Chapter 4

Quantitative genetics: measuring heritability

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Introduction

4.1 The field of quantitative genetics originated around 1920, following statistical demonstrations that traits which are normally distributed can arise from the action of multiple genes, each with relatively small effects (either increasing or decreasing the value of the trait).[1] Various complex statistical techniques are employed in such research. In this chapter, we explain the concept of heritability, but do not provide a detailed account of the statistical methods.[2] We then go on to describe the three ways in which data about human behaviour are obtained in this field of research, namely twin, adoption and family studies.

How is population variation examined using genetic studies?

4.2 Influences on the total population variation that is observed for a particular characteristic can be subdivided into different components:

- Genetic influences
- Environmental influences
- Gene–environment correlation (see Box 3.3)
- Gene–environment interaction (see Box 3.3)

The following paragraphs 4.3 – 4.12 explain how these factors are accounted for, statistically, in quantitative research.

Genetic influences on variation

4.3 Quantitative research techniques can be used to estimate the influence of unspecified genetic factors on behaviour. This is done by using a statistical concept called 'heritability', which was first derived by plant breeders to help them reproduce desirable characteristics in agricultural products such as corn and wheat. It is a complicated concept that can be used in various ways. It is frequently misinterpreted by scientists and other commentators on research in behavioural genetics.[3]

4.4 There is a common sense notion of heritability or inheritance that is concerned with the extent to which particular characteristics in an individual are the result of what one inherits (nature), the environment and world one grows up in (nurture) or some combination of these two (see paragraph 2.10). Most developmental psychologists adopt a perspective of 'interactionism' – a process of development involving both factors. In the context of research in behavioural genetics, however, heritability has a more precise statistical definition. This defines heritability as a statistical ratio that, for a given quantitative character and against a fixed environmental background, estimates the proportion of the observational differences in that characteristic across a population that can be attributed

[1] See paragraphs 2.10-2.11

[2] For further information in this area, see: Carey, G. (2002). *Human Genetics for the Social Sciences*. London: Sage Publications; Plomin, R., DeFries, J. C., McClearn, G. E. & McGuffin, P. (2000). *Behavioral Genetics*. 4th ed. New York: Worth.

[3] For a very clear discussion of concepts of heritability, see Daniels, M., Devlin, B. & Roeder, K. Of genes and IQ. In Devlin, B. *et al*. (1997). *Intelligence, Genes and Success*. New York: Copernicus.

to genetic influences. It is a statistic that refers solely to a group of individuals and does not concern the process of development in the individual.

4.5 Estimates of heritability may be divided into two types, which depend on the way in which variation within a population is accounted for. There are four aspects of variation: additive genetic variance, variance due to genetic interaction (epistasis), variance due to interaction between alleles (dominance), and variance due to environmental causes. Narrow-sense heritability is defined as the proportion of variance that can be attributed to transmissible genetic factors. Narrow-sense heritability measures the part of variance attributable in a population to the additive effect of genes, independently of interaction effects between alleles, between loci and between the genetic make-up and the environment. This provides a statistical estimate to answer the question that an animal or plant breeder will ask: if selective breeding is applied for a particular characteristic, will it work?

4.6 There is a different concept of heritability, which is also used in research in behavioural genetics that examines human populations, known as broad-sense heritability. This deals with the total variance due to genetic differences, whatever their origin (additive or interactive). Heritability in the broad-sense does not yield a figure that is predictive and therefore helpful to a breeder of plants or animals. Nor, of course, does it answer the common sense question about the extent to which genetic factors and environmental factors influence the development of characteristics in an individual. The estimate of heritability most commonly used in research studies is narrow-sense heritability, which accounts only for additive genetic variance. (All figures for heritability quoted in this Report are narrow-sense values, unless stated otherwise).

