.

Despite these disadvantages mainly relevant to model assumptions, we note several advantages of our study. First, this is the first study proposing an obesity prevalence model that accounts for both phenotypic and genetic obesity heredity and social contagious risk in a single model. This enabled us to compare the impacts of different types of risk factors. Second, compared with conventional epidemiologic studies, we modeled the time course of the obesity epidemic, which enabled us to predict future obesity prevalence.

We have refined the mathematical framework incorporating the genetic heredity of obesity. The model assumptions in Table S1 are oversimplified and are in no way intended to undermine the complexity of the obesity prevalence, nor undermine prior studies and findings. Those findings are helpful for constructing the more valid obesity epidemic model, which will be used in predicting obesity prevalence and understanding the current and future epidemic in the US and worldwide.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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What is already known about this subject?

- Obesity is transmissible across generations through both genetic and nongenetic routes.
- The complex interactions between the risk factors for obesity makes it challenging to assess the influence of the different risk factors on obesity prevalence.

What does your study add?

- By combining our mathematical model and observational data, we were able to evaluate the contribution of genetic and nongenetic factors on obesity prevalence under varying assumptions.
- The model projected that obesity prevalence reaches 41.03% (95% CI: [39.28, 44.31]) and 26.77% (25.62, 28.06) at 2030 in the United States and the United Kingdom, respectively.
- By using simulations with different scenarios, we were able to assess plausible genetic influences on obesity prevalence across generations.

