Review Article

The Genetics of Intelligence

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Summary

Background: Intelligence is defined as general mental capacity, which includes the abilities to reason, solve new problems, think abstractly, and learn quickly. Genetic factors explain a considerable fraction of inter-individual differences in intelligence. For many years, research on intelligence was limited to estimating the relative importance of genetic and environmental factors, without identifying any individual causal factors.

Methods: This review of the literature is based on pertinent original publications and reviews.

Results: Genome-wide association studies (GWAS) have shown that certain gene loci are associated with intelligence, as well as with educational attainment, which is known to be correlated with intelligence. As each individual gene locus accounts for only a very small part of the variance in intelligence (< 0.02%), so-called "polygenic scores" (PGS) have been calculated in which thousands of genetic variants are summarized together. On the basis of the largest GWAS performed to date, it is estimated that 7–15% of inter-individual differences in educational attainment and 7–10% in intelligence among persons of European descent can be explained by genetic factors. These genetic effects are partly indirect. At the same time, the relative importance of genetic factors in determining complex features such as intelligence and educational attainment must always be seen against the background of individual environmental conditions. In the presence of difficult social conditions, for example, the influence of genetic factors is typically lower.

Conclusion: At present, the polygenic scores generated from genome-wide association studies are primarily of scientific interest, yet they are becoming increasingly informative and valid for individual prediction. There is, therefore, a need for broad social discussion about their future use.

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The high heritability of cognitive abilities, also termed intelligence, and the enormous influence of this trait on many aspects of life and health explain the wide scientific and public interest in this subject. For a long time, studies of the genetic influence on intelligence were limited to estimates of the relative importance of genetic and environmental factors, with individual causal factors not known. In the past decade, however, important new insights into the genetic and molecular foundations of this trait have been gained, which will enable not only their application or use in science/academia but also in practice. These developments are presented here.

What is intelligence, and how is it measured?

Intelligence ranks among the best studied constructs in the empirical behavioral sciences (1). A consensus also

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exists in psychometric intelligence research regarding the core components of intelligence and the type of testing procedures that can be used to measure them (2). Consequently intelligence is a very general mental capacity that—among others—includes the abilities to reason, solve new problems, think abstractly, and learn quickly (3). Nowadays the dominant idea is that of a hierarchic model of intelligence with a global general factor ("g") at the top and underlying factors of different breadth, which in turn bundle different specific cognitive achievements (*Figure I*).

Furthermore, intelligence has a major role in explaining and predicting individual differences with partly considerable associated effect sizes in central areas of social life and advancement, including successful schooling and education (4), professional/vocational success (5), socioeconomic status (6), and health behaviors (7). Data from a metaanalysis of 240 independent studies including 105,185 individuals, furthermore, showed a strong population correlation between intelligence and school grades of p=0.54 (mean r=0.44, corrected only for the sampling error), which makes intelligence by some margin the strongest predictor of school success (4).

Numerous psychometric tests are available to measure intelligence; these can differ in terms of the task format and specific abilities assessed. Test batteries are used for individual diagnosis (for example, the intelligence structure test, IS-T 2000R; [8]), which include tasks to capture different primary factors of intelligence-among others, inductive reasoning, verbal comprehension, figural relations, and dealing with numbers. Empirically, achievements in these different partial areas consistently show positive intercorrelations-the prerequisite for aggregating such partial achievements into a total score (9). Relevant intelligence testing methods enable determining such a total value for each person tested. By applying norms these can then be converted into immediately interpretable standard values, such as the intelligence quotient (IQ). According to a recent comprehensive meta-analysis, inter-individual differences in intelligence scores from young adulthood display a mean differential stability over a five-year period (ranking stability) of p=0.76, which tends to increase at an older age (10). This means that if the test is repeated, the rank of a person among holders of a trait remains very stable over time.