4.7 It is vital to understand that neither concept of heritability allows us to conclude anything about the role of heredity in the development of a characteristic in an individual. Heritability refers to the proportion of variation in the population attributable to genetic influences. Thus, for example, an estimate of heritability of 0.60 does *not* mean that 60% of a particular person's trait is explained by their genes. What it does mean, is that in a given population that varies for a particular trait, 60% of that variation *across the whole population* is the result of differences in their genotypes. As heritability is a proportion of the total variance, the estimate will vary depending on the variation in the population of genetic and environmental factors. For example, if there is a population of individuals who are genetically identical for all relevant genes contributing to a given trait (that is, they all carry the same alleles for those genes; clearly a hypothetical situation), the narrow-sense heritability for the phenotypic characteristic related to those genes would be zero, because any differences must, by definition, be attributed to environmental factors.

4.8 It is important to distinguish heritability from genetic determination. Novel environmental changes might have dramatic consequences on a phenotype. A standard example is height. The heritability of height in most populations is probably over 0.90, that is to say, 90% of variation in height in most human populations can be attributed to genetic factors.[4] But the

[4] See for example, Phillips, K. & Matheny, A. P., Jr. (1990). Quantitative genetic analysis of longitudinal trends in height: preliminary results from the Louisville Twin Study. *Acta Genet. Med. Gemellol. (Roma)* **39**: 1,143–63; Carmichael, C. M. & McGue, M. (1995). A cross-sectional examination of height, weight, and body mass index in adult twins. *J. Gerontol. A Biol. Sci. Med. Sci*. **50**, 237–44; Preece, M. A. (1996). The genetic contribution to stature. *Horm. Res.* **45 Suppl 2**, 56–8; Silventoinen, K., Kaprio, J., Lahelma, E. & Koskenvuo, M. (2000). Relative effect of genetic and environmental factors on body height: differences across birth cohorts among Finnish men and women. *Am. J. Public Health* **90**, 627–30.

average height of most Western populations increased by 1.0 cm per decade between 1920 and 1970, even though the genes in those populations could not have changed substantially. In large outbred populations, any noticeable change in the frequency of particular genes will take many centuries. The example is apposite, because a similar increase in IQ test scores also occurred throughout most of the twentieth century in most industrialised countries. At different times and places, this increase ranged from 0.3 to 10 IQ points per decade. However high the heritability of IQ might be, and it is certainly not as high as 0.90, environmental changes can potentially have a substantial impact.[5] It is worth noting that any society that succeeds in reducing differences in the environments experienced by different members of that society, for example, by improving education services in deprived areas, will probably increase the heritability of their characteristics – in this case, intelligence.

Environmental influences on variation

4.9 Environmental variance includes a proportion of variance that can be explained by shared or common environmental influences and a remaining proportion accounted for by non-shared environmental factors, random effects and error. The terms 'shared' and 'non-shared' environment refer to the effects of the environmental influence, not their origins (as previously assumed by many researchers); that is whether they increase or decrease similarity between family members for a given characteristic. For example, social disadvantage is an environmental factor to which all family members are exposed. However, its effects on a particular behaviour may appear as 'non-shared' in genetic analyses if social disadvantage has a different effect on each individual within the family; that is, if its effect is to enhance differences between family members. The categories of shared and non-shared environmental influences are statistical notions and each category contains many unidentified factors that are not necessarily specifically investigated in a quantitative research project.

4.10 Many studies in this field have reported that the proportion of variation in behavioural traits that can be attributed to factors shared by family members is relatively low. These findings have been used to claim that an individual's shared environment, particularly the family, has little effect on his or her behaviour.[6] Interestingly, an exception to this finding is in the case of antisocial behaviour. Significant effects of shared environments are routinely reported in research in behavioural genetics in this area. Moreover, many researchers have now rejected the conclusion that the role of the family in affecting behaviour is unimportant.[7]

Gene–environment correlation and interaction

4.11 In most studies in behavioural genetics, the effects of gene–environment correlation and gene–environment interaction cannot be estimated separately and are included within the estimate of heritability. This means that even when a trait is highly heritable, environmental influences may still be important in mediating the effects of the genes on behaviour. For example, in the case of gene–environment correlation, if exposure to friendly company were correlated with a person's genotype, sociability could be found to be heritable even though it may have arisen as a result of increased exposure to company.

[5] See Chapter 7.