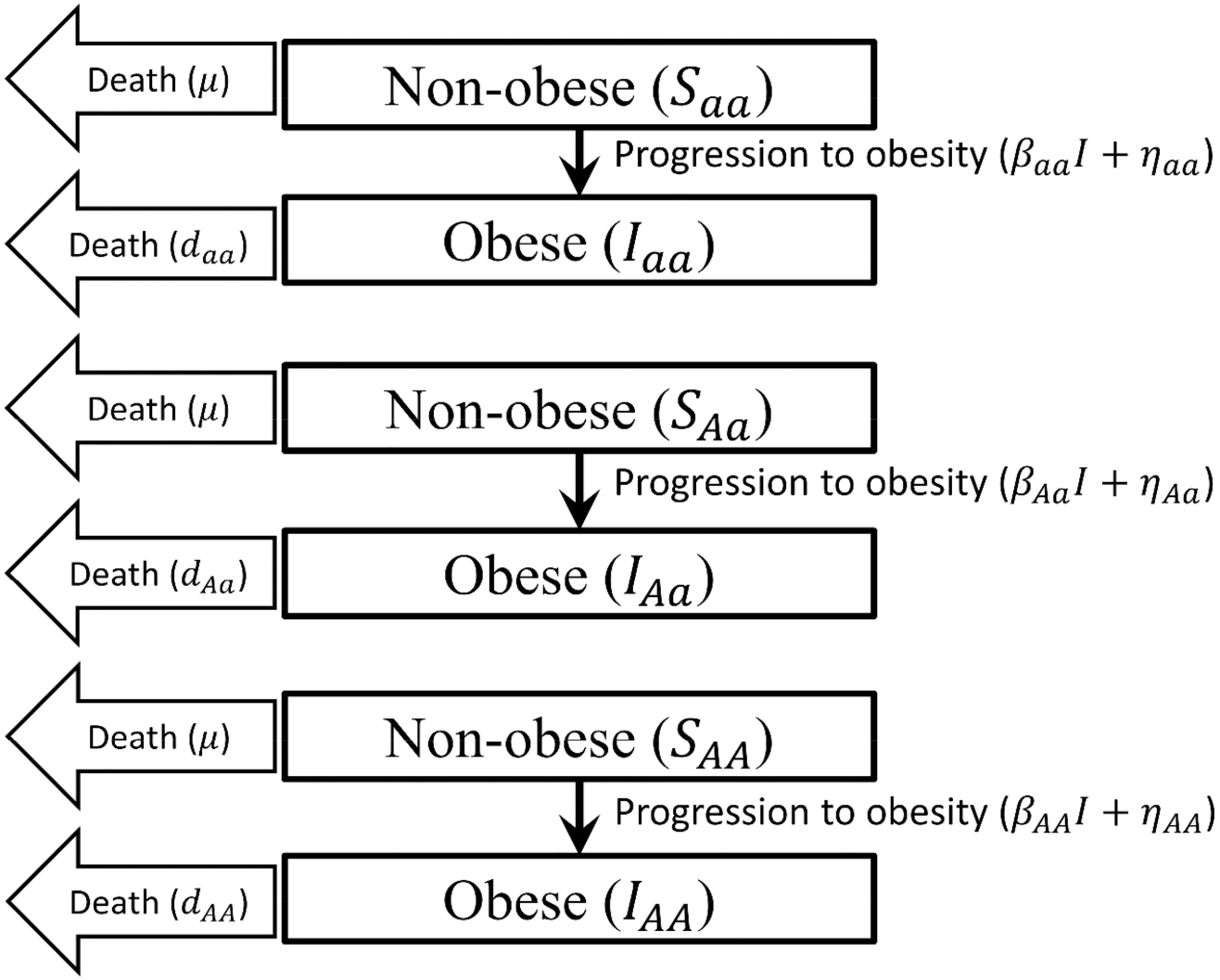

Figure 1. Schematic illustration of the obesity epidemic model

The model describes the time-variant dynamics of the population with and without obesity differentiated by genotype. S_{ij}, I_{ij} are the proportion of the population without and with obesity with genotype *ij* among the total population. The rate of transition from classes without obesity to classes with obesity is dependent on genotype.

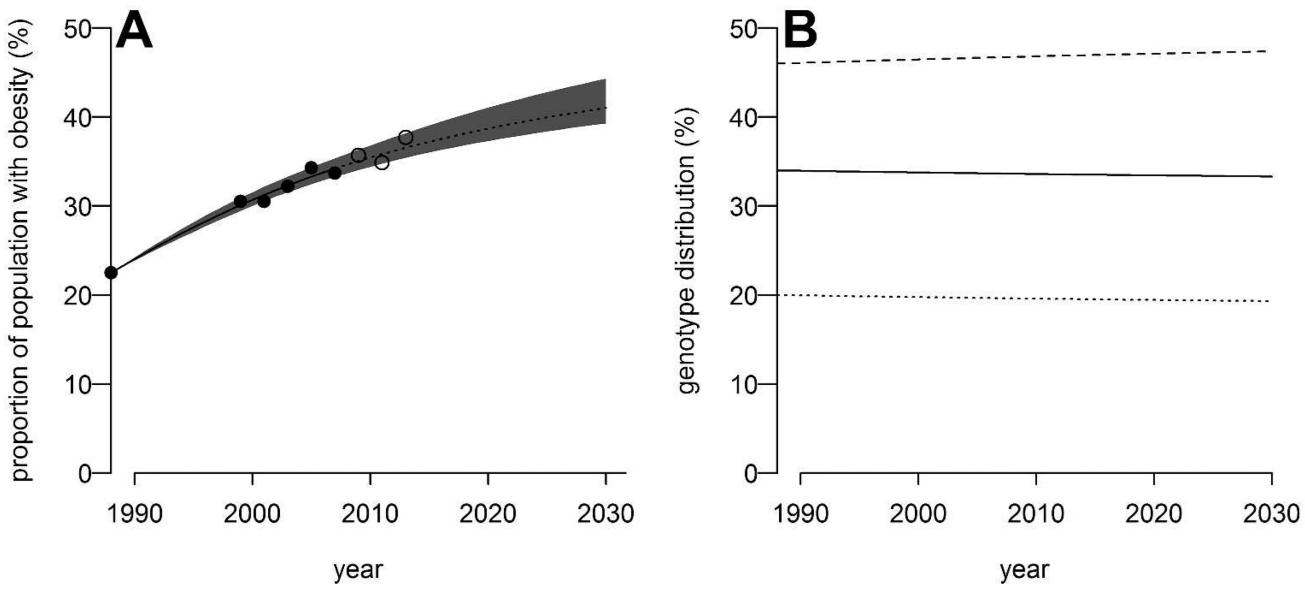

Figure 2. Obesity prevalence and genotype distribution from 1988 to 2030 in the US

(A) Obesity prevalence. The dots show the obesity prevalence from NHANES, and the line is the fitted curve realized by the parameters estimated by the shooting method[21]. The grey area shows the 95% confidence interval of the prediction. The closed circles show the data used for the parameter estimation (1988–2007) and open circles (2009–2014) are plotted for the purpose of model validation. (B) Each line shows the proportion of the genotypes *aa*, *Aa*, and *AA* among the total population.

