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Idealisation, genetic explanations and political behaviours: Notes on the anti-reductionist critique of genopolitics

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ABSTRACT

The rapid development of genetic research, determined, among others, by the requirements of The Human Genome Project, and a gradual reorientation in the perception of the role of nature and culture in the process of shaping complex networks of human relations by some political scientists, result in the increasing application of genetic data and methods in research regarding political behaviours. One of the key philosophical objections against the studies of the genetic foundations of political behaviours is that of excessive reductionism. This is supposed to manifest itself in the inadequate selection of the level of analysis for the explained phenomenon, the incompleteness of explanations and their low utility. My findings show that this objection is not sufficiently supported by contemporary science. Both studies using classical behavioural genetic methodologies and studies using DNA-based methods show that genes most likely play a role in political behaviours. Emphasising the significance of genetic influences in the midst of multiple extra-genetic interactions generates highly idealised explanations. Using the conceptual apparatus of the deformational concept of culture, I have demonstrated that the omission of a number of important extra-genetic influences by researchers is a consequence of focusing on specific causal patterns. This omission, however, does not entail negating the influence of non-genetic factors and, importantly, it may not have to be permanent. Following this approach, if correct, the reductionism of research into the genetic foundations of political behaviours is a standard cognitive procedure applied in science.

1. Introduction

After decades of the total dominance of environmentalism, social scientists now increasingly frequently recognise the relevancy of issues concerning the role of genetic influences on the behaviour of individuals. Psychologists, economists, sociologists, and political scientists use various genetic methods to show the genetic foundations of the analysed traits. Their research is very frequently met with far-reaching scepticism resulting, as it seems, from the historical development of the respective academic fields. This situation is particularly evident in political science, where the belief that the behaviour of an individual is determined solely by environmental factors still prevails. However, interdisciplinary fields emphasising the relevance of biological factors are emerging and growing outside the mainstream of political science research. One such field is genopolitics. It was formed by introducing the data and methods using in behavioural genetics into political science studies. Its goal is to discover the genetic foundations of political behaviours.[1] Genopolitical studies can be roughly divided into two types: classical heritability studies and molecular genetic studies. The first type enables estimating the magnitude of the contribution of genetic and environmental factors to the variance of the measured trait. The following research methods are used in heritability studies: twin, adoption and family methods. The second type also provides information on the heritability of the studied trait and enables identifying gene variants or loci correlated with the trait. The two main research methods used in the molecular approach are: candidate gene association studies (CGAS) and genome-wide association studies (GWAS) (Hatemi et al., 2012; Ksiazkiewicz & Friesen, 2017).

One of the key philosophical objections against genopolitical studies is that of excessive reductionism.[2] This objection was, admittedly, the subject of intense discussion some time ago (e.g. Charney, 2008; Charney & English, 2012; Engelmann, 2010; Weiss, 2016); however, I think it warrants a reconsideration, focusing on aspects that have not been noted and/or exhaustively discussed. The excessive reductionism objection

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[1] I understand the notion of political behaviour in the broad sense; it refers to both physical and mental components of activities affecting politics.

[2] Excessive reductionism is a type of reductionism that tries to explain complex phenomena with factors that can be considered as too simple in nature. Terms of identical or similar meaning that are used in the literature are: 'unreflective', 'destructive', 'illicit' and 'greedy reductionism'.

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may result, I believe, from underestimating the role of the idealisation method in scientific research, in particular, lack of correct recognition of its application's cognitive consequences. I will demonstrate that the idealising assumptions adopted by the researchers of genopolitics are not only justified, but even necessary to meet the adopted research objectives, and that the reductionism of genetic studies, which is actually implied by the idealisation method, is a standard procedure used in science. The findings of this article, however, should not be equated with the unconditional affirmation of genetic reductionism, nor are they in any case the expression of a view that allows for the possibility of purely genetic explanations of political behaviours. Research carried out on the basis of various behavioural sciences clearly shows the importance of environment and learning in the process of the formation and shaping of behaviours in politics. In analysing the process leading from the formulation of pre-theoretical objectives to the construction of genetic explanations of political behaviours, I will use the conceptual apparatus of the deformational concept of culture introduced by Nowak (1990, 2012). Nowak treats idealisation as one of several deformational procedures applied by humans. This approach contributes to a better understanding of the essence and meaning of the cognitive method involving counterfactual simplification of the studied phenomena.

I will start by discussing the basic methodological and epistemological issues concerning the idealisation method. I will then focus on the conceptual apparatus of the deformational concept of culture, juxtaposing idealisation with the deformational procedures utilised in fields of culture other than science. In the next section, I will briefly describe examples of the studies regarding the genetic foundations of political behaviours and the manner of linking political science with behavioural genetics. I will further discuss the objection of excessive reductionism made against the studies of the genetic foundations of political behaviours. This discussion will serve as a starting point for showing the role of idealisation in research that reveals relationships between genes and political behaviours, followed by a description of the reductionism of genopolitical research. In the final section, I will summarise the presented reflections.

2. Idealisation

One of the most significant features of human cognition is its fragmentary nature. Due to our brains and minds' limited capabilities, we are unable to register and internalise all aspects of the objects and phenomena we experience. We take into account only those elements and characteristics that we see as the most important in terms of current and planned activities. This practice is present in all areas of human activity. In science, it takes the form of a deformational procedure called idealisation.

