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DEFINING GENETIC DETERMINISM: THREE OLD CONCEPTS, ONE NEW PROBLEM AND A MODEST PROPOSAL

Abstract: *In this paper, I assess whether certain concepts of genetic causation, namely, the "gene for a trait," norm of reaction and heritability can capture a feasible version of genetic determinism in the postgenomic era. The result is mostly negative, due to the various shortcomings of those concepts. "Gene for a trait" is obsolete because it implies monogenic causality for human behavioral traits. Norm of reaction, although theoretically the best alternative, is not an option in human subjects, due to ethical considerations. The strength and the weakness of heritability lies in its being obtained by non-experimental methods. The advantage is that it is compatible with polygenic inheritance models and can be estimated by non-experimental methods. The disadvantages are related to its causal interpretation, especially in humans. Besides, the missing heritability problem demonstrated that modern genomic methods like genome-wide association studies come short on accounting for the causal paths from genomes to highly heritable traits. Based on the new understanding of genetic causation, I define a weak form of genetic determinism.*

Keywords: *genetic determinism; reaction norm; heritability; missing heritability; GWAS*

Definice genetického determinismu: Tři staré koncepty, jeden nový problém a skromný návrh

Abstrakt: *V tomto článku hodnotím, zda určité koncepty genetické příčinnosti, konkrétně „gen pro znak", norma reakce a dědičnost, mohou zachytit proveditelnou verzi genetického determinismu v postgenomické éře. Výsledek je většinou negativní, a to kvůli různým nedostatkům těchto konceptů. „Gen pro znak" je zastaralý, protože předpokládá monogenní kauzalitu pro lidské behaviorální znaky. Norma reakce, ačkoli je teoreticky nejlepší alternativou, nepřichází u lidských subjektů v úvahu z etických důvodů. Síla i slabina dědičnosti spočívá v tom, že se získává neexperimentálními metodami. Výhodou je, že je kompatibilní s polygenními modely dědičnosti a lze ji odhadovat neexperimentálními metodami. Nevýhody souvisejí s její kauzální interpretací, zejména u lidí. Kromě toho problém chybějící dědičnosti ukázal, že moderní genomické metody, jako jsou celogenomové asociační studie, jsou nedostatečné při zohledňování kauzálních cest od genomů k vysoce dědičným znakům. Na základě nového chápání genetické kauzality definuji slabou formu genetického determinismu.*

Klíčová slova: *genetický determinismus; reakční norma; dědičnost; chybějící dědičnost; GWAS*

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1. Introduction

Genetic determinism seems to be a resolved issue in the 21st century. The so--called interactionist consensus has become common parlance. At the very least, we do not frequently encounter crude deterministic ideas that were popular in the early 20th century Mendelian genetics, such as monogenic explanations of social ills.

Charles Davenport,[1] an American geneticist and an ardent defender of eugenic projects, published a paper on the genetic basis of nomadism, in which he defined the condition as a sex-linked Mendelian trait. Nomadism in the US was the lifestyle of so-called hobos, homeless, unemployed young men who wandered from one state to another by train, making a living by begging, stealing or working in temporary jobs. Davenport classified it as a form of feeble mindedness, a popular psychological diagnosis of cognitive deficit, considered to underlie various social problems like pauperism and criminality. At around the same time, others, such as Henry Herbert Goddard and Lewis Madison Terman, were advertising the view that intelligence, as measured by IQ tests, was an innate ability that runs in families and was unmodifiable by environmental means.[2]

Davenport, like many other eugenicists of his time, had transformed a social problem into a biological one, to be solved by enforced sterilization. In the US, the eugenics program had resulted in confinement of the "feeble minded" in institutions or worse, in enforced sterilization.[3] The eugenic vision was carried to its extreme by the Nazis in Germany. Nazis were not only confining or sterilizing those with "genetic" defects, but they ran a program to eradicate them altogether, by euthanasia.

Those dark days are long over. Eugenicists' simplistic Mendelian explanation of social traits now looks as preposterous as astrology or demonic

[1] C. B. Davenport, "The Feebly Inhibited. II. Nomadism or the Wandering Impulse, with Special Reference to Heredity," *Proceedings of the National Academy of Sciences of the United States of America* 1, no. 2 (1915): 120–22. Davenport was the president of the Eugenics Record Office at the time of this publication.

[2] Henry Herbert Goddard, *The Kallikak Family: A Study in the Heredity of Feeble-Mindedness* (New York: The Macmillan Company, 1912); Lewis M. Terman, *The Intelligence of School Children: How Children Differ in Ability, the Use of Mental Tests in School Grading and the Proper Education of Exceptional Children* (Boston: Houghton, Mifflin & Company, 1919). The chapter on the hereditarian theory of IQ in Gould's *The Mismeasure of Man* contains a detailed historical sketch of similar misuses of genetics in psychometric intelligence research: Stephen Jay Gould, *The Mismeasure of Man* (New York: W. W. Norton, 1996).

[3] Siddhartha Mukherjee, *The Gene: An Intimate History* (New York: Scribner, 2016).

possession. But the tensions surrounding the issue of the genetic determination of human behavioral traits have not disappeared completely. In the early 2000s, the hype of the Human Genome Project led to sensational statements about genes for sexual orientation, genes for psychological diseases, genes for aggression, genes for intelligence, etc. However, the next two decades buried the hopes for simple genetic explanations for complex traits. They were replaced by a more balanced view, where massive numbers of genes with weak and unspecific associations to complex traits became the norm. What does genetic determinism mean under these conditions? This is the main question that I want to answer in this paper. But first, let me mention one typical definition of genetic determinism:

> Genetic determinism promotes morally problematical claim that *socially significant* traits, traits we care about, such as gender roles, violence, mental illness, intelligence, are *fixed* by the genes and not much alterable by environment, learning or other human intervention.[4]

This definition resonates with Davenport's and other eugenicists' vision but in contemporary debates, no one holds such extreme and simplistic beliefs. No scientifically informed thinker believes in the absolute fixity of all behavioral characters and more importantly, the influence of the environment in the development of those socially significant traits is conceded by everyone – hence the interactionist consensus. However, the interest in the genetic basis of socially significant traits did not fade away. Is there a form of genetic determinism worthy of discussion in the 21st century, or what remains from that perspective?

Genomic technologies such as Genome Wide Association Studies (GWAS) make it possible to trace the gene variants that "influence" behavioral phenotypes like IQ or educational attainment.[5] The framework emerging from modern genetics is different from the old school eugenics, but genetic

[4] Alexander Rosenberg, *Darwinian Reductionism, or, How to Stop Worrying and Love Molecular Biology* (Chicago: University of Chicago Press, 2006), 222.

