

<Commentary Lee & Chabris on Burkart et al. [BBS 40, 2017]>

<CT>**Genomic data can illuminate the architecture and evolution of cognitive abilities**

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<C-AB>**Abstract:** Does general intelligence exist across species, and has it been a target of natural selection? These questions can be addressed with genomic data, which can rule out artifacts by demonstrating that distinct cognitive abilities are genetically correlated and thus share a biological substrate. This work has begun with data from humans and can be extended to other species; it should focus not only on general intelligence but also specific capacities like language and spatial ability.

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In 1904, Charles Spearman discovered g , the factor measured in common by correlated tests of diverse human mental abilities. The existence of possible g homologues in other species and the extent to which the evolutionary trend in our own primate lineage can be characterized as an increase in g are among the most important issues facing researchers across the disparate fields interested in cognitive evolution. We applaud Burkart et al. for recognizing the centrality of g to any complete understanding of human and animal differences.

Burkart et al. are not alone in expressing concern over the possibility that the correlations between factors defining a statistical g (and G) might not reflect common information-processing mechanisms (general intelligence) but rather artifacts of various sorts (e.g., Hampshire et al. 2012). In humans, at least, data from twins and genome-wide association studies (GWAS) can rule out various conceivable artifacts by demonstrating that distinct abilities are genetically correlated. The existence of a genetic correlation means that there are polymorphic sites in the genome affecting both traits – either because one trait is on the causal path to the other, or because distinct causal paths emanate toward both traits from a common biological substrate (whose function is influenced by the genetic variants). Empirically estimated genetic correlations between ability tests of different kinds are as large as the simple phenotypic correlations (Kovas & Plomin 2006; Trzaskowski et al. 2013), thus pointing to common biological mechanisms. For instance, Trzaskowski et al. estimated the genetic correlation between g and a test of mathematics to be 0.74. A genetic correlation is a coarse-grained summary statistic, but in the near future we believe it will be possible to use DNA-level data to determine whether a given polymorphic site is associated with multiple abilities in a manner consistent with a common mediating mechanism (van der Sluis et al. 2010).

The methodology of GWAS is enabling this revolution because certain special properties of genomic data – such as the natural randomization of genotypes within the offspring of the same parents – enable a high degree of trust in the causal inferences that can be drawn from it (Lee 2012; Lee & Chow 2013; Lee et al. 2016). Unfortunately, genetic

methods along these lines may be somewhat difficult to apply to nonhuman species because of the large sample sizes required for adequate statistical power (Chabris et al. 2015). Even in the face of this obstacle, however, indirect progress may be possible. In recent work, we identified a large number of polymorphic sites in the human genome associated with educational attainment, a heritable trait (Heath et al. 1985) that is genetically correlated with both g and intracranial volume (Okbay et al. 2016). More specifically, we found that sites associated with education are much more likely to be found in regions of the genome annotated as likely to affect gene expression in the brain. Armed with such predictive functional annotations, we may be able to determine whether a substitution of one allele for another that has occurred at any point in mammalian evolution would be likely to affect educational attainment – even if the site of the substitution is not polymorphic in modern human populations.

There are outstanding methodological issues with this approach, such as which parts of the genome should be used as a control for purposes of determining whether likely g -affecting sites have undergone an unusual number of base-pair substitutions that would be consistent with the action of natural selection (e.g., Dong et al. 2016). More work also needs to be done to ensure that the functional annotations truly predict causal effects on g or some cognitive trait rather than other intermediate phenotypes (e.g., personality traits like neuroticism) that are also genetically correlated with years of education in modern Western societies. If these issues can be addressed, however, then many powerful inferences become possible. For instance, we may be able to find evidence of directional selection increasing g in the human lineage or a correlation between the number of

substitutions from the time of the common ancestor to the present and the rank of a taxon in some measure of G (Johnson et al. 2002). Such findings would bolster many of the points tentatively advanced in the target article, including the identification of the statistical g/G factors in other species with general intelligence in *Homo sapiens*.

We also urge Burkart et al. and other researchers to consider important ability factors other than g . The correlations between distinct human abilities can be attributed to their common measurement of g , but the “error” or “residual” inherent in each ability when it is regarded in this way is also of substantive interest. The authors mention the CHC model of these lower-order factors; setting aside various controversies over terminology and substance, we single out two of these factors because of their ecological validity in the prediction of human behavior (Kell et al. 2013; Lee & Kuncel 2015). The factor that we will call Verbal Comprehension is characterized by tasks requiring the translation of meanings into verbal units (words, sentences, discourses) and vice versa. Burkart et al. do not emphasize human language, but the search for its evolutionary antecedents has raised many issues – including whether language is independent of other cognitive capacities – that may be illuminated by an interdisciplinary approach (Hauser et al. 2002; Pinker & Jackendoff 2005; Hurford 2007). We call the other non- g factor of interest Spatial Visualization, which is characterized by tasks requiring the mental transformation of representations of objects and scenes in a manner preserving spatial relationships. We suspect a relationship between spatial visualization and tool manufacture analogous to the one between verbal comprehension and language; confirming such a relationship may prove to be a worthwhile research program.

Given the prominence of both language and tool manufacture in human evolution, we are intrigued by the prospect of a mapping between these two capacities and the two arguably most important lower-order ability factors in the hierarchy of human individual differences. Of course, these are not the only abilities relevant to human evolution; various aspects of social cognition, such as face recognition and theory of mind, should also be explored. But in any case, it is now time for this line of research to incorporate and make maximal use of the abundance of genetic data that is becoming available.

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