Idealisation is a subject of continuing interest for philosophers of science. The procedure for creating idealised representations (models, laws, theories etc.) of real objects can be found in: physics (Cartwright, 1983; Hartmann, 1998; Liu, 1998; McMullin, 1985), chemistry (Fernández-González, 2013; Hendry, 1998; Seifert, 2020; Tobin, 2013), geology (Shrader-Frechette, 1989), evolutionary biology (Godfrey--Smith, 2009; Love, 2010; Sintonen & Kiikeri, 1994; Strevens, 2019), ecology (Odenbaugh, 2005; Tuomivaara, 1994), economy (Mäki, 1994; Morgan, 2006; Nowak, 1989; Svetlova, 2013), cognitive science (Rantala & Vadén, 1994), psychology (Brzeziński, 1990; C. J. Lee, 2010), linguistics (Blutner, 2011; Botha, 1982; Nowak, 2000a) and history (Brzechczyn, 2009; Szwochert, 2016; Topolski, 2009). Philosophers focus on the nature of idealisation and its functions. They are also interested in the relationship between idealisation and other cognitive procedures applied in science, as well as the role and importance of idealisation in the context of the dispute regarding the epistemic status of scientific theories (Ladyman, 2008). The relationships between idealisation and abstraction (Nowak, 1990), idealisation and modelling (Batterman, 2009), idealisation and explanation (Jebeile & Kennedy, 2015), idealisation and understanding (Potochnik, 2020), idealisation and scientific realism/anti-realism (Cartwright, 1983) are just some examples of issues discussed in the literature.

2.1. Core ideas and issues

Science is full of fiction. Point mass, ideal gas, perfectly round ball, ideally smooth and spherical plane, infinite population, perfectly informed economic agents – these are just a few examples of fiction, highly useful in studying phenomena and processes within various fields of science. These constructs are called idealisations and arise when the complexity of the empirical systems studied or their conceptual representations are subject to simplification (other terms used by philosophers: reduction (Strevens, 2019, p. 1715), deformation (Nowak, 2000b, p. 110) or distortion (Weisberg, 2015, p. 98)).

The counterfactual nature of the adopted assumptions is one of the characteristics that distinguish idealisation from other cognitive strategies used in science, such as abstraction:

> An abstract description of a system leaves a lot out. But it is not intended to say things that are literally false. An idealized description of a system is a description that fictionalizes in the service of simplification, in the way described above. The idealized description is often presented verbally as a description of a real system, but not a description that is literally true (Godfrey-Smith, 2009, p. 48).

Thanks to idealisation, the analysed phenomenon is represented as if it did not have the characteristics that it actually possesses. The result is a counterfactually deformed and ontically poorer representation. Conversely, abstraction also involves ignoring certain characteristics but without any particular consequences for the representation itself. It enables obtaining the general concept from the knowledge of individual objects. The already mentioned perfect roundness of a rolling ball, which is one of the assumptions that Galileo Galilei made to explain the nature of the movement, can be used as an example of idealisation. An example of mental activity typical for abstraction can be the omission of any property irrelevant to movement, such as the colour of the ball, in Galileo's model.

The reconstruction of the research procedure, in which the idealisation method was used, shows several key stages according to Nowak (2000b, p. 111, 2012, p. 22). First, the researcher makes a division into factors that exert and do not exert influence on the analysed magnitude *F*. This creates the space of factors essential for *F*. Then, in the set of essential factors, it distinguishes two subsets: principal factors and secondary factors. By prioritising the power of influence of individual principal and secondary factors, the essential structure of *F* is created. In the next step, the subject of research is deformed by adopting idealising assumptions that ignore secondary effects. As research develops, there is an accumulation of knowledge and the emergence of new cognitive needs. The requirements for simple initial models are then increased. As a result, the process of abandoning subsequent idealising assumptions may begin. The initial models are then subject to concretisation (factualisation (Krajewski, 1977), de-idealisation (McMullin, 1985)) by gradually taking into account the previously omitted secondary factors. The process of concretisation is continued until an approximation to the facts sufficient for the specific field of science is achieved.

This reconstruction is in itself a far-reaching simplification and, therefore, requires several additions and reservations. First of all, the counter factuality of the assumptions is a necessary condition for idealisation, but no less important is the relevance of these assumptions. As well as being in some ways false, an idealised representation should also be useful. Perfect rationality of voters will not be an idealisation helpful in explaining the socio-psychological conditions of electoral behaviour, as it does not focus on the relevant causal relationships (Odenbaugh, 2005, p. 233). Secondly, the division into principal and secondary factors is not always permanent. Over time, the magnitude of the effect of individual variables may vary, as shown (for example) by climate models.

The current anthropogenic impact on the extent and rate of climate change is quite different from the impact in the period immediately preceding the First Industrial Revolution. Thirdly, the role of idealisation in the sequence of cognitive activities leading to the explanation of the target phenomenon is not always limited to identifying causally irrelevant factors. It turns out that representationally inaccurate components can be key in constructing an explanation, as shown by Jebeile and Kennedy (2015) is using the example of the analysis of cosmological hydrodynamical simulations. Fourthly, and finally, not all idealisations can be concretised. The reasons for maintaining idealising assumptions on a permanent basis may be the need to identify key causal patterns, cognitive limits and absolute computational limits (Potochnik, 2017, pp. 58–60; Rice, 2019, p. 195).