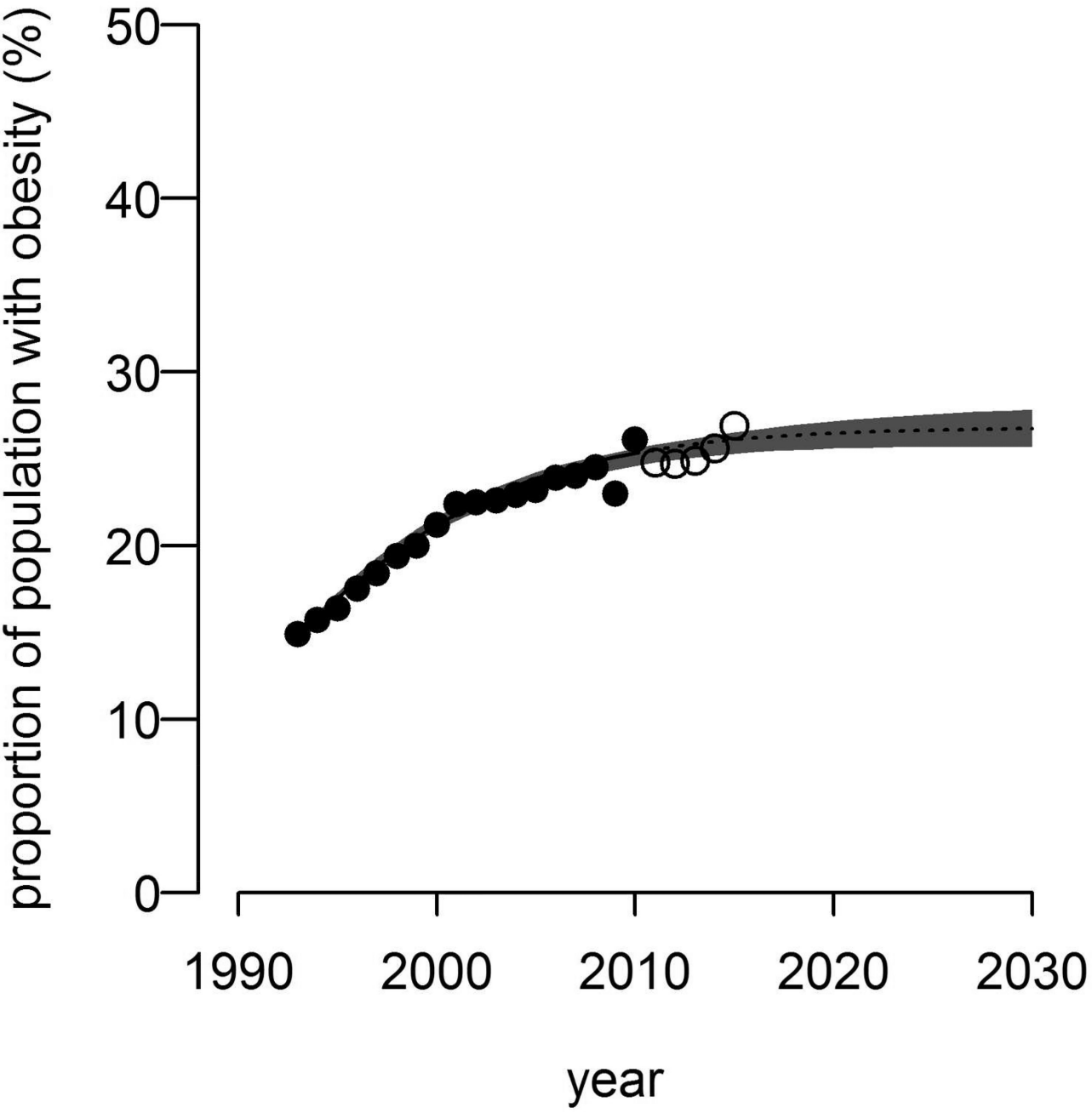

Figure 3. Obesity prevalence and genotype distribution from 1991 to 2030 in the UK

Obesity prevalence. The dots show the obesity prevalence from the Health Survey for England, and the line is the fitted curve realized by the parameters estimated by the shooting method[21]. The grey area shows the 95% confidence interval of the prediction. The closed circles show the data used for the parameter estimation (1993–2010) and open circles (2011– 2015) are plotted for the purpose of model validation.