[5] Jonathan R. I. Coleman et al., "Biological Annotation of Genetic Loci Associated with Intelligence in a Meta-Analysis of 87,740 Individuals," *Molecular Psychiatry* 24, no. 2 (2019): 182–97; James J. Lee et al., "Gene Discovery and Polygenic Prediction from a Genome-Wide Association Study of Educational Attainment in 1.1 Million Individuals," *Nature Genetics* 50, no. 8 (2018): 1112–21; Aysu Okbay et al., "Polygenic Prediction of Educational Attainment within and between Families from Genome-Wide Association Analyses in 3 Million Individuals," *Nature Genetics* 54, no. 4 (2022): 437–49.

determinism of a different sort, with thousands of tiny genetic effects determining "who we are" is still popular among some behavioral geneticists.[6,7]

In this paper, I will evaluate three concepts related to genetic causation, namely, gene for a trait, heritability, and norm of reaction, to make sense of genetic determinism. I will try to show that none of these concepts can define genetic determinism that can survive in this era. In the last section, I will offer a weaker and up to date version of genetic determinism that I believe to be worthy of consideration.

2. Gene for X: Two Definitions

One of the connotations of the phrase "gene for X" is that few alleles of major effect can determine physiological, anatomical and even behavioral traits. This is a nonstarter for almost any interesting human trait. Proposing genes that correspond to complex behavior has served a rhetorical function after the demise of Davenport style eugenics. A historically influential example of such rhetoric can be found in Dawkins's *The Selfish Gene*.[8] Genes for altruism, selfishness, alarm calls, etc. were proposed without any precautions.[9] Later, Dawkins [10] felt the need to clarify his position and moderated some of his claims. His later definition of "gene for X" is a good starting point, for it relies on Fisher's idea of the average effect of a gene substitution and his infinitesimal model.[11]

[6] Nathaniel Comfort, "Genetic Determinism Rides Again," *Nature* 561, no. 7724 (2018): 461–63; Robert Plomin, *Blueprint: How DNA Makes Us Who We Are* (Cambridge, MA: MIT Press, 2018).

[7] One insider critique of Plomin style determinist ideas is Kathryn Paige Harden. In one of her papers, she criticizes Plomin for using polygenic scores as fortune tellers K. Paige Harden, "'Reports of My Death Were Greatly Exaggerated': Behavior Genetics in the Postgenomic Era," *Annual Review of Psychology* 72, no. 1 (2021): 48.

[8] Here the almost 50 years old Dawkins reference might look outdated, but his understanding of genetic causality (i.e., probabilistic difference-making) reflects the idealizations used by most population geneticists, and especially R. A Fisher fairly well. Fisher's infinitesimal model is a foundational idea for modern association studies.

[9] Richard Dawkins, *The Selfish Gene* (New York: Oxford University Press, 1976).

[10] Richard Dawkins, *The Extended Phenotype: The Gene as the Unit of Selection* (Oxford: W. H. Freeman & Co, 1982).

[11] R. A. Fisher, "XV. – The Correlation between Relatives on the Supposition of Mendelian Inheritance," *Transactions of the Royal Society of Edinburgh* 52, no. 2 (1919): 399–433; R. A. Fisher, "Average Excess and Average Effect of a Gene Substitution," *Annals of Eugenics* 11, no. 1 (1941): 53–63.

According to Dawkins, genetic causation is no more "deterministic" than environmental causation. More importantly, Dawkins stated that genetic causes are not *different in kind* from environmental causes. An event C is the cause of an event R means:

1. C is reliably followed by R
2. Experimentally producing C events will lead reliably to R events.
3. Knowledge of C will provide a more accurate prediction than the ignorance of it, regarding the question of whether R events will happen or not.[12]

In the context of genetics, event C would correspond to a gene substitution whereas event R would be a corresponding change in the phenotype. Reliable association means neither necessity nor a strong association. It just means that the probability of R happening given that C happened is higher than the probability of R happening when C did not happen if every other variable is held constant. In the genetic context, this means that having a certain version of a gene raises the probability of having a certain trait, on average. Genetic causes are not insulated in the process of development. Thus, genetic effects and environmental effects are not categorically different from each other.

Dawkins's views on genetic causation, as summarized above, do not promote a problematic form of genetic determinism. But when it comes to defining "a gene for X," his ideas are ambiguous. Dawkins equated "genetic variation for a trait X" with "gene for X" and presented this as an "inevitable," "routine" practice in genetics.[13] This equivocation is a source of confusion. "Genetic variation for X" is synonymous with "gene for X" only if the trait X is monogenic and this conflicts with the qualifications he made about genetic causation.

Apart from this ambiguity, which I suspect to be originating from a confusion between genes in population genetics with genes in developmental contexts,[14] Dawkins provides a very liberal concept for the "gene for X":

[12] Dawkins, *Extended Phenotype*, 11–12.
[13] Ibid., 21.
[14] This distinction roughly corresponds to Dupré's distinction between genes for phenotypic traits (differences), Moss's preformationist vs epigenetic gene distinction (gene-p vs gene-d) and Griffiths and Stotz's Mendelian vs material genes: John Dupré, "15 What Genes Are, and Why There Are No 'Genes for Race,'" in *Processes of Life: Essays in the Philosophy of Biology*, ed. John Dupré (Oxford: Oxford University Press, 2012); Lenny Moss, *What Genes*

> A gene for X is a version of a certain region of the genetic material, which raises the probability of having the trait X in comparison to the alternative versions of that region, ceteris paribus.

It is obvious that this differs from a monogenic trait like *Drosophila* eye color or tallness/dwarfness in Mendel's peas. The genetic basis of the trait includes many genes with small effect and the total set of those genes are not transmitted as a unit. In this sense, tallness/dwarfness or red/white alleles of Mendelian genetics are at one extreme of a spectrum and an allele with an infinitely small average effect would be at the other end.

Another concept, more like typical Mendelian disorders, has been offered by Kenneth Kendler in the context of psychiatric genetics.[15] He defines the conditions for the validity of the statement "X is a gene for Y" as follows: "If X has a strong, specific association with disease Y in all known environments and the physiological pathway from X to Y is well understood, then it may be appropriate to talk of X as a gene for Y."[16] The strength of association is similar to the penetrance of an allele. High penetrance for a gene implies that the probability of having the trait is high if the gene is present. But a strong association also means that the probability of having the respective gene is also high, given that the trait is present. Mendelian (monogenic) disorders conform to this scheme. For complex traits like psychiatric conditions, there are no Mendelian genes in this deterministic sense. It is possible to have the gene without having the trait and it is also possible to have the trait without having the gene.