The heritability of intelligence

Numerous twin studies and adoption studies have shown that almost all human behavioral traits are subject to genetic influences (11), which-especially for intelligence-contribute substantially to explaining inter-individual differences. However, the relative importance of this influence changes over the lifespan. Whereas in early childhood, inter-individual differences in intelligence are influenced primarily by effects of the so-called shared environment (environmental factors that contribute to similarity in individuals growing up together-for example, parental education styles or socioeconomic status), these factors lose influence during childhood and adolescence, and no longer play a significant role from early adulthood. The decrease in the importance of shared environmental factors is contrasted by the increase in the importance of genetic influences, which account for slightly more than 20% of differences in intelligence in early childhood, about 40–50% at the start of school, and up to 60% and more in adulthood (12). Finally, so called non-shared environmental influences also increase with age and explain a substantial proportion (about 35%) of differences in intelligence in adulthood.

This increase is attributed, among other things, to the so called active genotype-environment correlation, whereby persons whose genotype confers advantages in the context of learning and performance/behavior and contributes to experiences of success also tend to seek out to a greater extent those environments that promote learning and achievement (1, 13). The genetic effects are reinforced to the extent that these environments have a feedback effect on trait development. This dynamic and bidirectional process is also known as



Three-stratum model of intelligence based on the reanalysis of 460 studies from the years 1930 to 1985, adapted from Carroll (9). A shorter arrow between general intelligence in Stratum III and any factor in Stratum II expresses a stronger association. The factor "fluid intelligence" is therefore a better indicator for general intelligence than "processing speed," for example.

genotype-environment transaction (14). Other hypotheses stipulate in the course of development an increasing importance of biological processes over environmental influences. The estimated heritabilities also include such indirect genetic effects. *Figure 2* summarizes the results described here.

The heritability of intelligence also varies depending on the family's socioeconomic status; in more favorable socioeconomic circumstances, higher heritabilities are found and in more difficult circumstances, partly notably lower ones. This interaction between genes and the environment is also known as the Scarr-Rowe effect and occurs in particular in view of large social inequalities, which is consistent with the results of a meta-analysis that identified the effect mainly in US samples (15).

The molecular genetic basis of intelligence

For many years, research into the molecular genetic foundations of intelligence were shaped by the non-replicable genetic associations and false-positive findings from candidate gene studies with limited statistical power (16). Only the development of the method of genome-wide



Summary of results from twin studies of the relative contribution of genetic and nongenetic factors to the development of inter-individual differences in general intelligence (12). Inner circle: in childhood, outer circle: in adulthood. "Error" is the term of the proportion of the measurement error in the empirically determined total variance of the trait intelligence. Modified from (1).

Box 1

Genome wide association studies

The genome-wide association study (GWAS) method involves systematic testing of a representative selection of genetic variants of the genome for association with a trait or disease. To this end, a selection of a million common single nucleotide polymorphisms (SNPs) (allele frequency in the population of the rare allele > 1 %) is typically used. Subsequently, statistical methods can be used to interpolate to up to 6 million SNPs and a comparatively tight net can be placed over the 3 billion bases of the total genome.

Methodological advances in determining SNPs by means of micro-arrays (DNA chips) and the improved biomathematical evaluation of the association findings, combined with the use of GWAS in extremely large study collectives, have enabled the discovery of thousands of robustly replicable association findings. These have not only contributed considerably to etiological research but have also enabled new therapeutic strategies. Currently, GWAS are increasingly conducted using genome sequencing and extended to include epigenetic variants, such as DNA methylation.

associations studies (GWAS) on the one hand (*Box 1*) and the combination of large study populations led to the discovery of robustly replicable association findings (17).

After an initial study in 2015 (IQ1) with limited success (18), in 2017 a meta-analysis of previous studies (IQ2) including a total of 78 000 participants found for the first time 18 significantly associated gene loci (19). An extended meta-analysis (IQ3), published in 2018 and including a sample of 280 000 participants, identified 206 independent loci (20) (*eFigure*). The effect size of each individual gene locus was very small and when combined they explained only some 5.2% of the trait variance (*Figure 3*). However, these studies successfully delivered the proof of principle of the identifiability of individual genetic factors for intelligence.