Researchers are therefore guided by different, often intertwined motivations when they introduce idealising assumptions into their models. According to Batterman (2009, pp. 428–429), the two main reasons for using the idealisation method are the need to improve the computational efficiency of the model and to increase its explanatory power. They result directly from the complexity of empirical systems. Numerous non-linear causal relationships and feedback loops effectively complicate the construction of highly detailed representations. Other reasons for using the idealisation method include temporary and absolute computational limits, as well as cognitive limits (Potochnik, 2017, pp. 47–49). The aspect nature of human cognition forces us to focus on only a few causal factors, using the techniques, tools and computational powers available at a given time. The widespread use of computer simulations in the analysis of highly complex phenomena shows how important research progress can be made when temporary computing limits are systematically overcome.[3]

2.2. Idealisation as one of the deformational procedures

The human inclination to distort empirical reality is reflected in various manifestations of cultural activity. Referring to the deformational concept of culture (Nowak, 1990, pp. 196–198, 2012, pp. 33–35), two weak-deformational procedures can be distinguished: positive and negative potentialisations and two strong-deformational procedures: reduction and transcendentalisation. When a representation has all the properties of an original object, but at least one of them occurs at a degree above the actual state, then we talk of positive potentialisation (of which an extreme case is mythologisation). The opposite situation, i.e., the presence in the representation of at least one property with a degree lower than in the original object, means negative potentialisation (of which an extreme case is ideation). A notion overestimating the actual military potential of one's own country is an example of positive potentialisation. Views that diminish the role of lobbying in perpetuating inequalities in democratic systems can, in turn, be considered examples of negative potentialisation. Counterfactually omitting some of the characteristics of the original is a procedure typical of reduction, while counterfactually adding new characteristics to an object without basis in reality is called transcendentalisation. Nazi racial hygiene was an ideology that reduced the humanity of the representatives of the persecuted ethnic groups. It resulted in reducing human individuals to a concentration camp number tattooed on the forearm. The doctrines emphasising the supernatural character of royal power can serve as examples of transcendentalisation. The image of the king as a superhuman being, anointed by God, was the foundation for the legitimacy of power in medieval Europe.[4]

Positive and negative potentialisation, reduction and transcendentalisation are of elementary nature. Their combinations occur in different areas of culture, creating deformational procedures with a higher level of complexity. The use of reduction and positive potentialisation results in fictionalisation – a cognitive activity characteristic for literature and art. Every literary character, a figure depicted in a painting or rendered in a sculpture, either because of technical limitations or as a result of deliberate action by the artist, is devoid of certain features while other features are exaggerated. The political caricature from the time of the Watergate scandal, depicting Richard Nixon as Pinocchio, is one possible example. The combination of transcendentalisation and positive potentialisation results in absolutisation – a procedure commonly used in religious and ideological narratives. It manifests itself in assigning to different deities attributes that are not possessed by real beings. Usually, these attributes appear in the maximum degree, making a given deity an infinitely perfect being in every aspect. Appropriate examples can be found in all the major monotheistic religions. Conversely, the combination of reduction and negative potentialisation is characteristic of idealisation – a method that is the domain of science. In terms of the deformational concept of culture, idealisation entails not taking into account factors considered to be irrelevant in the essential structure of the studied magnitude, as well as assuming a minimum value of other factors, whose actual value can be taken into account in subsequent stages of the study.[5] The one-shot two-person Prisoner's Dilemma game is both a product of reduction (it does not take into account the influence of, e.g. the Earth's magnetic field or weather conditions on the interaction) and an extreme case of negative potentialisation (it reduces to zero the properties that can be sensibly attributed to the interaction, e.g., the biological and psychological characteristics of the players).

3. Political science and genetic studies

For a long time, political studies have been conducted solely within the framework of the paradigm considering the mechanisms of learning and gaining experience to be the key determinants of political behaviours. Opinions emphasising the importance of biological factors have appeared in political science literature since the 1970s. The ground for the changes, which were to come a few decades later, was laid, for example, by such scholars as Merelman (1971), Peterson and Somit (1979), Schubert (1983) and Masters (1990). They were convinced that political behaviours are the result of the interaction of two great systems: culture and nature, and not the sole result of the socialisation and culturalisation processes. They pointed to the significant role of genetic mechanisms in the intergenerational transmission of political behaviours and to the urgent need to integrate the traditional approaches of political science with the perspective of political issues as biological phenomena.

Until the publication of the results of the study by Alford et al. (2005) in the *American Political Science Review*, hypotheses regarding the relationship between genetic factors and political behaviours were occasionally empirically tested (Bouchard et al., 2003; Eaves et al., 1999; Martin et al., 1986; McCourt et al., 1999). Alford, Funk and Hibbing assumed that political attitudes are heritable, i.e., they are conditioned not only by environmental factors but also by genetic ones. The results confirmed the assumptions of the researchers, showing that a part of the variance of conservative and liberal attitudes can be explained by individual genetic differences in the population. Alford, Funk, and Hibbing

[3] See Winsberg (2010) for much more detailed discussions on this and related issues.

[4] The key difference between weak- and strong-deformational procedures is that while the former merely modify the values of a given factor (quantitative transformation), the latter affect the space of properties of the object (qualitative transformation). Both weak- and strong-deformational procedures are of a counter-empirical nature, their essence is to distort reality and, as such, they constitute the foundations of all intellectual activity of man (Nowak, 2012, p. 34).