The second condition is the condition of specificity. According to this condition, the gene version (X) should specifically influence the respective trait (Y) and nothing else. Let us begin from a counterfactual example. Suppose that a mutation causes blindness. Blindness also inhibits reading, watching TV, and understanding facial expressions. Can we say that the gene which is mutated is a gene for understanding facial expressions? Certainly not, because the mutation does not cause a specific deficit in this capacity. Ignoring pleiotropy – a single gene influencing many traits – has led to fallacious attributions of function in animal genetics.

Can't Do (Cambridge, MA: MIT Press, 2003); Paul Griffiths and Karola Stotz, *Genetics and Philosophy: An Introduction* (Cambridge: Cambridge University Press, 2013).

[15] Kenneth S. Kendler, "'A Gene for…': The Nature of Gene Action in Psychiatric Disorders," *The American Journal of Psychiatry* 162, no. 7 (2005): 1243–52.

[16] Ibid., 1245.

In *Drosophila* behavioral genetics, many genes that were discovered to be specifically related to certain behavioral tendencies, were found to have other functions as well. For instance, *dunce* was thought to be a gene for associative conditioning, but it turned out to be functional in embryonic patterning and female fertility.[17] Another gene, *latheo,* was thought to be responsible for associative conditioning but it also took part in imaginal disc formation and cell proliferation in the central nervous system. The same is true for the so-called genes for geotaxis. Pleiotropy is the rule rather than the exception.

More surprisingly, there was no overlap between the genes found to affect wing development discovered by artificial mutagenesis and selection experiments.[18] In other words, the intentionally mutated genes which affect a trait are different from those which are associated with the trait after 80 generations of selection. The upshot is that a similar phenotypic variability can be achieved by mutating a non-overlapping set of genes. Thus, the causal relation of a gene variant to a trait of interest is not one-to-one in most cases.

In psychiatric genetics, the situation is similar except that we cannot compare artificial mutations with natural variation. A gene variant found to be associated with a specific disease is also associated with other diseases. For instance, serotonin receptor gene variants are associated with schizophrenia as well as bulimia and anorexia. A dopamine receptor variant raises the probability of both schizophrenia and Bipolar Disorder.

These observations tell us that genetic changes are not so specific in their effects. This is because genes do not do anything in isolation and our trait (e.g., disease) categories are not fine grained enough, which brings us to the third criterion proposed by Kendler. This condition is the noncontingency of association between a gene and its phenotypic outcome. The condition is aimed to ensure that the effect of a gene should not depend crucially on an environmental factor, as in cases where the social environment picks certain genetic traits and differentially treats their bearers, regardless of the functional connection between the gene and the resultant trait. For example, skin color might be genetic, and discrimination based on skin color might lead to low income. However, skin color genes do not count as "income genes" in any intuitively reasonable concept of genetic causation.

[17] Ralph J. Greenspan, "The Flexible Genome," *Nature Reviews Genetics* 2, no. 5 (2001): 383–87.
[18] R. J. Greenspan, "Selection, Gene Interaction, and Flexible Gene Networks," *Cold Spring Harbor Symposia on Quantitative Biology* 74 (2009): 131–38.

The causal proximity condition can be understood better if we compare the "gene for X" concept with the inborn errors of metabolism. According to Garrod, some mutations block certain biochemical pathways and thus, result in specific deficits.[19] It is safe to call some gene variant a gene for a trait when we know the biochemical steps from the gene product (e.g., enzyme) to the ultimate phenotype. Alkaptonuria and other inborn errors of metabolism were of this sort. The "one gene one enzyme" hypothesis was also proposed in this spirit. The question is whether we have such biochemical knowledge on the etiology of complex phenotypes such as behavior. We are not even close to it.

According to the criteria given above, there are no genes for complex and interesting traits. Thus, the "gene for X" concept is not suitable for defining contemporary versions of genetic determinism. The Mendelian few-to-few scheme of representing genotype-phenotype relations is just one of the possible models. There are other means to deal with complex causal relations between genotypes and phenotypes. Norm of reaction is a concept developed to deal with such complex cases.

3. Norms of Reaction

Phenotypic properties being fixed by genotypes and their being unmodifiable by environmental intervention are at the core of the debates concerning genetic determinism. But what does it mean for a phenotypic character to be fixed by the genotype?

Let us begin with the most typical examples: single gene disorders. Cystic Fibrosis (CF) is an autosomal recessive disorder caused by mutations in the CFTR gene. Patients show pancreatic insufficiency, pulmonary infections, sterility, and other symptoms with varying intensities. It is a single gene disorder, but its severity and the comorbidity of symptoms associated with the disease are influenced by at least two other factors, one in the first chromosome and one in the 19th chromosome.

When a child inherits two copies of the mutated-dysfunctional copies of the CFTR gene, it is inevitable that the disease will show up at a certain stage of development. There is, however, a phenotypic variability in the severity of disease. Some of this variability can be attributed to the variability

[19] Archibald E. Garrod, *Inborn Errors of Metabolism* (London: H. Frowde and Hodder & Stoughton, 1909).

in the mutations in CFTR. There are almost 900 different dysfunctional alleles of CFTR.[20]

A peculiar character of single gene disorders is, as said above, that they occur whatever the environment one lives in. Severity is influenced for sure by environmental as well as purely stochastic factors, but the disease phenotype cannot be undone by means of changing the diet or any similar environmental intervention.[21] A more definite condition is that one cannot get the disorder without having the genes. There is no such thing as an environmentally induced CF. There is obviously a linear, deterministic causal relation here. How does such a case show up in a norm of reaction?

A norm of reaction (NOR) represents phenotypic variation as a function of environmental *and* genetic variables. NORs are usually depicted as two-dimensional figures where the abscissa is some environmental variable of interest and ordinate represents the phenotypic variable. With respect to the concept of norm of reaction, to say that a trait is fully determined by genes is to say that the norm of reaction for that trait is flat.[22] A flat NOR means that modifying the environment has no effect on the phenotype.

Suppose that G1 is the genotype with two defective CFTR alleles and G2 is the genotype with two normal alleles. Let the ordinate represent the level of pancreatic insufficiency and abscissa represent the level of some environmental variable. To build a NOR, individuals with the genotypes G1 and G2 are raised in a range of environments and their level of pancreatic insufficiency is measured in each environment. The resultant function is the NOR, and if it is flat, the trait is said to be totally under genetic control.

The case so far seems simple enough. But even in the case of monogenic disorders, matters get complicated when one looks at the details. First, phenotypic variability cannot be mapped neatly onto genetic variation.

[20] Ayman El-Seedy and Véronique Ladeveze, "CFTR Complex Alleles and Phenotypic Variability in Cystic Fibrosis Disease," *Cellular and Molecular Biology* 70, no. 8 (2024): 244–60; Daniel L. Hartl and Andrew G. Clark, *Principles of Population Genetics* (Sunderland, MA: Sinauer Associates, 2007).