[6] An influential book arguing that parenting does not matter is Harris, J. R. (1998). *The Nurture Assumption*. New York: The Free Press.

[7] Rutter, M. & Silberg, J. (2002). Gene-environment interplay in relation to emotional and behavioral disturbance. *An. Rev. Psychol*. **53**, 463–90.

4.12 Since estimates of heritability in traditional studies in quantitative genetics might be due not just to the direct effect of genes, but also to the indirect effects of environmental factors that correlate with genes and that have an effect contingent on genotype, they are likely to overestimate the contribution of genetic factors to variation. Because of the complex relationship between genetic and environmental factors, it can be difficult for statistical approaches to model them accurately, meaning that the many complicated relationships that may exist between genetic and environmental factors are often over-simplified.

Family, twin and adoption studies

4.13 Family, twin and adoption studies are used to examine the contribution of genetic and environmental influences on traits and disorders. Each of these methods has its own merits and disadvantages, but as for all research, consistent findings from different types of studies allow for greater confidence in drawing conclusions.

Family studies

4.14 Family studies are designed to examine whether the chance of having a particular characteristic is increased in the relatives of those who are have the characteristic, compared to the relatives of those who do not. An increased incidence in relatives of affected individuals indicates that the trait is familial, that is, that it appears to run in families. For continuously distributed characteristics, rather than calculating relative risks, researchers estimate the similarity of biological relatives in families for these traits by calculating a correlation coefficient. A correlation of zero indicates no similarity and a positive correlation indicates similarity between relatives. Total similarity would result in a maximum correlation of 1. A significant positive correlation suggests that the trait is familial (but not necessarily genetic).

4.15 Family studies of behavioural characteristics such as personality, IQ test scores and childhood behaviours have consistently shown that family members are more similar to each other than unrelated individuals. It is also clear from family studies that these sorts of characteristics show a complex pattern of inheritance (such that they are sometimes termed complex traits), which suggests that they are influenced by a number of different genes in combination with environmental influences. That a characteristic is common to family members could be due either to genes that relatives share, or to environmental factors that impact on all family members in a way that makes them more similar. Thus, findings from family studies alone do not provide conclusive evidence of a genetic contribution. Twin and adoption studies allow us to disentangle, to some extent, the effects of genes and shared environmental factors.

Studies of twins

Methods

4.16 Monozygotic (MZ) twins come from the same fertilised egg and are genetically identical, that is, they have 100% of their genes in common. Non-identical or dizygotic (DZ) twins, like other siblings, share, on average, 50% of their genes. A greater similarity or correlation between MZ twins than DZ twins indicates a genetic influence. Studies of twins allow researchers to examine what proportion of the total phenotypic variance is explained by genetic factors, shared environmental factors and non-shared environmental factors.

4.17 Studies of twins are based on a number of assumptions. One is that pairs of MZ and DZ twins experience very similar environments. This assumption, called the equal environments assumption, has been criticised. Indeed, there is evidence that MZ twins do experience a more similar environment than DZ twins. In most studies, it is assumed that the equal environments assumption is correct when the degree to which twins share an environment has been measured by questionnaire, but these measures do not necessarily include the relevant environmental factors. There is increasing evidence that many environmental factors that are relevant for behaviour are more often shared by MZ twins than DZ twins.[8] Studies of twins also ignore the possible role of prenatal environment. Whether subsequently separated or not, twins, unlike other siblings, have shared the same prenatal environment at the same time.[9]

4.18 Another criticism is that findings in twins may not be so easily extrapolated to non-twins (singletons). Twins experience greater intrauterine and perinatal adversity, and the experience of being brought up as a twin is unusual. However, twins do not appear to differ markedly from singletons for most types of characteristics, other than in showing delays in the acquisition of language.

4.19 Despite the fact that MZ twins share the same genome, they are never truly identical. They differ in behaviour and physique as well as in intellectual abilities and personality traits. Some of these differences will be due to random or chance effects, others due to environmental influences that are not shared by the twins. However, although the assumption is made that MZ twins are genetically identical, the process of MZ twinning is complex and it is now known that there are various biological mechanisms that can lead to genetic differences between them.

