

Why are siblings different?

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Two children can have the same biological parents without receiving the same combination of inherited variants. Each conception samples a different pair of gametes. Development then unfolds through a different history, even when much of the family environment is shared. Neither “the same parents” nor “the same home” means identical starting material and identical experience.

The question also needs a specified difference. Eye color, height, an immune response and a personal preference are not one phenotype with one explanation. They can differ in their genetic architecture, environmental sensitivity and the ways they are measured. A general account of sibling variation should explain why differences are expected without pretending to predict every individual characteristic.

1. Chromosomes are inherited in combinations

During meiosis, paired homologous chromosomes segregate into gametes. Crossing over exchanges material between homologs, so an inherited chromosome can carry a mosaic of segments tracing to a parent's two corresponding copies. OpenStax describes these processes, and the NHGRI glossary distinguishes recombination as an exchange between related DNA molecules. [1,2]

The familiar phrase that siblings share half their genes needs care. Humans already share most of their DNA sequence. In this context, “half” usually concerns the expected sharing of inherited parental variants or chromosome segments by descent, not a claim that the remaining half of their DNA is unrelated biological material.

The expectation is also not an exact measured fraction for every pair. Meiosis produces variable combinations. A population average can be useful while leaving variation among particular siblings, just as an expected outcome of repeated sampling does not determine every draw.

2. A small inheritance model

Take one autosomal position and suppose the mother's two copies can be distinguished as M1 and M2, and the father's as F1 and F2. Assume each is transmitted with probability one half and the two children's transmissions are independent. The siblings have a one-half chance of matching their maternally inherited copy and a one-half chance of matching their paternally inherited copy.

Under these assumptions, they share both copies by descent with probability one quarter, one copy with probability one half, and neither with probability one quarter. The expected number shared is $2 \times 1/4 + 1 \times 1/2 + 0 \times 1/4 = 1$ out of 2. This is where the local one-half expectation comes from.

A run of positions along a chromosome is not a set of independent coin tosses. Linkage and recombination make nearby inheritance events correlated. The one-position model therefore cannot be multiplied across every DNA letter to calculate a real pair's whole-genome similarity. Its purpose is to clarify the expectation and its assumptions.

3. The famous count is only a starting point

Ignoring crossing over, 23 independently assorting chromosome pairs would give $2^{23} = 8,388,608$ combinations in a simplified gamete model. Combining one gamete from each parent gives $2^{46} = 70,368,744,177,664$ possible pairings in that same simplified model. These are combinatorial counts, not measured counts of viable embryos or distinct personalities.

Crossing over adds variation beyond intact-chromosome combinations. [1] But multiplying possibilities is not an explanation of any particular trait. Many sequence differences have little effect on a specified measurement, and many traits depend on combinations of influences. A large number of genetic combinations cannot be read as the same number of predetermined life outcomes.

The calculation is useful precisely when its boundary remains visible. It shows why repeated conception need not repeat a genotype. It does not assign probabilities to every possible appearance, ability or experience.

4. Development is a history

Inherited DNA operates in cells that receive signals, divide and interact over time. Two individuals do not occupy the same physical trajectory. Even a shared household includes different ages, relationships, illnesses, opportunities and sequences of events. Some differences are measured easily; others are difficult to record or separate causally.

This is not a license to call every unexplained difference an environmental effect. Measurement error, unmeasured genetic differences, interactions and developmental variation may all remain possible. A responsible analysis identifies what was actually compared instead of using “genes” and “environment” as containers into which every residual result must fit.

Monozygotic twins provide an important comparison because they originate from the same fertilized egg and have nearly the same initial genetic makeup. The NHGRI cloning fact sheet explicitly describes this near identity rather than promising identical organisms. [3] Similarity between such twins is informative, but it does not erase different developmental histories or make every trait identical.

5. What a family comparison can establish

If a trait resembles a parent's, several explanations may coexist. Parents transmit genetic variants, but they also influence environments, resources and learned practices. Resemblance alone does not isolate the size of each contribution. Conversely, a difference between siblings does not prove that inheritance was irrelevant: they did not receive identical combinations.

A hypothetical trait measured with an imprecise instrument adds another problem. Suppose the same person scores differently on two occasions because the task and circumstances vary. Some apparent difference between two siblings would then reflect within-person variability or measurement limitations. Before explaining a difference biologically, the reliability of the observation needs attention.

Population measures of genetic contribution also concern variation under specified conditions. They are not percentages of a particular individual's personality, nor fixed limits on what can change. The causal meaning of a population statistic cannot be transferred automatically to an individual future.

6. Similar origins are not identical outcomes

Siblings differ because inherited combinations differ and because development does not replay one identical history. Recombination and segregation provide well-established mechanisms for the first part. [1,2] Explaining the size and cause of a particular difference requires additional evidence about the trait, the individuals and their environments.

The common error is to treat a shared label as a shared state: the same parents, the same genes, the same upbringing. Each phrase compresses real variation. Unpacking it makes sibling differences less mysterious while preserving the distinction between explaining a mechanism and predicting a person.

Related reading

Article 030, “How can cells with the same DNA do different jobs?”, changes the comparison from different individuals to different cell states within an organism. The link is optional and reciprocal.

References

- [1] OpenStax. Biology 2e, section 11.1: The Process of Meiosis.
<https://openstax.org/books/biology-2e/pages/11-1-the-process-of-meiosis>
- [2] National Human Genome Research Institute. Homologous Recombination.
<https://www.genome.gov/genetics-glossary/homologous-recombination>
- [3] National Human Genome Research Institute. Cloning Fact Sheet.
<https://www.genome.gov/about-genomics/fact-sheets/Cloning-Fact-Sheet>