Educational attainment and intelligence

In contrast to intelligence, which has to be ascertained by using appropriate tests, educational attainment (EA)—operationalized as the number of years in school and education—can easily be determined from details in the personal (medical) history. It is therefore included as a covariate in the cohorts of many association studies of very diverse phenotypes. Different studies have shown, furthermore, that educational attainment correlates substantially (r=0.70) with cognitive abilities (19, 21).

In spite of this high association, however, it would be incorrect to equate educational attainment with intelligence. A metanalysis found lower heritability for educational attainment of around 40% (22) as well as important contributions from shared environmental factors, which can be interpreted as the influence of the family of origin on educational attainment. Furthermore, individual differences in educational attainment persist even after cognitive abilities and familial origin have been considered. Some of these differences can be attributed to motivational and non-cognitive factors (for example, selfefficacy beliefs [23]). Additionally, it was shown that school and university education in return have a positive effect on intelligence test results (24).

At the same time, the use of EA in the relevant GWAS has played such an important role in research into the molecular genetic basis of intelligence over the past decade that this development will be briefly outlined here. The first study (EA1), conducted in 2013, included 100 000 participants and identified only three genome-wide significant single nucleotide polymorphisms (SNPs). But this was successfully replicated in independent cohorts, which was considered an important indication of the robustness of the approach and the trait (25). Furthermore, a polygenic score (PGS) calculated from the EA1 study explained 2% of the total variance in a replication study—that is, 100 times more variance than the best SNPs (*Box 2*).

In the past decade, three further, and increasingly comprehensive, EA studies were published. In 2016, EA2, which included 300 000 participants, identified 74 independent SNPs, and explained 3.2% of the trait variance (26). Furthermore, the calculated PGS was able to predict 4% of the variance for the EA associated trait intelligence. EA3 in 2018 included a sample of 1 million subjects and identified 1271 significantly associated independent SNPs. The explained variance was 3.2-12.7% for years in education and 5.1-9.7% for intelligence performance. (27). The latest published study, EA4, included 3 million subjects and revealed 3952 SNPs. The explained weighted variance in US Americans of European origin was 13.3% (range 7.0-15.8%) (Figure 3) (28), which represents a substantial increase in predictive power. For example, the prevalence of university degrees of persons in the top decile of the PGS was 60%, compared with 10% in the bottom decile. However, an estimated 69% of genetic variance on years in education may beattributed to indirect effects-that is, not directly hereditary influences in the populations under study (for example, choice of partner or parental behavior determined by socioeconomic stratum) (29). The non-inherited part of the genome of parents and grandparents, which is also associated with PGS, is also among the indirect effects. This is interpreted as a genetic effect on the environment of the offspring (30).

Challenges associated with determining and using PGS

For biologically distal traits, such as educational attainment, polygenic scores are influenced to a not insubstantial degree by environmental factors, which are difficult to separate from genetic factors (31). This seems to also be the case for the trait intelligence, albeit to a lesser extent. Generalizability and transfer of polygenic scores to other populations also require critical examination; populationspecific differences in particular may lead to polygenic scores calculated in Europeans not having the same validity in other populations (32).

Furthermore, studies to date have used almost exclusively commonly occurring SNPs, which can typically be determined by using micro-arrays. But they reflect only a part of heritability in the wider sense-which is, for example, found by means of twin studies-and does not include non-additive gene effects and the influence of rare gene variants. Recently, a different approach was used for another polygenic trait with high heritability: body height. Here, too, 12,111 independent SNPs in the largest GWAS to date (including more than 5.4 million examined individuals) explained some 40% of trait variance in Europeans, which is close to the theoretical upper limit of 40-50% for the total of average additive genetic effects (SNP heritability) detectable by micro-arrays for the trait body height (33). Only the inclusion of rare variants that were determined by genome sequencing led to an increase in the explained trait variance to 68%, which is very close to the estimated heritability of 80% known from twin studies (34).