4.20 Overall, although there are criticisms of the twin method, these are not sufficient to cast doubt on the usefulness of this study design. Nevertheless, there are clearly good reasons to use a variety of research strategies in examining the contribution of genetic and environmental influences to behaviour before drawing conclusions.

Interpretation of twin study findings

4.21 Studies involving a large number of pairs of twins can be useful in providing basic information about what sorts of factors influence variation in a trait, and in refining definitions of characteristics. Studies of twins are increasingly being used to assess the contribution of environmental factors and to examine the pathways mediating the effects of environmental factors on behavioural traits. This type of design has also been used to examine the overlap of different traits (for example, studies of twins suggest that common genetic factors influence both anxiety and depressive symptoms), and in examining the underlying influences on normal variation compared with extremes. Caution, however, is also needed to avoid over-interpreting the meaning of heritability. There is a considerable literature discussing these concerns and we highlight two key areas:

[8] Rutter, M., Pickles, A., Murray, R. & Eaves, L. (2001). Testing hypotheses on specific environmental causal effects on behavior. *Psychol. Bull*. **127**, 291–324.

[9] There is another potentially important difference in the prenatal environments of twins. All DZ twins, and some MZ twins, are surrounded by different sacs or chorions in the uterus. But some MZ twins are monochorionic: they share the same chorion. If monochorionic MZ twins experience a more similar prenatal environment than dichorionic twins, this might explain why MZ twins as a group resemble one another more closely than DZ twins. The possibility is open to a simple test: dichorionic MZ twins should resemble one another less than monochorionic MZ twins, and no more than DZ twins. However, studies that have focused on these different types of twin do not yet provide conclusive evidence either way.

- *Studies of twins focus on populations, not individuals*

  Studies of twins have revealed that variation in many different characteristics is heritable. Estimates of heritability and the proportion of variance attributable to environmental factors only refer to the population studied. Thus, for example, many studies of twins have used representative twins born within a defined geographical area, in general a sound strategy. However, findings will refer to the population studied and may not generalise to other groups, for example, to those exposed to severe adversity or from different age and ethnic groups.

- *Extremes versus normal variation*

  In population-based samples of twins, most participants do not show extreme scores. The origins of severe or extreme behaviours may be different from those for characteristics within the normal range and thus the estimates of heritability and environmental variance obtained from twin study samples may not necessarily apply to groups of extremely high or low scorers. However, a type of statistical analysis known as 'extremes analysis'[10] allows for the testing of whether the relative contribution of genes and environment for extremely high or extremely low scores differs from that for variation across the normal range. For example, it may be that genetic factors influence normal variation in a trait, but that environmental factors are more important for extremes. This type of analysis has suggested that the magnitude of genetic and environmental influences on high levels of overactivity and inattention in children appears to be no different from that on 'normal variation' in these types of symptoms.[11] However, very large sample sizes are needed to pick up differences between normal variation and extremes.

Adoption studies

4.22 Adoption studies involve studying the biological and adoptive relatives of individuals who have been adopted. If individuals who are genetically related (biological relatives) are more similar for a particular characteristic than adoptive relatives, this suggests that genetic factors influence that trait. If relatives who are genetically unrelated are more similar for that trait, this is suggestive of a contribution from environmental factors. Adoption studies provide a powerful means of examining genetic and environmental influences and investigating gene–environment interaction. However, two difficulties with such studies are that adoptees are not placed randomly into adoptive families (they tend to be chosen to provide environments that are low-risk), and adoption is an unusual event in itself.

4.23 For traits such as intelligence, personality and antisocial behaviour, adoption studies have added to evidence from studies of twins in demonstrating a genetic contribution to variation. Adoption studies have also demonstrated important effects of gene–environment correlation. For example, adoption studies have found that the adoptive parents of children who are thought to be at increased risk of antisocial behaviour because their biological parents show similar behavioural traits, display

[10] DeFries, J. C. & Fulker, D. W. (1988). Multiple regression analysis of twin data: etiology of deviant scores versus individual differences. *Acta Genet. Med. Gemellol. (Roma)* **37**, 205–16.

