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Letters to the Editor

Authors' Response to Kaufman and Muntaner

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We thank Kaufman and Muntaner (K&M) for their interest in our work. In our response we have not addressed their ideological comments; instead we concentrate on rationale, empirical data and statistical analysis. In our study we asked: 'Why do brighter people tend to live longer?' To test this empirical question, we turned to three samples of twin data.

All data have limitations. We devoted several paragraphs to discussing those in our data; one anonymous reviewer noted the 'honestly portrayed results'. We were constrained to analysing data from twin pairs where at least one member had died and we noted that this reduced mortality variance. We also stated that ideal data would include intelligence assessed in childhood, completed mortality data and much larger samples.

Regarding statistical analysis, K&M claim that, by reporting results of null hypothesis testing rather than effect size estimates, we do not follow current conventions. This is an odd complaint since, as readers can see, we report only effect size estimates and no results of null hypothesis tests, in the abstract.

Concerning K&M's complaint that we have no direct measures of genes or environments, the power of pedigree-based studies of trait (co)variation is that genetic parameters can be estimated without information on individual genes or their effect sizes. Concerning the equal environments assumption in general, empirical data based on most twin studies ever published point to little or no influence of shared environmental factors on twin similarity.[1] K&M assert that the equal environmental similarity assumption invalidates our analysis of twin data. In fact, as we stated in our paper, monozygotic (MZ) twins are more likely to have more similar environments than dizygotic (DZ) twins, but this is because they create this greater similarity. The most comprehensive published evaluation of equal environmental similarity, based on environmental characteristics outside the twins' control, concluded that the available evidence supported the validity of the assumption.[2] With respect to our samples in particular, there is nothing in our ascertainment scheme that implies differential selection on twin zygosity.

K&M mention collider variables, but the essential information on which we base our inference is summarized in Figure 1. We do not claim that the slopes in Figure 1 are unbiased estimates of their population parameters, but rather draw conclusions about the differences between them.

It is correct that imputed missing data have different variance to observed data. K&M further state that if imputation and selection cause a greater bias in DZ than MZ twins, then the genetic contribution will be exaggerated.

Yet we find no evidence of the differential effects by zygosity that K&M expect. The mean and standard deviation (SD) lifespan in pairs, where one co-twin's data were imputed, differed minimally by zygosity for both twin 1 (MZ, 84.47 ± 7.55; DZ, 85.1 ± 7.65) and twin 2 (MZ, 85.09 ± 7.32; DZ, 85.22 ± 7.82) ($P > 0.05$); interaction effects between zygosity and cohort were also absent.

All methods make some assumptions, but we are no longer restricted to twin and adoption studies to probe genetic influence. Direct measures of DNA variation in large population samples can be exploited to test the same scientific questions. Shared genetic influences among dissimilar traits (pleiotropy) are widespread, in humans and other species. For example, a recent genetic analysis using data on over 112 000 unrelated people in a large population-based sample (thus no environmental covariance) showed shared genetic aetiology between cognitive functions and physical and mental health.[3] These kinds of analyses side-step twin methods, yet deliver broadly consistent findings.

K&M make an astonishing claim that the investigation of the health-related consequences of general cognitive ability has no place in epidemiology. Here, we refer the readers to Lubinski and Humphreys [4]

> It is time that measures of general intelligence be given the opportunity to reveal fully the scope of their scientific and practical significance. They should be incorporated into broad-spectrum epidemiological and social science investigations of human phenomena ... For general intelligence to remain unassimilated into much of the social sciences is scientifically indefensible. For many disciplines, it may even be scientific malpractice.

Cognitive epidemiology is the field of study that explores links between intelligence, health and mortality.[5,6] It includes exploring multiple pathways and mediators between scores on cognitive tests and outcomes that include low-level measures, such as C-reactive protein levels,[7] and higher-order traits such as cardiovascular disease.[8] A theoretical logic provides a useful framework for considering the empirically discovered links between intelligence and health. This framework is useful in generating empirical research questions such as ours. The theory is this: cognitive test scores are an indicator of overall brain function. Overall brain function is affected by the number, or load, of harmful mutations. Harmful pleiotropic mutations also influence measurable physical traits (such as heart, liver or kidney function). Brain function and physical traits may be genetically correlated to a small, but discernible, extent through the mechanism of overall mutation load and pleiotropy. This logic has been explored in detail in a paper focused on psychiatric traits.[9] Differences in measurable adversity (such as being malnourished in childhood), habits such as smoking and workplace hazards such as pollutants: each of these may create links between brain function (indexed by cognitive test scores) and physical health. Resolving these relationships and their causes is an empirical project, one that is advancing as we develop new experimental designs and analytical methods. We will learn more about the links between intelligence and life expectancy by welcoming new approaches.

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