Further progress in the field of educational attainment and intelligence is therefore to be expected on the one hand as a result of further increases in sample size and on the other hand from using genome sequencing, which is likely to enable the identification of individual genes and gene variants as well as explain associated biological signalling pathways. Epigenetic factors also play a role, even though research of distal phenotypes such as educational attainment in the context of so called epigenome wide association studies (EWAS) is still in its infancy (35). A more detailed explanation of such studies would exceed the scope of this article.

Initial biological annotations

The described increase in the predictive validity of polygenic scores for complex traits such as intelligence or educational attainment is currently still offset by a comparatively rudimentary understanding of the function of specific gene loci and the identification of the causal DNA variants. Notwithstanding, the results from the two large EA3 and EA4 studies are comparable and biologically plausible. The associated variants are enriched in genes and in evolutionarily conserved genome segments, which is an indication of their functional relevance. The very small effect sizes and the nearly 4000 associated gene loci indicate a pan-genomic etiology of intelligence. As expected, these genes are expressed in the central nervous system—not only during the embryonic and fetal de-

Box 2

The development of polygenic scores

The small effect size of every single nucleotide polymorphism (SNP) (< 0.02 % of the trait variance) is characteristic of complex traits, which are based on a polygenic model with hundreds to thousands of gene variants and sometimes very small, additive effects, which is why individual SNPs are inappropriate for phenotypic predictions from the genotype. Instead, for the past several years, polygenic scores (PGS) have been calculated and used to predict complex traits. These polygenic scores represent the weighed sum of all (associated) SNPs in the form of a single total value with a continuous distribution (40).For example, a PGS from genome-wide association studies explained 5.2 % of the variance in intelligence in independent cohorts (20).



Explained variance by polygenic scores in the traits intelligence (IQ) and educational attainment (EA) viz-a-viz the sample size of the most important studies published to date (for details see main text). h^2_{SNP} = maximum average heritability theoretically detectable with SNPs. Modified from (1).

GWAS, genome wide association study; PGS, polygenic scores;

SNP, single nucleotide polymorphism

velopment but also postnatally. Many of them code for proteins with neurophysiological functions, such as secretion of neurotransmitters, activation of ion channels, and metabotropic signaling pathways, and synaptic plasticity (20, 26–28).

Predicting intelligence using genetic tests

In addition to measuring intelligence directly by means of an intelligence test, the predictability of hereditary traits such as intelligence from the genome assumes an importance that exceeds mere scientific insights in the sense of basic research and has the potential to influence society as a whole. The unchecked availability of such tests in an uninformed environment is obviously associated with risks. In addition to the possibility of opportunistic examination in the context of diagnostic genome sequencing, direct-to-consumer tests from private suppliers are already available in other countries, which offer genome analysis and calculation of polygenic scores for a broad spectrum of traits. Customers are in no position to ascertain the quality of such scores. There is also the risk that the probabilistic nature of a PGS profile and the limits of its informative value in individual cases are difficult to categorize adequately for those seeking information, meaning that the results in question run the risk of being misleading. It is to be expected that in the coming years, providers of laboratory services will expand polygenic scores to include the trait intelligence and offer such tests to consumers in Germany. Finally, expanding polygenic scores to include preimplantation diagnostic evaluation for embryo selection seems possible (36). This is subject to critical reflection and discussion in the specialist academic literature in terms of opportunities and risks (29, 37). A more detailed presentation of this topic will be reserved for a later article. Notwithstanding, such trends show how urgently an intensive scientific-ethical, political, and societal discourse of this subject area is needed.