[5] The influence of both reduced and negative potentialisation factors are known to researchers. It should not be forgotten, however, that they also ignore the influence of factors of which they are not aware (the ceteris paribus condition) and which can only be identified on the basis of an examination of differences between predictions and observations (Grobler, 2006, pp. 171–174).

used the twin method, which involves comparing phenotypic characteristics between pairs of reared-together monozygotic (identical, MZ) and same-sex dizygotic (fraternal, DZ) twins. Furthermore, the twin method has been used to study the genetic foundations of such traits and phenomena as, for example, political participation (Fowler et al., 2008), the transmission of political attitudes in different stages of one's lifetime (Hatemi et al., 2009), partisan attachment (Settle et al., 2009), foreign policy preferences (Cranmer & Dawes, 2012), ideological beliefs (Kalmoe & Johnson, 2021) or associations of political attitudes with religiosity (Friesen & Ksiazkiewicz, 2015), need to evaluate (Ksiazkiewicz & Krueger, 2017) and social dominance orientation (SDO) (Kleppestø et al., 2019). Then, extended research schemes, applying the data not only related to twins, but also parents, spouses, children, relatives, and non-twin full siblings of the twins, were used to study the genetic foundations of, e.g., liberal and conservative attitudes (Bell et al., 2018; Hatemi et al., 2010), the transmission of attitudes toward inequality and system change (Kandler et al., 2012) and political orientations over the course of an individual's life (Hufer et al., 2020).

The most common objection to the twin method is the risk of overestimating the magnitude of genetic influence due to a violation of the equal environment assumption (EEA). It appears that the greater similarity in the behaviours of the reared together MZ twins is not necessarily due to genetic influences but may be dictated by identical parenting practices or a tendency to maintain closer relationships compared to DZ twins. The risk of artificial inflation of heritability may also result from epigenetic influences and the correlation between the genotype and the environment. Concerns are also raised in the literature regarding the temporal and spatial relativisation of the conceptualisation of measured behaviours (Ksiazkiewicz & Friesen, 2017).

In addition to classical heritability studies, research using more sophisticated molecular techniques is also being conducted. CGAS, which involve discovering the relationship between the variation in the nucleotide sequence at a certain specified locus in the genome and the variation in a specific phenotypic trait in the population, were used, for example, to study the relationships between the genes encoding the enzymes responsible for regulating the metabolism of serotonin and electoral participation (Deppe et al., 2013; Fowler & Dawes, 2008) and political violence (McDermott et al., 2013), as well as the relationships between the genes encoding the enzymes participating in the regulation of the activity of dopamine with political ideology (Settle et al., 2010), and partisanship and voting (Dawes & Fowler, 2009). Conversely, GWAS, which enable the analysis of hundreds of thousands of single nucleotide polymorphisms (SNPs) within the entire genome, were used in studies of conservative and liberal attitudes (Hatemi et al., 2011), political and economic preferences (Benjamin et al., 2012), as well as political ideologies (Hatemi et al., 2014).

Molecular techniques saw first applications in the research of political behaviours relatively recently, so molecular studies' results should be considered in terms of new hypotheses rather than mature and validated knowledge. Molecular techniques, like all research techniques, also have their limitations. Because of the enormous complexity of political behaviours and the small effect sizes of individual genetic variants, considerable difficulties may be experienced in detecting specific associations. However, this situation is not particularly surprising, given that political behaviours are likely influenced by thousands of genes interacting with one another and the environment. Therefore, the identified genetic markers serve only as clues to show which genomic, epigenetic and neural pathways may be significant in the emergence and formation of the analysed behaviours: 'The finding that a single genetic marker has some influence on a trait, may implicate a particular biological pathway consisting of hundreds or thousands of genetic and neurobiological mechanisms that result in hormonal release and cognitive and emotive changes, which in turn influence behaviour' (Hatemi et al., 2012, pp. 313–314).

In the analysis of the manner of linking genetics with political science, the typology of Remisiewicz (2017), originally created to discuss the types of influence exerted by biology on sociology, seems highly useful. Adapting it to the needs of the reflection presented herein, three possible types of links between biology and political science can be distinguished:

- Proper biologism – data and methods, as well as biological theories, are incorporated into political science;
- Biologism without biology – only biological theories are transposed from biology to political science;
- Biology without biologism – biological data and methods are introduced into political science without incorporating the theoretical structures of biology.[6]

The studies of the genetic foundations of political behaviours seem to point to the third method of linking political science with genetics. The transfer of genetic data and methods to political science is not accompanied by the transfer of genetic theories, which could be used in the analysis of political processes and phenomena. Genetic studies add new aspects to the structure of the political science explanatory chain, without replacing any of its links. They are, thus, far from the 'imperialist' inclinations of Wilsonian sociobiology, which postulated the lossless reduction of sociology to biology.

4. Excessive reductionism objection

A common philosophical objection against the studies of the genetic foundations of political behaviours is that of excessive reductionism. The explication of the concept of reductionism in texts critical of genopolitics is characterised by high heterogeneity and, therefore, requires detailed analysis. The allegation of excessive reductionism usually appears in the context of three arguments. The first concerns the lack of adequacy between the phenomenon explained and the adopted level of analysis. The second raises the issue of the incompleteness of genetic explanations of political behaviour. The third indicates the low explanatory utility of genopolitical studies.