[21] There are various exceptions to this description, where the causal variant leads to the aberrant phenotype only under certain environmental conditions. The case of phenylketonuria (PKU), a monogenic disorder that can be remedied by restricting the intake of phenlylalanine, is one such example.

[22] Philip Kitcher, *In Mendel's Mirror: Philosophical Reflections on Biology* (Oxford: Oxford University Press, 2003); Paul E. Griffiths, "The Fearless Vampire Conservator: Phillip Kitcher and Genetic Determinism," in *Genes in Development: Re-Reading the Molecular Paradigm*, eds. Eva M. Neumann-Held and Christoph Rehmann-Sutter (Durham, NC: Duke University Press, 2006), 175–98.

The severity of the CF cannot be mapped neatly onto the different mutant versions of the gene. Knowing which of the 900 CFTR alleles (along with a knowledge of the alleles at two other locations) a patient has does not give precise information for a physician to predict how severe the complications will be.

The central problem with invoking NORs in the debates about genetic determinism is that there are no NORs for human traits. NORs are acquired by experimental intervention. Individuals are raised in controlled environments. It is ethically unacceptable to raise human infants in environments of a researcher's choice. The only thing that can be done is to look for statistical associations between certain environmental variables and the variability in the presence/absence or the level of expression of a trait.

NOR has been offered as a model that has richer information content concerning the causal relations between genotypes, environments, and phenotypes.[23] This rich content is obtainable only if many dimensions of the environment are controlled and many genotypes are raised in those environments. In the end, the aim of constructing a NOR is to gain global causal-functional knowledge about the genotype-environment-phenotype relations.[24] Global causal knowledge requires complete NORs: ideally, a multidimensional function which incorporates matchings between many possible environments with many possible genotypes. It is theoretically possible to construct multidimensional NORs with prior knowledge of possible causal factors.[25] This is done by building computer simulations. However, constructing a NOR by experimental methods is much more difficult than estimating it by computer simulations.

In experimental practice, a NOR is usually obtained by a much simpler method. NORs are constructed by raising individuals with different genotypes in *two* environments and then connecting the two mean phenotypic values by a straight line [26]. The slope of this straight line is considered to show the degree of phenotypic plasticity (i.e., environmental modifi-

[23] R. C. Lewontin, "Annotation: The Analysis of Variance and the Analysis of Causes," *American Journal of Human Genetics* 26, no. 3 (1974): 400–411.
[24] Gry Oftedal, "Heritability and Genetic Causation," *Philosophy of Science* 72, no. 5 (2005): 699–709. As Oftedal correctly observed, global-causal knowledge was the benchmark against which Lewontin judged heritability analysis.
[25] Philip Kitcher, "The Transformation of Human Sociobiology," *PSA: Proceedings of the Biennial Meeting of the Philosophy of Science Association* 1986, no. 2 (1986): 63–74.
[26] Massimo Pigliucci, *Phenotypic Plasticity: Beyond Nature and Nurture* (Baltimore: Johns Hopkins University Press, 2001).

ability) of the genotype. Although there are multidimensional models for constructing NORs, it would be difficult to interpret the biological meaning of the mathematical function for that NORs and finding a NOR with a "reliable fit" in a multidimensional state space – there are many possible curves that can fit the environment/genotype/phenotype matchings and the NOR is the curve with the best fit – would require a very large data set.[27] In short, practical constraints force researchers to use simple two-dimensional NORs with only two environments, and the phenotypic values in the intermediate environments are filled in with a linear function drawn, without even using regression.

Despite these difficulties, NORs in model organisms provide ample evidence against a simple genetic determinist view of development. For instance, in Drosophila developmental genetics, serious genotype-environment interactions in diet response have been illustrated by using a reaction norm approach.[28] There is no reason to suppose that human behavior would be an exception to this, and in this regard, NOR is a useful concept to illustrate the degree of phenotypic plasticity. The problem is that it is too demanding in human behavioral genetics.

NORs have been originally invoked against the importance attributed to the results of ANOVA (analysis of variance) studies in human behavioral genetics.[29] In those studies, the core measure of the degree of genetic determination of a trait was heritability. NOR has practical shortcomings as I tried to show. Heritability escapes some of them – the need for experimentation – but it has its own set of problems, which are more serious that make a causal interpretation almost impossible.

3.1 Heritability and Genetic Causation

Heritability is the proportion of phenotypic variance that can be predicted from genetic variance. Despite being derived from the analysis of variance, it is commonly interpreted as a causal concept, especially in behavior genetics. Phenotypic variance (i.e., mean square of deviations from the phenotypic mean= VP) can be partitioned into three components: variance due to genes (VG), variance due to environment (VE) and error variance (e). Thus, ANOVA for a metric trait is expected to give this equation:

[27] Ibid., 8.
[28] Mirre J. P. Simons and Adam J. Dobson, "The Importance of Reaction Norms in Dietary Restriction and Ageing Research," *Ageing Research Reviews* 87 (2023): 101926.
[29] Lewontin, "Annotation."

VP = VG + VE + e. Gene-environment interaction (VGE) can also explain some proportion of the phenotypic variance. So, an adequate equation will be VP = VG + VE + VGE + e.

VG can further be partitioned into variance due to additive genetic effects (VA), variance due to dominance (VD) and variance due to interaction among genes in different loci (VI). The sum of these constitutes the board-sense heritability of a trait. Thus, board-sense heritability is VG/VP (=H). Narrow-sense heritability is the measure of phenotypic variance due to additive gene effects. It is given by the formula VA/VP (=h). Broad-sense heritability is said to be "the extent to which individuals' phenotypes are *determined* by the genotypes."[30] In this regard, it is apparently more important for the discussions on genetic determinism, however, in human behavior genetics and especially in genome-wide association studies, additive genetic variance (narrow-sense heritability) has been at the center stage. Here, additive means that the contributions of allele substitutions on the total variation in a population are *statistically independent from each other and the environment*. In other words, it can be treated as an aggregate measure of individual genetic effects.

Heritability can be estimated by experimental methods in animal and plant breeding. VG and VE can be measured by holding either the environment or the genotype constant and thus, nullifying their contribution to the total variance. One possible way to do this is to standardize environments. Quantitative geneticists can follow the other road: keep genotypes constant and see how environments influence the phenotypic outcome. This is achieved by using inbred lines, which are thought to be identical in almost every loci. The variance in such a line should solely be environmental. In such a case, VG will be calculated by VG = VP – VE.