Finally, it should be emphasized once again at this point that the relative importance of genetic factors influencing complex traits such as intelligence will always have to be considered on the background of realized environmental conditions. Furthermore, environmental influences over the entire lifespan are important for understanding inter-individual differences in intelligence (cf Figure 2). Additionally we need to remember that polygenic scores do not only reflect genetic traits of an individual but are also confounded by environmental factors. Parents pass to their children in addition to genetic information also status, education, world views, values, habits, and much else (38). Such effects can propagate themselves across generations through social mechanisms-in the sense of "dynastic effects"-which is consistent with more recent findings that show that the prediction of polygenic scores for educational attainment was worse for adopted children than for non-adopted children who grew up in their families of origin (39), which is a clear indication of environmental effects.

Conclusions

Intelligence has a strong influence on multiple aspects of life. In childhood, shared environmental factors have an important role in explaining inter-individual differences, whereas in adults, genetic factors are dominant. For the longest time these were appreciable only globally, but in the past decade, rapid developments in the area of genome wide association studies have enabled important progress in elucidating the genetic basis. So called polygenic scores that can be determined at the individual level even now reach a substantial predictive quality for complex traits, such as intelligence or educational attainment. In addition to their importance for basic research, these findings are also highly relevant to society, which requires informed and careful handling of predictions based on polygenic scores as well as their limitations and potential risks.

Conflict of interest statement

The authors declare that no conflict of interest exists.

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References (abbreviated)

- 1. Hagemann D, et al.: Stuttgart: Kohlhammer 2023; 525-605.
- Snyderman M. et al.: Am Psychol 1987: 42: 137-44. 2
- Gottfredson L: Intelligence 1997; 24: 13-23. 3 Λ
- Roth B, et al.: Intelligence 2015; 53: 118-37. 5. Schmidt FL, et al.: J Pers Soc Psychol 2004; 86: 162-73.
- 6. Strenze T: Intelligence 2007; 35: 401-26.
- 7. Calvin CM, et al.: BMJ 2017; 357: j2708.
- 8. Amthauer R, et al.: Göttingen: Hogrefe 2001.
- Carroll JB: New York, NY: Cambridge University Press 1993. Q
- 10. Breit M, et al.: Psychol Bull 2024; 150: 399-439.
- 11. Polderman TJ, et al.: Nat Genet 2015; 47: 702-9.
- 12. Knopik VS, et al.: New York: Worth Publishers 2017.
- 13. Plomin R, et al.: Nat Rev Genet 2018; 19: 148-59.
- 14. Bronfenbrenner U, et al.: Psychol Rev 1994; 101: 568-86.
- 15. Tucker-Drob EM, et al.: Psychol Sci 2016; 27: 138-49.
- 16. Chabris CF, et al.: Psychol Sci 2012; 23: 1314-23.
- 17. Visscher PM, et al.: Am J Hum Genet 2017; 101: 5-22.
- 18. Davies G, et al.: Mol Psychiatry 2015; 20: 183-92.
- 19. Sniekers S, et al.: Nat Genet 2017; 49: 1107-12.
- 20. Savage JE. et al.: Nat Gen 2018: 50: 912-19.
- 21. Hill WD, et al.: Mol Psychiatry 2018; 24: 169-81.
- 22. Branigan AR, et al.: Social Forces 2013; 92: 109-40.
- 23. Richardson M, et al.: Psychol Bull 2012; 138: 353-87.
- 24. Ritchie SJ, et al.: Psychol Sci 2018; 29: 1358-69.
- 25. Rietveld CA, et al.: Science 2013; 340: 1467-71. 26
- Okbay A, et al.: Nature 2016; 533: 539-42.
- 27. Lee JJ, et al.: Nat Genet 2018; 50: 1112-21 28. Okbay A, et al.: Nat Genet 2022; 54: 437-49.
- 29. Schork AJ. et al.: Nat Genet 2022: 54: 372-3.
- 30. Kong A, et al.: Science 2018; 359: 424-8.
- 31. Burt CH: Behav Brain Sci 2022; 46: e207
- 32. Abdellaoui A, et al.: Nat Genet 2022; 54: 1345-54.
- 33. Yengo L, et al.: Nature 2022; 610: 704-12.
- 34. Wainschtein P, et al.: Nat Genet 2022; 54: 263-73.
- 35. Karlsson Linner R. et al.: Mol Psychiatry 2017: 22: 1680-90.
- 36. Lencz T, et al.: Elife 2021; 10: e64716.
- 37. Turley P, et al.: N Engl J Med 2021; 385: 78-86.
- 38. Shen H, et al.: Proc Natl Acad Sci USA 2020; 117: 25646-54.
- 39. Cheesman R, et al.: Psychol Sci 2020; 31: 582-91.
- 40. Boyle EA, et al.: Cell 2017; 169: 1177-86.