4.1. Inadequacy of the level of analysis

Drawing conclusions regarding political phenomena on the basis of genetic analyses can, according to critics, be considered as reaching too far. The reason for this is the lack of consistency between the explained phenomenon and the adopted level of analysis. Explaining political behaviours by genetic factors, if not inherently impossible, is, at best, pointless – given the state of knowledge and methodological potential. The currently insurmountable obstacle is the epistemic gap between genes and behaviours. According to this interpretation, genopolitical research provides only apparent knowledge that may mislead those who are not sufficiently familiar with the issue. The problem of the proper selection of the level of analysis to the explained phenomenon was raised by Charney (2008, p. 341):

> […] different kinds of explanation are appropriate to different kinds of phenomena, and it is only a misunderstanding of the phenomenon in question that allows one to seek an inappropriate explanation for it. The same is true in science. Quantum mechanics has very little to tell us about the functioning of the human heart, and if a physicist claimed that the resolution of remaining difficulties with string theory promised greater understanding of the etiology of heart disease,

[6] More specifically, the transfer of theory from one field to another applies, in Remisiewicz's view, only to those theoretical structures that could be used to explain the behaviours of entities of a different class than before the transfer. A situation in which the theoretical structures of one field are used to explain the behaviours of entities from another field occurs, for example, in memetics and in evolutionary psychology. These fields develop explanations for a variety of social phenomena based on concepts originally applicable only to the studies of biological organisms.

we would have to conclude that he did not know what heart disease was. (Note that this phenomenon, the "irreducibility" of our scientific knowledge about the human heart to our scientific knowledge about quantum mechanics, does not mean that the heart is a mystical phenomenon, or lead to the positing of a "heart-matter dualism").

Genetic explanations of political behaviours, as well as the quantum-mechanical aetiology of heart disease, according to Engelmann (2010, p. 61), are examples of 'misguided materialism' (Francis, 2004, pp. 94–95). Although biological entities are made up of chemical components, the gradation of matter itself does not imply a cause and effect relationship between the chemical and the biological. This observation also applies to higher levels of organisation. Societies consist of social groups, which in turn are formed by biological entities. This relationship, however, does not ultimately determine the role of genetic or neurobiological factors in the process of the occurrence of social facts.

4.2. Incompleteness of the explanation

Critics of genetic studies emphasise that the concentration of research efforts on individual genes or functionally isolated sets of genes is cognitively fruitless. With such complex phenotypic traits as political behaviours, a number of different factors can be expected to exert their influence, and among them genetic factors are likely to play a lesser role:

> The cogency of the search for single main-effect genes in complex human behavior must be reconsidered. Proteins encoded by at least 266 genes are involved in variation in aggression in fruit flies, yet at the same time, the heritability of aggression is less than ~0.1 because of the high level of environmental variance (even though the researchers assumed the environments were identical). If such is the level of genetic complexity and the importance of environmental interaction implicated in behavioral variation in fruit flies, why should we assume that, when it comes to human behavior, things are any simpler? We would expect all of the factors influencing political behavior to be several orders of magnitude more complex, at least on the order of the difference between the brain of the fruit fly, with ~100,000 neurons, and the human brain, with ~100 billion (Charney & English, 2012, p. 30).

The political phenotype is conditioned by multiple interacting factors; therefore, genetic explanations are characterised, according to Charney and English, by significant incompleteness. In the midst of different interactions, exposing the meaning of genetic influences seems to be a strategy that is cognitively wrong. This view consequently leads to questioning the validity of genopolitical studies.

4.3. Low explanatory utility

The two previous arguments explicitly or implicitly undermine the validity of the search for relationships between genetic factors and political behaviours, while the argument referring to the low explanatory utility of genopolitical research demonstrates what knowledge is not provided by this research:

> […] it is impossible to explain to a blind person what colours are by telling her about the neurophysiology of colour-perception; it is equally impossible to understand why someone has certain political views by looking at her genetic asset. The answer to the question why someone has a certain political opinion is part of an entirely different 'language-game' than the answer to the question of how two people with different political views differ genetically (Weiss, 2016, p. 324).

Weiss notes that genopolitical studies do not explain the key problem for a political scientist: why individuals display one type of political activity, and not another. Charney (2008, p. 342) went one step further, illustrating his position with an example of a study of pro and contra attitudes towards the US Constitution. In his opinion, even if the explanation of the 'aetiology' of attitudes towards the constitution was correct, genopolitical theory would not answer many other extremely highly relevant questions, such as when by whom and why the constitution was written or what ideological values it promotes.

5. Genetic explanations of political behaviours

Anti-reductionist criticism of the genetic explanations of political behaviours is a conglomerate of views with a common denominator in the form of the conviction as to the fruitlessness of the efforts to discover the ultimate causes of political behaviours. After all, numerous studies show that the importance of physico-chemical mechanisms decreases with the increasing complexity of biological hierarchical systems. Therefore, in the opinion of critics, genopolitical research is founded on equally erroneous ontological and epistemological premises as the crude mechanicism of the scientific revolution or the reductionist physicalism of the nineteenth century. The reductionism of genetic explanations diminishes the role of environmental influences, which, in addition to the purely cognitive consequences, may have undesirable social consequences. The analysis of genopolitical research, however, does not confirm such conclusions. Researchers of genopolitics are aware of the high level of complexity of the analysed phenomena and the limitations resulting from this fact.

5.1. Causal complexity

Even studies of very simple organisms show how complicated a phenomenon life is. The nematode *Caenorhabditis elegans (C. elegans)* was the first multicellular organism whose genome we were able to sequence. It has attracted the attention of biologists since the second half of the nineteenth century and has been a model organism since the second half of the twentieth century, which means that it is used to study biological processes occurring not only in representatives of related species, but also in organisms on a much higher level of complexity, including humans. The adult nematode is 1–2 mm long, inhabits soils in different parts of the world and feeds on bacteria. It has over 20,000 protein-coding genes. The adult hermaphrodite body (dominant sex) consists of 959 somatic cells, of which 302 are neurons, while adult males have 1031 somatic cells, including 381 neurons (Félix & Braendle, 2010). Researchers have extensively studied not only the genome of *C. elegans,* but also its connectome and have gained knowledge about the relationships between genes, the nervous system and the developmental environment. The studies of the biological and environmental conditions of behavioural patterns in nematodes show unusual complexity and multiple levels of interactions. Schaffner (1999, pp. 73–77) summarised their results by formulating eight general principles:

1) Any neuron is the result of the activity of multiple different genes;
2) A single behavioural pattern is created by the activity of multiple neurons (neural circuits);
3) Any gene, affecting multiple different neurons, can indirectly affect many different patterns of behaviour (pleiotropic genes);
4) One neuron may be involved in the formation of multiple patterns of behaviour (multifunctional neurons);
5) Different behavioural traits in genetically identical individuals, bred under the same environmental conditions, may result from random anatomical differences in the structure of nervous systems (developmental noise);
6) Different developmental environments result in different patterns of behaviour, even in genetically identical individuals (phenotypic plasticity);
7) Gene expression depends on epigenetic factors;
8) Genes interact with each other, affecting the development of neurons and the formation of phenotypes in multiple ways (epistasis).

The image of the network of relationships between genes, the nervous system, and the developmental environment in organisms as simple as *C. elegans* can serve as a starting point for the research into organisms with higher levels of complexity. Extrapolations of the regularities identified in simple organisms to human behaviour, however, should be carried out with due caution and any conclusions drawn on this basis are subject to many reservations. Comparisons between species are, however, not unwarranted, and, in the discussed case, their value is mainly manifested in highlighting the complexity of the problem.

Although living organisms display clear characteristics of hierarchical systems, phenomena from lower levels do not necessarily determine what happens at higher levels. If we even have a full physico-chemical description of molecular processes at our disposal, it is unlikely that we will ever be able to predict the phenotypic effect at a high level of complexity. Complex systems, therefore, do not display a simple, linear relationship between cause and effect. This is due to several reasons. Apart from unusual complexity, manifested by, for example, many mutually related determinants, lack of symmetry and the influence of random events, emergent properties appear on each level of the system, i.e., properties whose existence cannot be predicted on the basis of knowledge regarding the individual components of the system. An additional complication is generated by a multiple realisation of a specific behavioural pattern. It should not be expected that higher-level properties will be realised by strictly defined sets of lower-level properties. The realising elements themselves, however, when participating in the creation of a specific behavioural pattern, may occupy different levels in the system structure in different entities.[7]

5.2. Idealised explanations

The high degree of complexity of the system and its stochastic nature implies a need for high levels of caution in drawing conclusions from the relationships identified between genes and behaviours in *C. elegans*. The interpretation of the results of studies of organisms at a level of complexity higher by several orders of magnitude becomes much more difficult. While classical heritability studies show that usually between 30 and 40% of the variation in the analysed political behaviour can be explained by genetic variation, studies using molecular techniques do not, as of yet, allow for drawing any unanimous conclusions. The reason being methodological limitations. This problem was noted by Hatemi et al. (2014, p. 292), whose study relying on GWAS did not yield positive results:

> The failure to identify significant SNPs should not be surprising. Our findings are consistent with genome-wide explorations on almost any complex trait; a single gene or small group of genes does not directly influence ideological preferences. Rather, thousands of genetic variants of very small effects and constellations of genes interact with each other and the environment to influence behavior, indirectly. For social and behavioral traits, such as political attitudes and ideologies, in which measures and definitions change as a function of time, location and climate, sample size and measurement limitations present a challenge. Even if we could ensure the perfect measure, the plethora of relevant individual genes and their complex interactions with other genes, as well as the environment counsel against expecting that any individual genetic markers could explain a sizable amount of the genetic variance in political temperament and without a very large sample, identifying genes of small effects is unlikely. Our findings are consistent with this polygenic expectation, and spur us to gather larger samples.

Two previous GWAS-based studies (Benjamin et al., 2012; Hatemi et al., 2011) also failed to identify specific polymorphisms; however, estimates of heritability obtained in one of these studies partially corroborated heritability estimates from twin-based studies (Benjamin et al., 2012). Small sample sizes are a major problem with GWAS conducted to date. They did not exceed several thousand individuals. In comparison, GWAS conducted to identify genetic variants associated with income (Hill et al., 2019), social stratification (Abdellaoui et al., 2019) and educational attainment (J. J. Lee et al., 2018) were based on the sample sizes of, respectively: 286,301, 456,426 and 1,131,881 individuals.

The magnitude of the difficulty of discovering associations between single genes and political behaviours was also demonstrated by replications of CGAS-based studies. For example, the results obtained by Fowler and Dawes (2008) were only partially confirmed. The relationship between the polymorphism of the serotonin transporter gene (*5-HTT*) and electoral turnout was confirmed, while the assumed dependence of the monoamine oxidase A gene (*MAOA*) was probably a false positive (Deppe et al., 2013; Fowler & Dawes, 2013). This example and the failure to replicate research from other fields (Duncan et al., 2019) show that CGAS results should be approached with caution, at least until they are confirmed in studies with much larger sample sizes.

Either way, further molecular studies are necessary to more accurately assess the cognitive value of the studies conducted to date. As I have pointed out several times, due to the small effect sizes of SNPs, replications and new studies should be conducted using very large sample sizes; also, the applied research techniques require continuous development. Charney's comment concerning the lack of fitness of the analysis level to the phenomenon explained would only be justified if researchers of genopolitics interpreted political behaviours in terms of simple Mendelian traits. However, this is not the case, as the analysis of the research conducted so far clearly demonstrates.