Without controlled environments, the only clue to heritability is the correlation between trait values in diverse types of relatives. In humans, heritability has traditionally been estimated by family-based methods such as twin studies. In general, the degree of relatedness and heritability is key to explaining the observed correlations between relatives. Identical twins are supposed to share their complete set of genes, and fraternal twins share half. Thus, we would expect that the identical twin correlation to be twice the fraternal twin correlation if the trait is 100% heritable. However, it should be possible to distinguish between genetic and environmental causes of correlations (e.g., cultural transmission) to make an accurate estimate of herit-

[30] Douglas Scott Falconer, *Introduction to Quantitative Genetics* (Harlow: Longman, Scientific & Technical, 1989), 126.

ability. As Lewontin et al. have noted,[31] these two sources are conflated in the human case due to the lack of experimental control over environments. In twins-raised-apart style studies, part of the correlation can be explained by the fact that adopted twins and non-adopted twins lived in similar environments, sometimes in the same neighborhood, meeting each other frequently.

The estimation of heritability involves conceptual problems, additivity being the central issue. The environmental sensitivity of every genotype in a heterogeneous population might be different.[32] When estimating heritability in such a population, VG might be overestimated because some genotypes deviate from the mean not solely due to their genetic properties but also the specific interactions with the environment. In other words, there might be genotype-environment interaction, which will bias the estimation towards more genetic variance and less environmental variance. The additivity of genetic and environmental sources of variance can no longer be assumed if there is significant gene-environment correlation or gene-environment interaction.

Gene-environment correlation is a confounding factor which results from the nonrandom matching between certain genotypes and certain environments. The presence of GE correlation changes the equation to $VP = VG + VE + 2Cov(G, E)$. The last term is the term for the covariance of environments and genotypes. There are three types of gene-environment correlation. The first is passive GE correlation where the phenotypes of conspecifics (e.g., parents) influence the environment of the individuals (children) differentially which further leads to phenotypic differences. Dynastic effects, maternal effects or genetic nurture all point out to this type of indirect "genetic" influence, which leads to certain genotypes being differentially found in certain environments. It is passive because the genotypes of progeny have no power in determining the environments provided by the parents. This type of correlation is mostly considered to be a part of environmental variance.[33]

[31] Richard C. Lewontin, Steven P. R. Rose, and Leon J. Kamin, *Not in Our Genes: Biology, Ideology, and Human Nature* (New York: Pantheon Books, 1984).

[32] Not only the environment but also the genotypic background can be controlled in experimental organisms, as using inbred lines would homogenize this important confounding factor. This is also missing in the human studies.

[33] The so-called hereditarians prefer to give a genetic explanation to passive GE correlations such that the environment provided by the parents is itself explained as the expression of the parents' genotype. There are numerous examples of this reasoning and the most radical version – the socioeconomic environment of a country explained by race specific genotypes – coming from scientific racists such as Richard Lynn Cyril Burt, *The Backward Child* (New

Reactive GE correlation happens when the correlation is still imposed by the environment, but the environment is sensitive to genotypic differences between individuals. Douglas Falconer points that cows with high milk yield are given more food than cows producing less milk.[34] This creates a positive correlation between milk yield and food consumption. The heritability of milk yield is nearly 0.27, which suggests that there is a significant genetic component of the differences in milk yields.[35] If this is the case, dairy workers' decision to give more food to better cows is partially sensitive to the genetic differences. The environment (husbandry workers) is reacting differently because of genetic differences. In this case, variance is taken as genetic:

> The covariance, in practice being unknown, is best regarded as part of genetic variance because the nonrandom aspects of the environment are a consequence of the genotypic value and so an individual's environment can be thought as part of its genotype.[36]

This case is different from passive GE correlation because genes of the target individuals are part of the causal story. In passive GE correlation, target individual's genotype has no direct or indirect effect that explains phenotypic variation, in the reactive one, genes are mediating causes and partitioning of causal responsibility depends on the concept of causality employed as well as the specifics of the scenario. If, a non-agentive, difference-making concept is employed, the "causal structure" would be similar to active GE correlation and the correlation would be subsumed under VG.[37,38] If an intuitive,

York: D. Appleton-Century Company, 1937); Richard J. Herrnstein and Charles A. Murray, *The Bell Curve: Intelligence and Class Structure in American Life* (New York: Free Press, 1994); Richard Lynn and Tatu Vanhanen, *IQ and Global Inequality* (Augusta, GA: Washington Summit Publishers, 2006); Saskia Selzam et al., "Comparing Within- and Between-Family Polygenic Score Prediction," *The American Journal of Human Genetics* 105, no. 2 (2019): 351–63.

[34] Falconer, *Introduction to Quantitative Genetics*.

[35] W. G. Hill et al., "Heritability of Milk Yield and Composition at Different Levels and Variability of Production," *Animal Science* 36, no. 1 (1983): 59–68.

[36] Falconer, *Introduction to Quantitative Genetics*, 134.

[37] Kate E. Lynch and Pierrick Bourrat, "Interpreting Heritability Causally," *Philosophy of Science* 84, no. 1 (2017): 14–34.

[38] Although I agree with Lynch and Bourrat (see "Interpreting Heritability Causally") that active and reactive cases have the same "causal structure" under their definition of causality and "phenotype," I believe neither of them should be subsumed under VG in humans, if VG (and heritability) is to be interpreted causally and not merely for predictive purposes. When

commonsensical, agentive concept is employed, differential treatment by the society would be considered as causally more salient than the genetic difference itself.

More interesting cases lie in between arbitrary environmental influences and the interaction of genetic predispositions with the environments. Active GE correlations, along with GE interactions, provide such interesting cases.

Active GE correlation occurs when individuals with different genotypes actively select – or create – their environments and their choices causally depend on their genotypes.[39] Suppose that before the domestication of dogs, some wolves with a peculiar genotype tended to approach human encampments and began feeding on human waste. Further suppose that the genetic changes related to this type of behavior also reduced these breeds of wolves' hunting frequency and aggression towards humans. In addition to selecting their environments (i.e., preferring to wander around human settlements), imagine that the playful behavior of these protodogs change the behavior of humans against dogs. Playful behavior on the protodogs' side created a friendly response from humans, which propagated into other human settlements through cultural transmission and resulted in the culturally transmitted dictum "some wolves (protodogs) are the best friends of humans." This, in turn, created customs for taming dogs by special techniques. In this scenario, the behavioral difference between wild and pro-domestic wolves starts as purely genetic, and taming is a reaction that amplifies the already existing difference. The genetic difference also made protodogs prefer to live near humans. Thus, the protodogs were not just chosen due to their genetic propensities but their genetic propensities led them to choose (or even create to some degree) the most suitable environments for their phenotype. The differential sensitivity of protodogs to taming is an example of gene environment interaction.[40]

Apart from GE correlation and interaction, which might lead to overestimation of heritabilities, there are also doubts about whether heritability estimates can provide any kind of causal information at all. According to

the direct and additive genetic effects on human behavior cannot be inferred from heritability studies, we might expect further complications with indirect effects.