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Supplementary material

Complete list of references, eReferences, eFigure: www.aerzteblatt-international.de/m2024.0236

Supplementary material to accompany the article

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Complete list of full references

- 1. Hagemann D, Spinath FM, Mueller EM: Differentielle Psychologie und Persönlichkeitsforschung. Stuttgart: Kohlhammer 2023; 525–605.
- Snyderman M, Rothman S: Survey of expert opinion on intelligence and aptitude testing. Am Psychol 1987; 42: 137–44.
- Gottfredson L: Mainstream science on intelligence. An editorial with 52 signatories, history, and bibliography. Intelligence 1997; 24: 13–23.
- Roth B, Becker N, Romeyke S, Schäfer S, Domnick F, Spinath FM: Intelligence and school grades: a meta-analysis. Intelligence 2015; 53: 118–37.
- Schmidt FL, Hunter J: General mental ability in the world of work: occupational attainment and job performance. J Pers Soc Psychol 2004; 86: 162–73.
- Strenze T: Intelligence and socioeconomic success: a meta-analytic review of longitudinal research. Intelligence 2007; 35: 401–26.
- Calvin CM, Batty GD, Der G, et al.: Childhood intelligence in relation to major causes of death in 68 year follow-up: prospective population study. BMJ 2017; 357: j2708.
- 8. Amthauer R, Brocke B, Liepmann D, Beauducel A: Intelligenz-Struktur-Test 2000 R. Göttingen: Hogrefe 2001.
- Carroll JB: Human cognitive abilities: a survey of factor-analytic studies. New York, NY: Cambridge University Press 1993.
- Breit M, Scherrer V, Tucker-Drob EM, Preckel F: The stability of cognitive abilities: a meta-analytic review of longitudinal studies. Psychol Bull 2024; 150: 399–439.
- Polderman TJ, Benyamin B, de Leeuw CA, et al.: Meta-analysis of the heritability of human traits based on fifty years of twin studies. Nat Genet 2015; 47: 702–9.
- Knopik VS, Neiderhiser JM, DeFries JC, Plomin R: Behavioral genetics New York: Worth Publishers 2017.
- Plomin R, von Stumm S: The new genetics of intelligence. Nat Rev Genet 2018; 19: 148–59.
- Bronfenbrenner U, Ceci SJ: Nature-nurture reconceptualized in developmental perspective: a bioecological model. Psychol Rev 1994; 101: 568–86.
- Tucker-Drob EM, Bates TC: Large cross-national differences in gene x socioeconomic status interaction on intelligence. Psychol Sci 2016; 27: 138–49.
- Chabris CF, Hebert BM, Benjamin DJ, et al.: Most reported genetic associations with general intelligence are probably false positives. Psychol Sci 2012; 23: 1314–23.
- Visscher PM, Wray NR, Zhang Q, et al.: 10 years of GWAS discovery: biology, function, and translation. Am J Hum Genet 2017; 101: 5–22.
- Davies G, Armstrong N, Bis JC, et al.: Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53949). Mol Psychiatry 2015; 20: 183–92.
- Sniekers S, Stringer S, Watanabe K, et al.: Genome-wide association meta-analysis of 78,308 individuals identifies new loci and genes influencing human intelligence. Nat Genet 2017; 49: 1107–12.
- Savage JE, Jansen PR, Stringer S, et al.: Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nat Gen 2018; 50: 912–19.
- 21. Hill WD, Marioni RE, Maghzian O, et al.: A combined analysis of genetically correlated traits identifies 187 loci and a role for

neurogenesis and myelination in intelligence. Mol Psychiatry 2018; 24: 169-81.

