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2013 study on happiness and gene expression flawed, new research shows

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Credit: Bill Kuffrey/public domain

(Medical Xpress)—In 2013, a paper published in the *Proceedings of the National Academy of Sciences* suggested that people who pursue happiness by seeking pleasure, rather than by searching for meaning, experience changes in gene expression similar to those experienced by people suffering from chronic stress. Nicholas Brown of the New School of Psychotherapy and Counseling in London and his colleagues reviewed

the study and found it flawed. Their critique also appears in *PNAS*.

According to the earlier study, led by Barbara Fredrickson of the University of North Carolina at Chapel Hill, hedonists, people who seek happiness through pleasure, show changes in patterns of activity in 53 genes. People suffering from illness-inducing chronic stress also experience the same changes in gene activity. On the other hand, eudaimnonists, people who seek happiness through meaning, do not experience these epigenetic changes. News of the study spread throughout the media, with major news outlets reporting that seeking pleasure rather than meaning in life could make you physically ill.

Brown and his team questioned the validity of the study and examined it closely. They noted that the sample consisted of just 80 white American adults. The materials used to generate the results consisted of just one questionnaire on well-being, reliant on self-reporting and not originally designed to measure eudaimonism or hedonism, and one biological sample, taken one time only, from each participant. The researchers pointed out that well-being can be a permanent state or a temporary one, with eudaimonic well-being more likely to be permanent and hedonistic well-being more likely to be temporary. If well-being changes over time, a gene sample taken after the state of well-being has changed might not be relevant.

Other problems with the earlier study included the use of an inventory of minor health problems over the prior two weeks to control for the possible effects of ongoing infections or gene expression associated with the immune response and the use of previous work by one of the coauthors to choose the 53 genes, out of a possible 20,000, to examine.

Brown's team found yet more problems with the study's statistical analysis. People who scored high on questions supposed to identify hedonists also scored high on items supposed to identify eudaimonists.

When the team created random groupings of questions, to divide the subjects into two meaningless categories, they were able to identify characteristic patterns in gene activity for each category.

The researchers state that, because of its remarkable, unsubstantiated claims and its appeal to the popular media, the previous study was irresponsible.

More information: A critical reanalysis of the relationship between genomics and well-being, Nicholas J. L. Brown, *PNAS*, DOI: 10.1073/pnas.1407057111

Abstract
Fredrickson et al. [Fredrickson BL, et al. (2013) *Proc Natl Acad Sci* USA 110(33):13684–13689] claimed to have observed significant differences in gene expression related to hedonic and eudaimonic dimensions of well-being. Having closely examined both their claims and their data, we draw substantially different conclusions. After identifying some important conceptual and methodological flaws in their argument, we report the results of a series of reanalyses of their dataset. We first applied a variety of exploratory and confirmatory factor analysis techniques to their self-reported well-being data. A number of plausible factor solutions emerged, but none of these corresponded to Fredrickson et al.'s claimed hedonic and eudaimonic dimensions. We next examined the regression analyses that purportedly yielded distinct differential profiles of gene expression associated with the two well-being dimensions. Using the best-fitting two-factor solution that we identified, we obtained effects almost twice as large as those found by Fredrickson et al. using their questionable hedonic and eudaimonic factors. Next, we conducted regression analyses for all possible two-factor solutions of the psychometric data; we found that 69.2% of these gave statistically significant results for both factors, whereas only 0.25% would be expected to do so if the regression process was really able to identify

independent differential gene expression effects. Finally, we replaced Fredrickson et al.'s psychometric data with random numbers and continued to find very large numbers of apparently statistically significant effects. We conclude that Fredrickson et al.'s widely publicized claims about the effects of different dimensions of well-being on health-related gene expression are merely artifacts of dubious analyses and erroneous methodology.

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