[39] Robert Plomin et al., *Behavioral Genetics* (New York: Worth Publishers, 2008), 318.

[40] Dog domestication acted on various genes, mostly related to central nervous system functioning and some genes related to starch digestion: Erik Axelsson et al., "The Genomic Signature of Dog Domestication Reveals Adaptation to a Starch-Rich Diet," *Nature* 495, no. 7441 (2013): 360–64.

Lewontin,[41] heritability is a local value. It is valid only for a certain population at a certain time. One problem with locality – being dependent on population parameters – is that it constrains the generalizability of heritability across populations. The problem of portability implies that even if genes are causally relevant, the relation is fragile, or "low in stability."[42] And without the possibility of "intervention studies," heritability in a certain environmental range would not tell much about the global functional relations between genotypes, environments and phenotypes.[43]

Behavior geneticists have one commonly expressed reason to continue using heritability estimates: a high heritability (e.g., 0.5) shows that there is considerable genetic influence on the trait, which can be uncovered by molecular genetic methods. Heritability estimates show a researcher where to begin digging and highly heritable traits are prime targets for identification of genes related to behavior.[44,45] We are told that the genetic mechanisms that produce behavior will be uncovered by using the techniques developed in molecular genetics.[46] The problem with this promise is that even our best methods to detect the "genomic correlates of behavioral traits" have been short on providing any kind of functional understanding. The so-called missing heritability problem is just the tip of the iceberg, a superficial manifestation of the deeper difficulties in finding out the molecular genetic basis of almost any complex human trait.

3.2 Missing Heritability and Beyond: GWAS and Genetic Causation

The missing heritability problem arises out of a mismatch between what twin/family studies discover and what association studies detect. Classical quantitative genetic methods give fairly high heritability values for complex

[41] Lewontin, "Annotation."
[42] Pierrick Bourrat, "Heritability, Causal Influence and Locality," *Synthese* 198, no. 7 (2021): 6689–6715.
[43] Oftedal, "Heritability and Genetic Causation."
[44] Neven Sesardić, *Making Sense of Heritability* (Cambridge: Cambridge University Press, 2005).
[45] One obvious advantage of high heritability is that it would increase the statistical power of association studies and thus, would lead to smaller samples to be adequate for detecting genetic signals: Alexander Gusev, "A Molecular Genetics Perspective on the Heritability of Behavior and Group Differences," 2023, http://gusevlab.org/projects/hsq/. However, the causal interpretation of those "genetic" signals rehearse the same conceptual problems with heritability itself, the assumption of additivity being the basic shortcoming.
[46] Plomin, *Blueprint*.

human traits whereas the most up-to-date genomic method – namely, genome wide association studies (GWAS for short) – detects many variants that can explain only a small fraction of those heritabilities.[47] This original formulation of the problem is further extended to the lack of mechanisms that connect single nucleotide polymorphisms (SNP) with phenotypic variation, and the lack of an actionable level of predictive power.[48] Before handling these key issues, we might mention the historical roots of the problem.

Early association studies were performed in small samples, and the main question was whether variation in quantitative traits were due to few large effect variants or many small effect variants.[49] Early studies confirmed the former, but when the same studies were conducted in larger samples, it was discovered that there were many more QTLs with smaller effects and more importantly, the effect sizes discovered beforehand were exaggerated. These results gave support to a model with few genes of high effect and many genes with small effects. This type of genetic architecture might be called the exponential architecture because there is an exponential distribution of effect sizes and number of genes involved.[50]

Given the exponential model, the expectation in human medical genomics was to find those high effect variants. If a marker is tightly associated with a large increase or decrease in a quantitative trait, it is reasonable to search for the genes responsible for the change, in the vicinity of that marker. These genes are candidate genes. There were initial successes such as the case of the epsilon 4 apolipoprotein (*APO*E4*) variant in late onset Alzheimer's disease but as more and more such studies were conducted, almost all candidate genes were rejected because the results of earlier studies could not be replicated.[51]

GWA studies were introduced in the 2000s as a high resolution, hypothesis free method for detecting the genetic basis of complex traits such as body mass index or schizophrenia. The high resolution of GWA studies is a result of using hundreds of thousands of single nucleotide polymorphisms

[47] Brendan Maher, "Personal Genomes: The Case of the Missing Heritability," *Nature* 456, no. 7218 (2008): 18–21.
[48] Lucas J. Matthews and Eric Turkheimer, "Three Legs of the Missing Heritability Problem," *Studies in History and Philosophy of Science* 93 (2022): 183–91.
[49] Cecelia M. Miles and Marta Wayne, "Quantitative Trait Locus (QTL) Analysis," *Nature Education* 1, no. 1 (2008): 208.
[50] Jonathan Flint and Trudy F. C. Mackay, "Genetic Architecture of Quantitative Traits in Mice, Flies, and Humans," *Genome Research* 19, no. 5 (2009): 723–33.
[51] Naomi P. Friedman, Marie T. Banich, and Matthew C. Keller, "Twin Studies to GWAS: There and Back Again," *Trends in Cognitive Sciences* 25, no. 10 (2021): 855–69.

(SNP) at once and in large samples. GWA is hypothesis free in the sense that it does not depend on prior causal knowledge on genomic locations.[52]

GWA studies were first aimed at discovering disease-associated single nucleotide polymorphisms (SNP) by comparing the differential distribution of these SNPs in the genomes of case (i.e., those having the disease) and control groups. Once a SNP with significant association is found, its position gives researchers hints where to look for causally relevant genomic regions. The number of variants discovered and replicability is much higher in GWAS than earlier methods. However, the variants discovered are inadequate for explaining the high heritability estimates found in twin/family studies. One example of this phenomenon is found in schizophrenia genetics.

The narrow sense heritability obtained by the classical methods of quantitative genetics (i.e., twin and family studies) of Schizophrenia is 0.6–0.8.[53] In a GWAS study conducted on nearly 150,000 people, 128 genomic regions have been found to be significantly associated with the condition, but these SNPs could explain only 7% of the phenotypic variation.[54] In a more recent study, SNP-based heritability was estimated to be 0.24, when all variants – significant or not – were taken into account and when the significant hits were taken into account, the variance explained was about 2% of total variance.[55] This gap in numbers is just tip of the iceberg, considering the complexity of the functional biology of the trait.

One common finding in complex trait genomics has been the extremely small effect sizes of single variants.[56] In Fisher's infinitesimal model,[57] quantitative traits (i.e., continuous or metric traits such as height) are deemed to be influenced by indefinitely many genes with infinitesimal effects for each.