- Branigan AR, McCallum KJ, Freese J: Variation in the heritability of educational attainment: an international meta-analysis. Social Forces 2013; 92: 109–40.
- Richardson M, Abraham C, Bond R: Psychological correlates of university students' academic performance: a systematic review and meta-analysis. Psychol Bull 2012; 138: 353–87.
- Ritchie SJ, Tucker-Drob EM: How much does education improve intelligence? A meta-analysis. Psychol Sci 2018; 29: 1358–69.
- Rietveld CA, Medland SE, Derringer J, et al.: GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. Science 2013; 340: 1467–71.
- Okbay A, Beauchamp JP, Fontana MA, et al.: Genome-wide association study identifies 74 loci associated with educational attainment. Nature 2016; 533: 539–42.
- Lee JJ, Wedow R, Okbay A, et al.: Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nat Genet 2018; 50: 1112–21.
- Okbay A, Wu Y, Wang N, et al.: Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nat Genet 2022; 54: 437–49.
- Schork AJ, Peterson RE, Dahl A, Cai N, Kendler KS: Indirect paths from genetics to education. Nat Genet 2022; 54: 372–3.
- Kong A, Thorleifsson G, Frigge ML, et al.: The nature of nurture: effects of parental genotypes. Science 2018; 359: 424–8.
- Burt CH: Challenging the utility of polygenic scores for social science: environmental confounding, downward causation, and unknown biology. Behav Brain Sci 2022; 46: e207.
- Abdellaoui A, Dolan CV, Verweij KJH, Nivard MG: Gene-environment correlations across geographic regions affect genome-wide association studies. Nat Genet 2022; 54: 1345–54.
- Yengo L, Vedantam S, Marouli E, et al.: A saturated map of common genetic variants associated with human height. Nature 2022; 610: 704–12.
- Wainschtein P, Jain D, Zheng Z, et al.: Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nat Genet 2022; 54: 263–73.
- Karlsson Linner R, Marioni RE, Rietveld CA, et al.: An epigenome-wide association study meta-analysis of educational attainment. Mol Psychiatry 2017; 22: 1680–90.
- Lencz T, Backenroth D, Granot-Hershkovitz E, et al.: Utility of polygenic embryo screening for disease depends on the selection strategy. Elife 2021; 10: e64716.
- Turley P, Meyer MN, Wang N, et al.: Problems with using polygenic scores to select embryos. N Engl J Med 2021; 385: 78–86.
- Shen H, Feldman MW: Genetic nurturing, missing heritability, and causal analysis in genetic statistics. Proc Natl Acad Sci USA 2020; 117: 25646–54.
- Cheesman R, Hunjan A, Coleman JRI, et al.: Comparison of adopted and nonadopted individuals reveals gene-environment interplay for education in the UK Biobank. Psychol Sci 2020; 31: 582–91.
- Boyle EA, Li YI, Pritchard JK: An expanded view of complex traits: from polygenic to omnigenic. Cell 2017; 169: 1177–86.



Manhattan plot of the meta-analysis of SNP based GWAS for intelligence in N = 269 867 independent subjects from Savage et al. (2018) (20). Each dot represents an SNP according to its position in the genome. The significance on the Y-axis is displayed as a negative logarithm of the P value. All values above the dotted red line at 5×10^{-8} are considered genome-wide statistically significant (corrected according to Bonferroni). Independent, significantly associated SNPs are marked with a diamond. With permission from Springer-Nature Group. GWAS, genome wide association study; SNP, single nucleotide polymorphism

Questions on the article in issue 2/2025

The Genetics of Intelligence

The submission deadline is 26 January 2026.

Only one answer is possible for each question. Please select the answer that is most appropriate.