Because of the cumulative effect of thousands of genes, it will probably never be possible to identify specific alleles that can explain a substantial part of the variation in complex behavioural traits in a population. Each studied gene's influence is only a small part of a much larger and extremely complex system. Researchers of genopolitics, however, are aware of the limitations. They usually emphasise that their goal is to focus on selected dependencies but at the same time point out the important role of factors, which they do not take into account in their analyses. Fowler and Dawes (2008, p. 590), for example, clearly state that the existence of a single gene responsible for electoral participation is unlikely; at the same time, they note the relevancy of entire sets of genes and environments. Similarly, Hannagan and Hatemi (2008, p. 333) note: 'It is unlikely that "the" gene for conservatism, financial success, a great golf stroke, or any other complex trait will be identified. It is more likely that complex networks of genes, for which causal variation might be specified, are the appropriate targets for future research. Genes likely establish general inclinations or predispositions that shape our interpretation and reaction to experiences. Those experiences increase the likelihood of developing a specific trait or attitude.' McDermott et al. (2013, p. 1058) stipulate, however, that their analysis involves only one gene product that is likely not irrelevant to neuronal transmission in serotonergic and dopaminergic pathways as well as other related systems. These systems consist of thousands of gene products, and therefore individual markers are unlikely, as it seems, to have a major impact on any complex social behaviour.

Two further reservations with regard to genopolitical studies: incompleteness and low explanatory utility, therefore, seem just as questionable, particularly when we consider the role played by the idealisation method in the study of complex systems. In explaining the variance of a particular behaviour, we could take into consideration a number of factors whose impact is found in different scientific disciplines, frequently by using entirely different methodologies. Behavioural geneticists, neurobiologists, political scientists or sociologists focus their attention on factors that are considered key from the point of view of their theoretical perspectives while ignoring the influence of factors deemed less important. None of the approaches is able to obtain a comprehensive picture of the analysed phenomenon on its own;

[7] Potochnik and McGill (2012) provide an excellent account of the issue of the hierarchical structure of life.

therefore, the explanations formulated on their basis are necessarily partial. The orientation of individual approaches towards different causal patterns may be one of the obstacles to building a unified approach in the future.

Researchers of genopolitics follow the same cognitive procedure as sociologists or political scientists focusing exclusively on environmental influences. According to Nowak's model, the process leading from the establishment of pre-theoretical goals to the formulation of a genetic explanation of a studied political behaviour takes place in several stages, in which the researcher:

1) Simplifies reality on the basis of the adopted ontological perspective, i.e., makes a demarcation between factors that affect and those that do not affect the analysed behaviour. The latter are then reduced, which means that they are not taken into account in the next research stages. Among those can be included, for example, the physical parameters of the Earth or the type of diet adhered to by the respondents. As a result, the space of essential factors for the analysed behaviour is created, consisting of physiological, neurobiological, psychological, cultural, social etc. factors, in addition to the genetic ones;
2) On the basis of the adopted theoretical perspective, determines which of the factors in the space of essential factors are principal and which are secondary to the analysed behaviour;
3) Etablishes the hierarchy of the power of influence of particular principal and secondary factors, thanks to which an essential structure of the examined behaviour is created;
4) Introduces idealising assumptions under which the effect of secondary factors is subject to ideation (extreme case of negative potentialisation). In other words, recognises that physiological, neurobiological, psychological, social, or cultural factors assume the value of zero and, therefore, do not affect the analysed magnitude;
5) Finally, can modify the initial claim by way of concretisation. By abandoning subsequent idealising assumptions, the researcher will demonstrate how the examined behaviour depends on the influence of secondary factors.

As I mentioned in Section 2.1, the model presented above is in itself a highly idealised construct; therefore, when taking into account specific genetic studies, one should take into account the possibility of smaller or larger deviations. These will mainly concern the last step, which is rare. However, some molecular studies also uncover the influence of environmental factors, specifically the gene-environment interaction (G × E).[8] It appears, for example, that the association between the *5-HTT* gene and voter turnout studied by Fowler and Dawes (2008) was most likely moderated by exposure to religious activity. In contrast, McDermott et al. (2013) found that individuals with a low-activity *MAOA* allele who were exposed to violent behaviour in their youth were more likely to engage in physical violence later in life.

One area where concretisations will emerge along methodological development may be the interface between genopolitics and neuropolitics. Neurobiological data help to single out genes that may be important in the emergence and formation of a particular behaviour, while genetic data point to important neurobiological components. Thus, genes whose influence on bodily processes is fairly well known are subject to being singled out. These include the genes that determine brain development, hormone production, synthesis and uptake of neurotransmitters, as well as transcription factors. The development of connections between genopolitics and neuropolitics will perhaps provide a much broader picture of the biological determinants of political behaviours in the future. Until then, the connections between genopolitical and neuropolitical research can be considered, for example, in terms of mechanistic inter-field integration, which results in the formulation of mosaic-like mechanistic explanations. They bring together different types of evidence from different research fields (Craver, 2005, 2007).

However, as a rule, influences ignored in studies of the genetic foundations of political behaviour are analysed, as I mentioned earlier, in separate research approaches introducing their own idealising assumptions.[9] The reason for this may be the methodological limitations of the early stage of research development. Therefore, one would expect that with the emergence of new cognitive needs and the development of more effective research techniques, these limitations would be overcome. However, this scenario would require the emergence of unified approaches, which will be very difficult to achieve due to the focus of researchers on specific causal influences. However, a temporary or permanent lack of the possibility of concretisation of the claims made in a given research field does not necessarily entail a low explanatory power of these claims and that the field itself is regressive, which results, in a way, from concepts that tie the explanatory power of a representation only to representatively correct components (Bokulich, 2011; McMullin, 1985; Strevens, 2019). As I pointed out in Section 2.1, maintaining idealising assumptions may result from many reasons, chief among them being the realisability of the representation.