[52] Peter M. Visscher et al., "Five Years of GWAS Discovery," *American Journal of Human Genetics* 90, no. 1 (2012): 7–24.
[53] Vassily Trubetskoy et al., "Mapping Genomic Loci Implicates Genes and Synaptic Biology in Schizophrenia," *Nature* 604, no. 7906 (2022): 502–8; Naomi R. Wray et al., "Pitfalls of Predicting Complex Traits from SNPs," *Nature Reviews Genetics* 14, no. 7 (2013): 507–15.
[54] Schizophrenia Working Group of the Psychiatric Genomics Consortium, "Biological Insights from 108 Schizophrenia-Associated Genetic Loci," *Nature* 511, no. 7510 (2014): 421–27.
[55] Trubetskoy et al., "Mapping Genomic Loci Implicates Genes and Synaptic Biology in Schizophrenia." The studies mentioned here are population level studies and if GWAS is carried out within families, heritabilities of almost all behavioral traits or social outcomes are almost halved.
[56] Effect size in GWAS is not a causal concept as inferred from a real or hypothetical experiment. Rather, it is the percentage of the variance predicted from having this or that version of the SNP allele Okbay et al., "Polygenic Prediction of Educational Attainment."
[57] Fisher, "XV. – The Correlation between Relatives on the Supposition of Mendelian Inheritance."

Small mean effects can easily be swept by countering effects from either the environment or the genotypic background. Thus, small effects are of little value for a causal-mechanistic understanding unless the effects add up to a significant degree.[58]

These problems led researchers to include the SNPs below the significance threshold to solve the missing heritability problem. When the additive contributions of these thousands of SNPs are taken into account, GWAS heritability increases significantly. For instance, in 2010, nearly 50 SNPs had been discovered to be significantly associated with height but these explained only 5% of the variance. When all the common SNPs were taken into account, 45% of the heritability was explained.[59] The largest study so far has identified more than 12,000 SNPs that explain 40–50% of variance.[60]

Including tens of thousands of SNPs partly solves the missing heritability problem for certain traits but it also reduces the specific information gained from GWAS. This point is also true for polygenic risk scores (PGS). These scores provide a weighted sum of thousands of SNPs for genotypic prediction, but they also move away from the goal of identifying specific causal pathways.[61] The aim of GWAS was not to account for twin/family heritabilities but to find the genetic regions related to disease and other traits. The difficulty lies not in the numbers but in their causal interpretation. Which genes influence the trait of interest and by which mechanisms were the questions GWA studies were expected to answer. Such a causal story is still missing.[62] The "mechanism gap" is still out there.[63] Without specific genetic etiologies, high heritability values would not be definitive of genetic determinism.

The phrase "genetic determinism" loses much of its significance within the new conceptual framework of genetics. The prototypical examples of genetic determinism, as exemplified by Davenport and monogenic disorders, involved a few genes with fairly strong, direct links to the phenotype. The findings of new forms of genetic analysis such as GWAS cannot be

[58] The problem might be solved by focusing on higher-level genetic entities such as gene networks or network modules rather than SNP-trait regression: Gry Oftedal, "Proportionality of Single Nucleotide Causation," *Studies in History and Philosophy of Science* 93 (2022): 215–22.
[59] Jian Yang et al., "Common SNPs Explain a Large Proportion of the Heritability for Human Height," *Nature Genetics* 42, no. 7 (2010): 565–69.
[60] Loïc Yengo et al., "A Saturated Map of Common Genetic Variants Associated with Human Height," *Nature* 610, no. 7933 (2022): 704–12.
[61] The main function of PGS is prediction rather than explanation.
[62] Eric Turkheimer, "Still Missing," *Research in Human Development* 8, no. 3–4 (2011): 227–41.
[63] Matthews and Turkheimer, "Three Legs of the Missing Heritability Problem."

interpreted by those simple models. However, if the thousands of SNPs additively influence the trait distribution in a consistent manner, there can still be a form of genetic determinism, not as "determinist" as the outdated eugenical ideas but still considering the genotype as a significant constraint on the malleability of a trait. In short, massive polygenicity just makes the "gene for X" concept obsolete, but this is not an outright refutation of genetic determinism. A more refined form of genetic determinism, which allows for genetic heterogeneity and polygenic inheritance is still defensible. This new genetic determinism will be much weaker than the older versions, but it shares two common points: individual phenotypic differences have a significant genetic component, and the success of environmental intervention depends on genetic propensities.

4. The Polygenic Pint Jug: A Weak Form of Genetic Determinism

So far, I have tried to give a precise description of genetic determinism by using three concepts: the gene for X, norm of reaction and heritability. None could give a clear-cut description of genetic determinism. Nobody can charge the so-called genetic determinists for defending a monogenic perspective in human behavior. Neither is heritability a perfect ground for defining genetic determinism. A heritability above 0.5 cannot justify the thesis that the trait in question is more a matter of genes than the environment. NOR provides theoretically the best causal representation of the relationship between genotypes and phenotypes, but it requires experimentation, which is unethical in human subjects.

Behavior genetics have traditionally handled the relationship between genotypes and phenotypes within the quantitative genetic framework. This framework did not rely on a model with a few genes of deterministic influence, as was common in classical transmission genetics. However, polygenicity did not stop genetic determinists like Arthur Jensen or Hans Eysenck from taking high heritability as evidence for the practical immutability of IQ.[64] The thesis was that heritability provided a measure of how much IQ or scholastic achievement can be modified through the environmental interventions at hand. The genotype was setting the potential, just like the

[64] Hans J. Eysenck, *The Inequality of Man* (London: Temple Smith, 1973); Arthur R. Jensen, "How Much Can We Boost IQ and Scholastic Achievement?," *Harvard Educational Review* 39, no. 1 (1969): 1–123.

volume of a pint jug sets a limit to how much milk it can carry.[65] A similar idea is being proposed, albeit in a more careful language. Polygenic scores are replacing heritabilities.[66] I will abbreviate this weak genetic determinism as WGD from now on.

The surviving elements of genetic determinism consist of two related theses. The first is that, if a trait is significantly heritable, then the individual differences can be explained by genetic differences, at least in the actual range of environmental variation. Thus, genes are actual difference makers within a certain range. This thesis, by itself, has nothing to do with determinism for sure. However, when combined with a thesis on the limits of modifiability within the actual environmental range, it leads to a weaker version of determinism. A corollary to the latter is that, despite the possibility of changing the average value of a trait in the population, or the absolute value of the trait in each individual, the relative positions of genotypes would stay the same if the intervention is generalist. For instance, if a population level nutritional improvement program is applied, the individual heights and the mean height would increase, but the ranking would remain the same. In this regard, WGD is a thesis that can be represented by non-flat but parallel NORs in a fairly limited environmental range.

