Review of: "Correlations between Socioeconomic Status (SES) and Biogeographic Ancestries: Indirect Evidence of SES Model Misspecification"

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Potential competing interests: No potential competing interests to declare.

Even though I have not yet conducted any biogeographic ancestry admixture studies myself, I am an attentive recipient of all genetically informative studies (heritability, genetic markers, SNPs, ancestry, indirect indicators, etc.). Traditionally, these studies work with individual data (e.g., twin studies) and measure abstract heritabilities or correlations with genetic markers (usually without information on specific genes and their causal pathway).

Biogeographic ancestry admixture studies produce correlations with evolutionary origins. Initially, this is not information about genetic influence. For example, one could correlate sex (XY or XX) with hair length and find a high correlation. Nevertheless, the sex difference between men and women in hair length could still be explained purely culturally, namely through different ideals of beauty. These ideals of beauty could, in turn, have an evolutionary component, which has to be clarified theoretically. Long story short, correlations with biogeographic ancestry do not provide clear evidence of genetic influence, so environmental factors should be controlled for empirically and theoretically.

However, if high correlations are found between certain characteristics and biogeographic ancestry and these correlations are otherwise not taken into account in research, then one can speak of a possible bias in this research. And correlations with biogeographic ancestry provide indirect evidence for possible genetic influences, particularly when other relevant environmental factors have been controlled and the association with biogeographic ancestry still exists.

This is exactly where the study by Gregory Connor, John G.R. Fuerst, and Meng Hu comes in. It does not simply examine the relationship between socioeconomic status (SES) and biogeographic ancestry using a new sample, but has conducted a meta-analysis of the many single studies available to date. To do this, they searched for studies according to the usual methodological standards (documented in detail in the appendix), evaluated them for usability, calculated mean correlations, also for subgroups, and looked for outliers. Tables and figures present the mean results. The reported correlations are not high, but consistent.

Some suggestions:

In the abstract, include the average result (correlation in*r*), the final number of studies (k), and the final number of subjects (*N*).

This should be added to the abstract (also with an average correlation): "correlation estimates on samples restricted to

African-American SIRE and to Hispanic-American SIRE show essentially the same patterns as unrestricted samples". (Table 8)

It should also be emphasized (in the discussion section of the manuscript as well as very briefly in the abstract) that still existing correlations within the SIRE groups are an indirect indication of possible evolutionary-genetic effects.

Table 4: Describe what correlates with what (so that a quick reader can understand it without having to read the entire manuscript).

Figure 2: Describe what correlates with what (so that a quick reader can understand it without having to read the entire manuscript).

Tables 7, 8, 9, 10: Express the results in usualr-correlations, not Fisher's Z. What correlates with what?

What is the most meaningful end result?

Take into account the problem of unpublished studies.