6. Reductionism of genopolitics

If my findings are accurate, then the objection of excessive reductionism against the research of genetic foundations of political behaviours does not apply, and its origins probably lie in the insufficient appreciation of the idealisation method. What remains is to answer the question: what are the characteristics of the reductionism of genopolitics?

Political behaviours, like other biosocial phenomena, are not determined solely by a single causal pattern. Researchers are faced with many interrelated causal influences, and it is only up to their decision which factors they will adopt as the focus of their research and which they will permanently and/or temporarily ignore. This situation is a result of the very nature of the analysed system and human cognitive limitations. As a result, researchers of genopolitics, in formulating highly idealised explanations, follow the guidelines of methodological reductionism, a methodological directive that implies the division of the studied system into small components. Many scientific theories assume this type of reductionism, focusing on selected small elements of target systems. However, this does not mean that an analysis of all isolated elements can provide a basis for explaining the system as a whole:

> There is an integration of the parts at each level, from the cell to tissues, organs, organ systems, and whole organisms. This integration is found at the biochemical level, at the developmental level, and in whole organisms at the behavioral level. All holists agree that no system can be exhaustively explained by the properties of its isolated components. The basis of organicism is the fact that living beings have organization. They are not just piles of characters or molecules, because their function depends entirely on their organization, their mutual interrelations, interactions, and interdependencies (Mayr, 2001, pp. 18–19).

However, the nature of political behaviours calls into question such types of reductionism as ontological, causal, and epistemological. Ontological reductionism assumes that higher order beings are nothing more than the sum of their parts. Causal reductionism holds that a system's components' behaviour determines the system's behaviour as a whole. In contrast, epistemological reductionism claims that laws and theories about higher order phenomena can be derived from the laws and theories describing lower order phenomena and, ultimately, laws and physics theories without a loss (Murphy, 2009). According to the current state of

[8] G × E stands for genetic susceptibility to the environment.

[9] Similar conclusions were reached by Potochnik (2017, pp. 70–80), after analysing the studies on the genetic conditions of violence.

knowledge and methodological possibilities, these positions are not accurate when studying complex biosocial phenomena. Nor are they the assumptions adopted by scholars formulating genetic explanations of political behaviours.

7. Summary

Studies of the genetic foundations of political behaviours have caused much controversy in social sciences. One of the objections made against them is that of excessive reductionism. This is supposed to manifest itself in the inadequate selection of the level of analysis for the explained phenomenon, the incompleteness of explanations and low explanatory utility. Political behaviours are determined by many intertwined factors. In the opinion of the critics, this is not appreciated by the researchers of genopolitics, who focus exclusively on genetic influences, leaving much more relevant dependencies outside their scope of interests. In reality, however, researchers of genopolitics are well aware of the complexity of the process of translating genetic effects into behaviours and their focus only on selected causal influences is justified by methodological reductionism – a methodological directive that assumes the division of the studied system into small components. The analysis of the dispute over genopolitics clearly demonstrates the existence of cognitive and communication barriers between the disputing parties, as pointed out by Hatemi and McDermott (2012, p. 527): 'Most researchers consider political traits to be influenced by thousands of genetic markers both indirectly and through interactions with numerous environmental stimuli and other genes in complex genomic, epigenetic, and neural pathways. By contrast, many criticisms are developed as if responding to the view that political traits are simple Mendelian traits, governed by a single gene or a small set of genes.'

Political phenotype studies, depending on the research objectives and assumptions, take into account multiple different factors, among which genetic, neurobiological or physiological factors seem to be just as warranted as social or cultural factors. This is indicated by studies carried out using the best methodologies currently available to us. Political behaviours are, in all probability, the result of the interaction between culture and nature, and not the result of unilateral cultural influences. Research concerning the genetic basis of political behaviours is not a competitive position for traditional behaviouralism but one of its supplements and evolutions.

In order to obtain a more complete picture of the process of generation and formation of political behaviours, both the cumulative effect of thousands of individual genes and the influence of epigenetic, neurobiological and physiological factors, as well as the environment and random events, should be taken into account. The state of our knowledge and methodological possibilities, however, are not conducive to building a unified approach. This situation may be temporary or permanent. According to the first interpretation, the emergence of new cognitive needs and methodological development will enable the researchers of genopolitics to abandon gradually their idealising assumptions. According to the second interpretation, methodological limitations resulting from the fact that researchers working within different approaches focus on different causal patterns will prove insurmountable.

Explanations of political behaviours, whether they emphasise the relevance of environmental or biological determinants, are highly idealised in nature. The process – from the formulation of pre-theoretical objectives to the explanation of the analysed dependence – is carried out in several stages. First, a division is made into factors that affect and do not affect the analysed behaviour. The latter are then reduced, which means that they are not taken into account in the next research stages, while the former are divided into principal and secondary factors. Then, the secondary factors are subject to an extreme case of negative potentialisation – ideation. In other words, their value is counterfactually reduced to zero. If this does not conflict with research objectives and is feasible, then as the research evolves and new cognitive needs arise, some idealising assumptions may be concretised. Taking into account the impact of secondary factors brings the researcher closer to showing the actual dependence of the analysed behaviour on the influences considered to be essential. In the light of the findings described above, the reductionism of research into the genetic foundations of political behaviours can be considered as a standard cognitive procedure applied in science.

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