[11] Stevenson, J. (1992). Evidence for a genetic etiology in hyperactivity in children. *Behav. Genet*. **22**, 337–44.

increased negative parenting.[12] This is thought to provide a demonstration of how an environmental factor (negative parent response) may be influenced by the characteristics of the child and illustrates the complexity of the relationship between genetic and environmental factors.

4.24 Adoption studies have also shown that genes and environment can have an interactive influence; that is the effects of environmental adversity are much more marked when there is also genetic susceptibility. For example, analysis of data from three adoption studies showed significant increased adolescent antisocial behaviour in adoptees when they were both at increased genetic risk and then exposed to an adverse environment. This increased risk was significantly greater than the effects of genetic and environmental factors acting alone.[13]

Current uses of quantitative genetic studies

4.25 Quantitative genetic research is traditionally regarded as a way of examining whether or not a particular disorder or characteristic is genetically influenced. Since virtually every human characteristic is genetically influenced to some extent, attention is turning to using quantitative research to answer other questions. So why do researchers still conduct studies that involve estimates of heritability? The objective of family, twin and adoption studies is now much broader than simply examining whether genes influence a particular trait. These methods are now used to examine a much wider range of issues that are clinically and scientifically relevant, such as:

- *Examining the contribution of psychosocial factors*. For example, examining to what extent parenting factors might increase the risk of behavioural problems, even when genetic influences are taken into account.

- *Examining how psychosocial/environmental influences moderate genetic effects*. For example, as mentioned earlier (Box 3.3), studies of twins have shown that the impact of life events on depression varies depending on genetic susceptibility.

- *Examining why two traits may go hand in hand*. This type of analysis has shown that anxiety and depression often occur together and are influenced by the same set of genes.

- *Examining the relationship between symptoms within the normal range and extremes*. This type of work has shown that some traits (for example, Attention Deficit Hyperactivity Disorder symptoms) lie along a continuum, with similar genetic effects on high scores and on symptoms within the normal range. Findings for other traits have been different. For example, the relative contribution of genes and environment to variation in IQ scores appears to differ for very low IQ scores compared to scores in the normal range.

[12] Ge, X. *et al*. (1996). The developmental interface between nature and nurture: A mutual influence model of child antisocial behaviour and parenting. *Dev. Psychol*. **32**, 574–89; O'Connor, T. G., Deater-Deckard, K., Fulker, D., Rutter, M. & Plomin, R. (1998). Genotype–environment correlations in late childhood and early adolescence: Antisocial behavioural problems and coercive parenting. *Dev. Psychol*. **34**, 970–81.

[13] Cadoret, R. J., Cain, C. A. & Crowe, R. R. (1983). Evidence for gene-environment interaction in the development of adolescent antisocial behavior. *Behav. Genet*. **13**, 301–10.

Conclusion

4.26 In summary, family, twin and adoption study designs each have different strengths and weaknesses. It is important to recognise the limitations of any type of study design, to maintain a critical approach to interpreting findings and to avoid over-interpretation (see Box 4.1). Nevertheless, when findings from different studies are consistent, research in quantitative genetics provides a useful method for studying the factors that influence different human characteristics.

Box 4.1: Central points regarding research in quantitative genetics

- Quantitative genetics involves statistical methods that attempt to distinguish the effects of genetic and environmental factors on variation in certain behavioural traits, which can be quantitatively measured, between groups of individuals.
- The subjects of the research are usually twins, siblings, adopted children, and families.
- The statistics such as estimates of heritability generated by the research refer to groups of people, not to individuals. Nor do they refer to particular genes or regions of DNA or to specific environmental factors. This requires further research and additional measurement.
- Estimates of heritability and other statistical techniques are useful in understanding the relative contribution of different types of influence and their relation to each other. They are also useful for understanding why some types of behaviour often occur together. They do not, however, lead directly to predictive information regarding individuals, nor do they give reliable estimates of how strongly predictive a genetic test might be if it were developed.