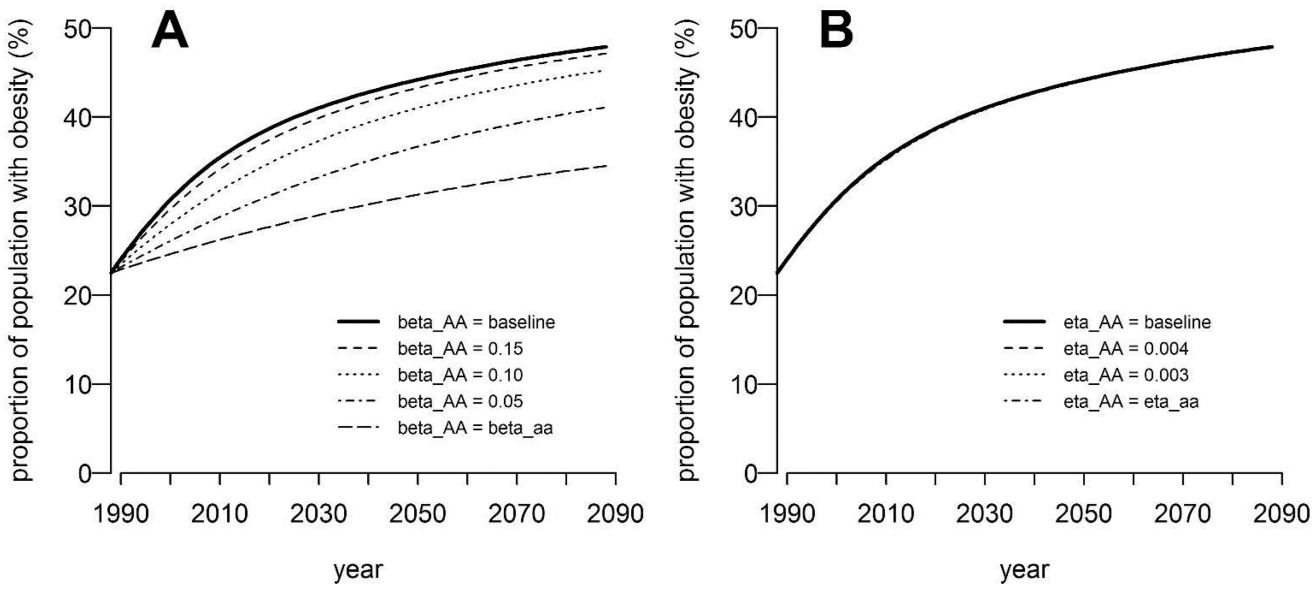

Figure 4. Simulated obesity prevalence varying the transition rate due to social contagious weight gain risk and the rate due to spontaneous weight gain risk for homozygotes of a hypothetical obesogenic gene

Each line corresponds to the time evolution of the obesity prevalence varying (A) the coefficient for the transition rate due to social contagious weight gain risk for homozygotes of the hypothetical obesogenic gene from the estimated value (0.184) to the level of that for the other genotype (0.012) and (B) the transition rate due to spontaneous weight gain risk for homozygotes of the hypothetical obesogenic gene from the estimated value (0.0046) to the level of that for the other genotype (0.0027).