Question 1

Which definition of intelligence is most likely to apply?

- a) Intelligence is the ability to develop and express artistic and creative talents.
- b) Intelligence describes an individual's capacity to store factual information (lexical knowledge) and access it at the right moment.
- c) Intelligence is a very general mental capacity, which among others comprises the abilities for reasoning and abstract thought as well as rapid learning.
- d) Intelligence relates primarily to a person's mathematical and verbal comprehension.
- e) Intelligence is a variable that relates above all to an individual's emotional capacity, which assesses largely a person's capability for empathy.

Question 2

Which statement regarding inter-individual differences in intelligence ratings applies most, according to a recent meta-analysis?

- a) From young adulthood, the rank of a person within the distribution of trait carriers is very stable over a period of five years.
- b) In childhood, the rank of a person within the distribution of trait carriers is very stable over a period of five years, but this stability in rank decreases in adulthood.
- c) Only at an older age (> 60 years) is the rank of a person within the distribution of trait carriers is very stable over a period of five years.
- d) The rank of a person within the distribution of trait carriers is not very stable and mostly changes substantially over a period of five years.
- e) The rank of a person within the distribution of trait carriers is fluctuating, for which reason relevant testing should be carried out annually.

Question 3

How does the importance of genetic influences on intelligence develop over the lifespan?

- a) It accounts for about 1–2 % in early childhood, 5–10 % at the start of school, about 20 % in adulthood.
- b) It accounts for about 5 % in early childhood, 10–20 % at the start of school, about 30 % in adulthood.
- c) It accounts for about 10 % in early childhood, 10–15 % at the start of school, about 5 % in adulthood.
- d) It accounts for about 20 % in early childhood, 40–50 % at the start of school, about 60 % in adulthood.
- e) It accounts for about 40 % in early childhood, 50–70 % at the start of school, about 90 % in adulthood.

Question 4

How many independent gene loci associated with intelligence did the 2018meta-analysis IQ3 identify?

a) 18, b) 27, c) 110, d) 206, e) 504

Question 5

Which of the statements about Carroll's three-stratum model of intelligence is correct, according to the information contained in the article?

- a) A shorter arrow between Stratum III (general intelligence) and a factor in Stratum II signifies a stronger association.
- b) In this model, fluid intelligence is the worst indicator for general intelligence.
- c) A shorter arrow between Stratum I (general intelligence) and a factor in Stratum II signifies a stronger association.
- d) In this model, processing speed is a better indicator for general intelligence than all other factors.
- e) Visual and auditory perception are not considered as factors in this model.

Question 6

Persons whose genotype confers advantages in the context of learning and achievement behaviors, to a greater extent turn to environments that promote learning and achievement, which in turn affect the development of traits. Which of the following terms is used in the article for this bi-directional association?

- a) Genotype-environment-adaptation
- b) Genotype-environment/setting-interaction
- c) Genotype-environment/setting-association
- d) Genotype-environment-transaction
- e) Genotype-environment/setting-acclimatization

Question 7

For which polygenic trait with a high heritability does the article describe that by conducting genome-wide association studies and including rare variants the variance of traits was explained up to 68%? a) Hair color; b) body height; c) eye color; d) skin type; e) visual disorder/defective vision

Question 8

What is the proportion of differences in intelligence in adulthood that can be explained with so-called non-shared environmental influences? a) about 5 %; b) about 15 %; c) about 20 %; d) about 35 %; e) about 55 %

Question 9

According to the article, how is educational attainment

(EA) operationalized?

- a) Number of years in education/formative years
- b) Average of grades in the final certificate
- c) Self-rated educational attainment
- d) Results from a standardized IQ test
- e) Number of schools and universities attended

Question 10

What does the abbreviation SNP stand for?

- a) "singular new pattern"; b) "severe nucleotide polymorphism"
- c) "simple nucleotide pattern"; d) "standard nucleotide profile"
- e) "single nucleotide polymorphism"