The second thesis is that if the trait is significantly heritable, environmental interventions should be *gene sensitive*. In other words, interventions should take into account genetic variation of the trait and the specific genotypes of the individuals or groups. For instance, in the case of major depression, drugs that act on specific genes or receptor proteins will be more efficient than generalist environmental interventions such as changing one's stressful work environment, if the trait at least partly genetic. Another version of this thesis is that, regardless of the causal-mechanistic details or the specific genes involved, polygenic propensities differ between individuals, and these make interventions more or less likely to succeed in different individuals. For example, the genetically predicted scholastic achievement can be used to categorize children into potentially high or low achievers, and this can be used to design efficient personalized training for each individual.[67]

[65] The metaphor of pint jug originates from Cyril Burt, *Mental and Scholastic Tests* (London: Staples Press, 1947). It has been criticized by Lewontin, Rose, and Kamin, *Not in Our Genes*.
[66] Here I refer to the rhetoric function of heritability being replaced by PGS. Technically, SNP heritability is replacing narrow-sense heritability.
[67] Kaito Kawakami et al., "Exploring the Genetic Prediction of Academic Underachievement and Overachievement," *NPJ Science of Learning* 9, no. 1 (2024): 1–11.

If an individual's genetic makeup determines how to improve their conditions, such as increasing the IQ or modifying temperament to fit a preset social standard, WGD can be used to defend a personalized behavioral improvement program, or a stratified intervention strategy based on personal genomes. Such a program would give individuals the opportunity to select the "best" environments for themselves – that is, the environments best suited to their genetically determined needs and capacities. The important point is to take genetic differences seriously, rather than ignoring them, for the new genetic determinist perspective.[68]

WGD is just another way of saying that genes make a difference in behavior and social outcomes and in this regard, it is much weaker than the traditional forms of genetic determinism where genes fix the trait values. However, even this weak thesis can be objected empirically, conceptually and ethically. At the empirical side, there stands the difficulties in discovering causal variants in modern genomic methods. Most of the GWAS hits in psychiatric diseases are not proper drug targets. The case is further complicated in normal behavioral variation where the only causal-functional insight is that the potential causal genes in LD with significant hits are differentially expressed in the brain. In short, the knowledge gained so far does not allow for targeted interventions.

Conceptually, the causal interpretation of GWAS and PGS invokes similar difficulties as traditional heritability estimates faced in the 20th century. Confounding factors such as population stratification, assortative mating or vertical cultural transmission makes it almost impossible to disentangle direct genetic effects from a mixture of various weak and interacting causes. In addition to the complexity of the causal paths, the heterogeneity at the phenotypic and genetic levels reduces the chances of developing concrete causal models out of GWAS findings.[69] The same phenotype – say, being diagnosed schizophrenic or having the same IQ – can correspond to different neural structures (i.e., endo-phenotypic heterogeneity) and different genotypes (genetic heterogeneity). The causal paths would be different and hence, the models would differ.[70] This would also reduce the actionability of the findings of contemporary behavioral genomics.

[68] Plomin, *Blueprint*.

[69] Carl F. Craver et al., "Gloomy Prospects and Roller Coasters: Finding Coherence in Genome-Wide Association Studies," *Philosophy of Science* 87, no. 5 (2020): 1084–95.

[70] Heterogeneity of the genetic basis of a trait does not refute determinism: Suppose that autism is not a common disorder but a collection of rare genetic disorders. In other words, every subgroup of autistic individuals has a common genetic defect not shared by the other

WGD proponents sometimes advertise their position as an alternative to diehard environmentalism and antiegalitarian hereditarianism. For instance, Kathryn Paige Harden suggests that genes being involved in social outcomes does not imply the futility of equity-promoting social interventions. In contrast, those generalist interventions help genetically disadvantaged strata more than the general population.[71] Robert Plomin, a more straightforward proponent of WGD, offers PGS stratified education as an efficient means to educational reform and warns parents and educators about exaggerating the effects of parenting and schooling. Genetic propensities are significant factors (the strongest systematic difference-maker according to Plomin) in deciding what life-path to choose: "It seems only sane to suggest that, when you can, try to go with the grain of genetics rather than fight against it."[72] These suggestions raise ethical questions about the misuse of genomics in labeling people and groups, a reminiscent of the 20th century eugenics, despite the assurances of Harden and Plomin. Harden, for instance, proposes a distinction between the natural fact of genetic diversity and the socially imposed and value-laden social hierarchy, and suggests that the former should not be translated into the latter in a just society. Plomin, on the other hand, leaves the choice to individuals when they are realizing their genetic potential and opposes the value system where high-paying occupations or better college degrees are seen as inherently more valuable. I would expect these well-intended proposals to be ineffective in preventing society from making value judgements based on genetic worth, if PGS or any other genetic profile is used to stratify people for educational or medical purposes.

5. Conclusion

Genetic determinism is at best a vague concept. If it is described as a viewpoint akin to Davenport style eugenics, it becomes a belief with no contemporary adherents. To make it more precise and in line with contemporary genetic research, conceptual tools of genetics have been invoked. "Gene for X" locution captures the most typical form of genetic determinism – few

subgroups. But the disorder is still genetically determined, because it is assumed to be caused by a few de novo mutations with large effect sizes. One might say that Autism Type 1 is caused by the rare variant 1, Autism Type 2 is caused by rare variant type 2, so and so forth.

[71] Kathryn Paige Harden, *The Genetic Lottery: Why DNA Matters for Social Equality* (Princeton, NJ: Princeton University Press, 2021).

[72] Plomin, *Blueprint*, 103.

gene variants explaining the whole variation in a trait – but it is common knowledge that this form of explanation cannot be extended to complex traits such as human behavior. NORs, if they were available in humans, would provide the ultimate answer to the question of genetic determinism, however, multidimensional NORs are technically difficult to obtain and NORs are unavailable due to ethical reasons.

Heritability is said to provide a crude and population specific measure of genetic influence on human traits. Causal interpretation of heritability relies on unrealistic assumptions, such as additivity. Studies performed at the whole genome level, such as GWAS, were expected to identify the physical basis of heritabilities. Missing heritability problem shows that the molecular genetic basis of heritable variation cannot be easily captured. The model emerging from GWA studies is that multiple gene variants with very small effects – Fisher's infinitesimal model – is valid for almost every behavioral trait. In addition to polygenic inheritance, another complication comes from the heterogeneity of the genetic bases of these traits. The new genetic determinism is the thesis that individual differences, be they concern dimensions of social behavior or common diseases, are determined to a significant degree by genetic differences, through complex and diverse pathways.

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