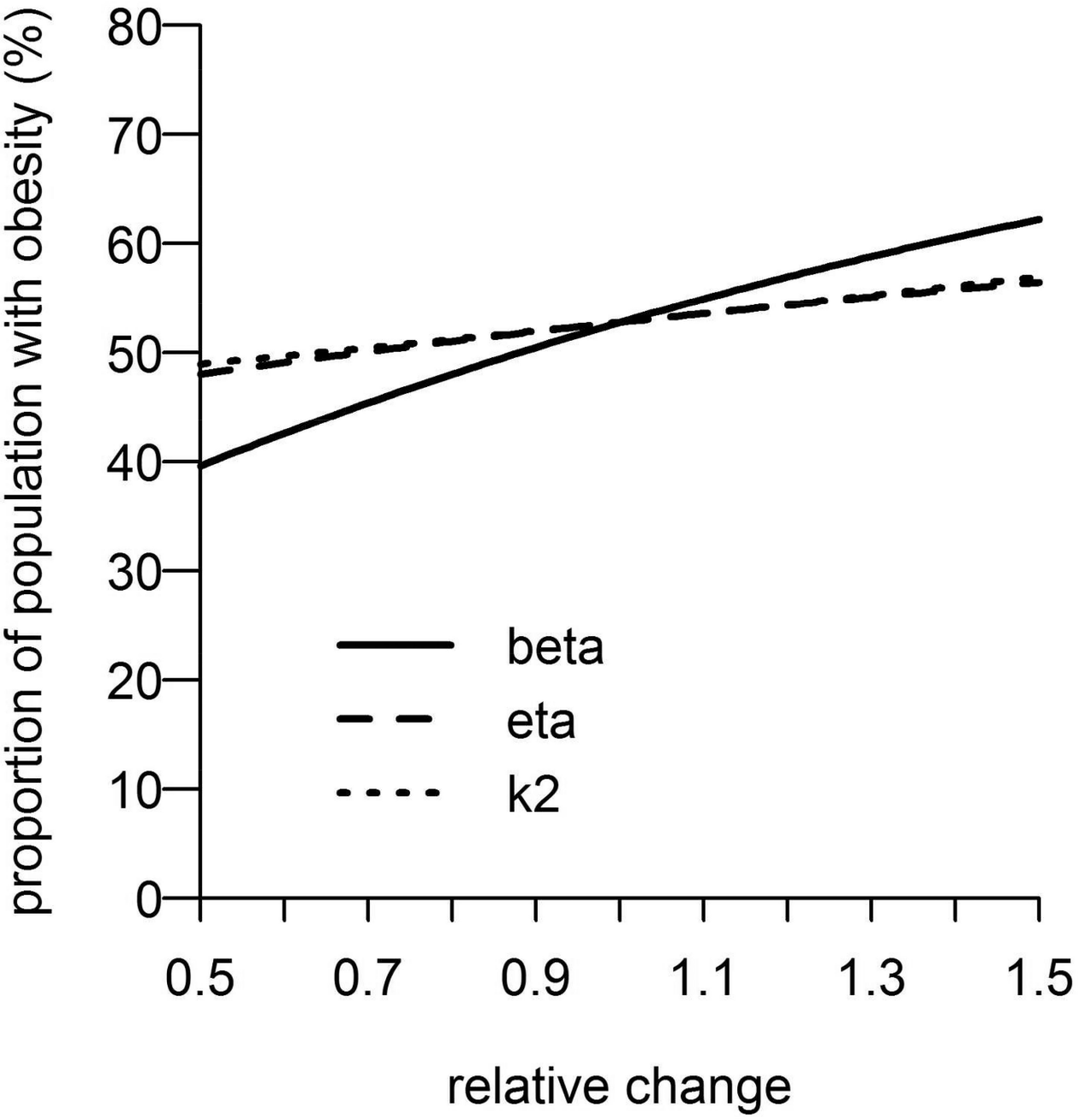

Figure 5. Converged obesity prevalence varying controllable parameters

Each line corresponds to the converged obesity prevalence relatively magnifying (or reducing) coefficient for the transition rate due to social contagious weight gain risk (β), the transition rate due to spontaneous weight gain risk (η), and phenotypic transmission risk (k_2) from the estimated values, respectively.

Table 1

Time-dependent variables in the obesity epidemic model

Variable	Description
S_{aa}	Proportion of population without obesity with no risk allele (genotype: *aa*)
S_{Aa}	Proportion of population without obesity with one risk allele (genotype: *Aa*)
S_{AA}	Proportion of population without obesity with two risk alleles (genotype: *AA*)
I_{aa}	Proportion of population with obesity with no risk allele (genotype: *aa*)
I_{Aa}	Proportion of population with obesity with one risk allele (genotype: *Aa*)
I_{AA}	Proportion of population with obesity with two risk alleles (genotype: *AA*)
N_{aa}	Proportion of population with no risk alleles (genotype: *aa*)
N_{Aa}	Proportion of population with one risk allele (genotype: *Aa*)
N_{AA}	Proportion of population with two risk alleles (genotype: *AA*)
c_a	Frequency of allele *a* among total population
c_A	Frequency of allele *A* among total population

Table 2

Baseline parameter values for the obesity epidemic model

Description	Notation	Estimated values (US)	Estimated values (UK)	Units	Method of estimation
Birth rate	ν	0.0144	0.0123	1/year	Central Intelligence Agency World Factbook[26]
The childhood obesity risk given the mother is nonobese	k_1	0.0000	0.0000	nondimensional	Assumed
The childhood obesity risk given the mother is obese	k_2	0.1901	0.1703	nondimensional	Fit to initial trends
Coefficient for the transition rate due to social contagious weight gain risk for the individuals with genotype aa and Aa	β_{aa}, β_{Aa}	0.0122	0.0054	1/year	Fit to initial trends
Coefficient for the transition rate due to social contagious weight gain risk for the individuals with genotype AA	β_{AA}	0.1838	0.4954	1/year	Fit to initial trends
The transition rate due to spontaneous weight gain risk for the individuals with genotype aa and Aa	η_{aa}, η_{Aa}	0.00270	0.00002	1/year	Fit to initial trends
The transition rate due to spontaneous weight gain risk for the individuals with genotype AA	η_{AA}	0.0046	0.0117	1/year	Fit to initial trends
Death rate	μ	0.0144	0.0123	1/year	Assumed to be same as birth rate